

SEQUENCE LISTING

<110> Dumas Milne Edwards, Jean Baptiste
Bougueleret, Lydie
Jobert, Severin

<120> FULL-LENGTH HUMAN cDNAs ENCODING POTENTIALLY SECRETED PROTEINS

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<150> US 60/169,629

<151> 1999-12-08

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<151> 2000-03-06

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cag	cta	gag	gtg	gcc	ctg	att	gga	gcc	tct	ccc	cgg	gga	aac	cgt	tcc	726
Gln	Leu	Glu	Val	Ala	Leu	Ile	Gly	Ala	Ser	Pro	Arg	Gly	Asn	Arg	Ser	
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Leu	Phe	Gly	Leu	Glu	Val	Ala	Thr	Leu	Gly	Gln	Gly	Pro	Asp	Cys	Pro	
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Ser	Met	Gln	Glu	Gln	His	Ser	Ile	Asp	Asp	Glu	Tyr	Ala	Pro	Ala	Val	
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Phe	Gln	Leu	Asp	Gln	Leu	Leu	Trp	Gly	Ser	Leu	Pro	Ser	Gly	Phe	Ala	
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Gln	Trp	Arg	Pro	Val	Ala	Tyr	Ser	Gln	Lys	Pro	Gly	Gly	Arg	Glu	Ser	
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gcc	ctg	ccc	tgc	caa	gct	tcc	cct	ctt	cat	cct	gcc	tta	gca	tac	tct	966
Ala	Leu	Pro	Cys	Gln	Ala	Ser	Pro	Leu	His	Pro	Ala	Leu	Ala	Tyr	Ser	
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Leu	Pro	Gln	Ser	Pro	Ile	Val	Arg	Ala	Phe	Phe	Gly	Ser	Gln	Asn	Asn	
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Trp	Asp	Gln	His	Tyr	Leu	Ser	Trp	Ser	Met	Leu	Leu	Gly	Val	Gly	Phe	

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Leu Leu His His Lys Lys Tyr Ser Glu Tyr Gln Ser Ile Asn				
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1 5	
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gcaaaactcc aatatgagga caagttccga aataatttga aaggcaaaag gctggatatc	403
aacaccaaca cctacacatc tcaggatctc aagagtgcac tggcaaaatt caaggagggg	463
gcagagatgg agagttcaaa ggaagacaag gcaaggcagg ctgaggtaaa gcggctcttc	523
cgccccattg aggaactgaa gaaagacttt gatgagctga atgttgtcat tgagactgac	583
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Met Ala
ccc cag agc ctg cct tca tct agg atg gct cct ctg ggc atg ctg ctt 164
Pro Gln Ser Leu Pro Ser Ser Arg Met Ala Pro Leu Gly Met Leu Leu
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Gly Pro Leu Met Ala Ala Cys Phe Thr Phe Cys Leu Ser His Gln Asn
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Leu Lys Glu Phe Ala Leu Thr Asn Pro Glu Lys Ser Ser Thr Lys Glu
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aca gag aga aaa gaa acc aaa gcc gag gag gag ctg gat gcc gaa gtc 308
Thr Glu Arg Lys Glu Thr Lys Ala Glu Glu Glu Leu Asp Ala Glu Val
25 30 35
ctg gag gtg ttc cac ccg acg cat gag tgg cag gcc ctt cag cca ggg 356
Leu Glu Val Phe His Pro Thr His Glu Trp Gln Ala Leu Gln Pro Gly
40 45 50
cag gct gtc cct gca gga tcc cac gta cgg ctg aat ctt cag act ggg 404
Gln Ala Val Pro Ala Gly Ser His Val Arg Leu Asn Leu Gln Thr Gly
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Glu Arg Glu Ala Lys Leu Gln Tyr Glu Asp Lys Phe Arg Asn Asn Leu
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Lys Gly Lys Arg Leu Asp Ile Asn Thr Asn Thr Tyr Thr Ser Gln Asp
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ctc aag agt gca ctg gca aaa ttc aag gag ggg gca gag atg gag agt 548
Leu Lys Ser Ala Leu Ala Lys Phe Lys Glu Gly Ala Glu Met Glu Ser
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tca aag gaa gac aag gca agg cag gct gag gta aag cgg ctc ttc cgc 596
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ccc att gag gaa ctg aag aaa gac ttt gat gag ctg aat gtt gtc att 644
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Ser	Ser	Ser	Ser	Leu	Glu	Glu	Lys	Ile	Ala	Ala	Leu	Phe	Asp	Leu	Glu	
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Phe	Leu	Lys	Leu	Gly	Gly	Leu	Gln	Val	Leu	Arg	Thr	Leu	Val	Gln	Glu	
		280			285			290								
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Leu	Val	Thr	Glu	Lys	Met	Phe	Ala	Glu	Glu							
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gct gcc ctg cgg gcg ctg caa gag tgt cag cgg caa cag gta cgg ccg      206
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ggc gct ggt ggt agc ttg gac ctt gtg tgc caa cgc ttc ctc agg tct      350
Gly Ala Gly Gly Ser Leu Asp Leu Val Cys Gln Arg Phe Leu Arg Ser
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ggg cct aac agc ctc cac tgc ctg ggc tca ctc agg gag cgc ctc att      398
Gly Pro Asn Ser Leu His Cys Leu Gly Ser Leu Arg Glu Arg Leu Ile
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att tgg gca gcc atg gat tct atc cca gcc cca tca tca gtt cag gga      446
Ile Trp Ala Ala Met Asp Ser Ile Pro Ala Pro Ser Ser Val Gln Gly
        80                85                90
cac aac ctg act gaa gat gcc aga cat cct gag agt tgg cag aac aca      494
His Asn Leu Thr Glu Asp Ala Arg His Pro Glu Ser Trp Gln Asn Thr
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Gly Gly Tyr Ser Glu Gly Asp Ala Val Ser Gln Pro Gln Met Ala Leu
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Glu Glu Val Ser Val Ser Asp Pro Leu Ala Ser Asn Gln Gly Gln Ser
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Leu Pro Gly Ser Ser Arg Glu His Met Ala Gln Trp Glu Val Arg Ser
        140                145                150                155
cag acc cat gtt cca aac aga gaa cct gtt cag gca ctg cct tcc tct      686
Gln Thr His Val Pro Asn Arg Glu Pro Val Gln Ala Leu Pro Ser Ser
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gcc agc cgg aaa cgt ctg gac aag aaa cgt tca gtg cct gta gcc act      734
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        175                180                185
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Arg Val Gly Thr Ala Ser Gln Arg Phe Ile Glu Leu Gly Ala Glu Ile	
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Lys Arg Val Arg Arg Gly Thr Pro Glu Tyr Lys Val Leu Glu Asp Lys	
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Lys Gly Leu Ile Leu Glu Phe Glu Lys Asn Arg Gly Ser	
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Glu	Leu	Glu	Leu	Pro	Glu	Ser	Pro	Val	Asn	Gln	Asp	Leu	Gly	Met	Phe	
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Leu	Val	Thr	Ile	Ser	Cys	Tyr	Thr	Arg	Gly	Gly	Arg	Ile	Ile	Ser	Thr	
				110					115					120		
tct	tgc	cgt	tgc	gtg	atg	ctg	cat	tac	cgc	tca	gac	ctg	ctc	cag	atg	663
Ser	Ser	Arg	Ser	Val	Met	Leu	His	Tyr	Arg	Ser	Asp	Leu	Leu	Gln	Met	
				125				130					135			
ctg	gac	aca	ctg	gtc	ttc	tct	agc	ctc	ctg	cta	ttt	ggc	ttt	gca	gag	711
Leu	Asp	Thr	Leu	Val	Phe	Ser	Ser	Leu	Leu	Leu	Phe	Gly	Phe	Ala	Glu	
		140					145					150				
cag	aag	cag	ctg	ctg	gag	gtg	gaa	ctc	tac	gca	gac	tat	aga	gag	aac	759
Gln	Lys	Gln	Leu	Leu	Glu	Val	Glu	Leu	Tyr	Ala	Asp	Tyr	Arg	Glu	Asn	
	155				160					165						
tgc	gtg	agt	gag	tac	gtg	ccg	acc	act	gga	gcg	atc	att	gag	atc	cac	807
Ser	Val	Ser	Glu	Tyr	Val	Pro	Thr	Thr	Gly	Ala	Ile	Ile	Glu	Ile	His	
	170				175				180					185		
agc	aag	cgc	atc	cag	ctg	tat	gga	gcc	tac	ctc	cgc	atc	cac	gcg	cac	855
Ser	Lys	Arg	Ile	Gln	Leu	Tyr	Gly	Ala	Tyr	Leu	Arg	Ile	His	Ala	His	
				190				195					200			
ttc	act	ggg	ctc	aga	tac	ctg	cta	tac	aac	ttc	ccg	atg	acc	tgc	gcc	903
Phe	Thr	Gly	Leu	Arg	Tyr	Leu	Leu	Tyr	Asn	Phe	Pro	Met	Thr	Cys	Ala	
			205					210					215			
ttc	ata	ggg	gtt	gcc	agc	aac	ttc	acc	ttc	ctc	agc	gtc	atc	gtg	ctc	951
Phe	Ile	Gly	Val	Ala	Ser	Asn	Phe	Thr	Phe	Leu	Ser	Val	Ile	Val	Leu	
		220					225					230				
ttc	agc	tac	atg	cag	tgg	gtg	tgg	ggg	ggc	atc	tgg	ccc	cga	cac	cgc	999
Phe	Ser	Tyr	Met	Gln	Trp	Val	Trp	Gly	Gly	Ile	Trp	Pro	Arg	His	Arg	
	235				240						245					
ttc	tct	ttg	cag	gtt	aac	atc	cga	aaa	aga	gac	aat	tcc	cgg	aag	gaa	1047
Phe	Ser	Leu	Gln	Val	Asn	Ile	Arg	Lys	Arg	Asp	Asn	Ser	Arg	Lys	Glu	
	250				255					260					265	
gtc	caa	cga	agg	atc	tct	gct	cat	cag	cca	ggg	gca	ggg	cct	gaa	ggc	1095
Val	Gln	Arg	Arg	Ile	Ser	Ala	His	Gln	Pro	Gly	Ala	Gly	Pro	Glu	Gly	
			270					275					280			
cag	gag	gag	tca	act	ccg	caa	tca	gat	gtt	aca	gag	gat	ggg	gag	agc	1143
Gln	Glu	Glu	Ser	Thr	Pro	Gln	Ser	Asp	Val	Thr	Glu	Asp	Gly	Glu	Ser	
			285					290					295			
cct	gaa	gat	ccc	tca	ggg	aca	gag	ggg	cag	ctg	tcc	gag	gag	gag	aaa	1191
Pro	Glu	Asp	Pro	Ser	Gly	Thr	Glu	Gly	Gln	Leu	Ser	Glu	Glu	Glu	Lys	
		300					305					310				
cca	gat	cag	cag	ccc	ctg	agc	gga	gaa	gag	gag	cta	gag	cct	gag	gcc	1239
Pro	Asp	Gln	Gln	Pro	Leu	Ser	Gly	Glu	Glu	Glu	Leu	Glu	Pro	Glu	Ala	

```

      315              320              325
    agt gat ggt tca ggc tcc tgg gaa gat gca gct ttg ctg acg gag gcc      1287
    Ser Asp Gly Ser Gly Ser Trp Glu Asp Ala Ala Leu Leu Thr Glu Ala
    330              335              340              345
    aac ctg cct gct cct gct cct gct tct gct tct gcc cct gtc cta gag      1335
    Asn Leu Pro Ala Pro Ala Pro Ala Ser Ala Ser Ala Pro Val Leu Glu
      350              355              360
    act ctg ggc agc tct gaa cct gct ggg ggt gct ctc cga cag cgc ccc      1383
    Thr Leu Gly Ser Ser Glu Pro Ala Gly Gly Ala Leu Arg Gln Arg Pro
      365              370              375
    acc tgc tct agt tcc tgaagaaaag gggcagactc ctcacattcc agcactttcc      1438
    Thr Cys Ser Ser Ser
      380
    cacctgactc ctctccctc gtttttcctt caataaacta ttttgtgtca gctccaaaaa      1498
    aaaaaaaaaa aa      1510

```

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<210> 9
<211> 882
<212> DNA
<213> Homo sapiens

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<220>
<221> CDS
<222> 78..410

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<220>
<221> sig_peptide
<222> 78..155
<223> Von Heijne matrix
      score 10.0731536331164
      seq LWLALVSCILTQA/SA

```

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<400> 9
    atggctggcc agaggaggaa cgctttgtgt tctcatcgga gctgcatggg aagtctgcat      60
    acagcaaagt gacctgc atg cct cac ctt atg gaa agg atg gtg ggc tct      110
              Met Pro His Leu Met Glu Arg Met Val Gly Ser
              -25              -20
    ggc ctc ctg tgg ctg gcc ttg gtc tcc tgc att ctg acc cag gca tct      158
    Gly Leu Leu Trp Leu Ala Leu Val Ser Cys Ile Leu Thr Gln Ala Ser
    -15              -10              -5              1
    gca gtg cag cga ggt tat gga aac ccc att gaa gcc agt tcg tat ggg      206
    Ala Val Gln Arg Gly Tyr Gly Asn Pro Ile Glu Ala Ser Ser Tyr Gly
              5              10              15
    ctg gac ctg gac tgc gga gct cct ggc acc cca gag gct cat gtc tgt      254
    Leu Asp Leu Asp Cys Gly Ala Pro Gly Thr Pro Glu Ala His Val Cys
              20              25              30
    ttt gac ccc tgt cag aat tac acc ctc cta gat ttg ggg ccc atc act      302
    Phe Asp Pro Cys Gln Asn Tyr Thr Leu Leu Asp Leu Gly Pro Ile Thr
              35              40              45
    cgg aga ggt gca cag tct ccc ggt gtc atg aat gga acc cct agc act      350
    Arg Arg Gly Ala Gln Ser Pro Gly Val Met Asn Gly Thr Pro Ser Thr
              50              55              60              65
    gca ggg ttc ctg gtg gcc tgg cct atg gtc ctc ctg act gtc ctc ctg      398
    Ala Gly Phe Leu Val Ala Trp Pro Met Val Leu Leu Thr Val Leu Leu
              70              75              80
    gct tgg ctg ttc tgagagctcc gctgagcacc tggccttgaa gtttgtgttc      450
    Ala Trp Leu Phe
              85

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ttccctctgg	caatggctcc	cttcagcact	tctgctttcc	actccaattc	acacaggctt	510
ggtattaaca	gaatcaaggc	caggctaggt	taggaaaagg	gaagagcttt	caccttcttt	570
aaaactctcg	gctgggcgca	gtggctcatg	cctgtaatcc	cagcattttg	ggaggctgag	630
gcagggtgat	cacctgaggt	cagcagttca	aaatcagcct	ggccaaaatg	ctgaaactcc	690
gtctctacta	aaaatacaaa	aattagccag	gcatggtgac	aggcgctgt	aatcccagct	750
actcgggagg	ccaaggcagg	agaattgctc	gaactcaggg	ggtggagggt	gcagtgagtt	810
gagattgtgc	cattgcactc	cagcctgggc	aacagagcaa	gactctgtct	caggcaaaaa	870
aaaaaaaaaa	aa					882

<210> 10
 <211> 1849
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> 84..299

<220>
 <221> sig_peptide
 <222> 84..134
 <223> Von Heijne matrix
 score 3.86022363031904
 seq GFVAALVAGGVAG/VS

<400> 10						
aaacatggcg	gcgcccagcg	cgcgaggacg	tgatccgctt	ctgctccggc	ttggattgta	60
gccttgacga	ggtctgagcg	acc atg gac	cgg ccg ggg	ttc gtg gca	gcg ctg	113
Met Asp Arg Pro Gly Phe Val Ala Ala Leu						
-15 -10						
gtg gct ggt	ggg gta gca	ggt gtt tct	ggt gac ttg	ata tta ttt	cct	161
Val Ala Gly	Gly Val Ala	Gly Val Ser	Val Asp Leu	Ile Leu Phe	Pro	
-5 1 5						
ctg gat acc	att aaa acc	agg ctg cag	agt ccc caa	gga ttt aat	aag	209
Leu Asp Thr	Ile Lys Thr	Arg Leu Gln	Ser Pro Gln	Gly Phe Asn	Lys	
10 15 20 25						
gct ggt ggt	ttt cat gga	ata tat gct	ggc gtt cct	tct gct gct	att	257
Ala Gly Gly	Phe His Gly	Ile Tyr Ala	Gly Val Pro	Ser Ala Ala	Ile	
30 35 40						
gga tcc ttt	cct aat ggt	tgc ctg cct	gat tgc agt	tcc atc		299
Gly Ser Phe	Pro Asn Gly	Cys Leu Pro	Asp Ser Ser	Ser Ser Ile		
45 50 55						
tgaagtgggt	aagcagaggg	cacaggtatc	tgcttctaca	agaacatttc	agattttctc	359
taacatctta	tatgaagagg	gtatccaagg	ggtgtatcga	ggctataaaa	gcacagtttt	419
aagagagatt	cctttttctt	tgggtccagtt	tcccttatgg	gagtccttaa	aagccctctg	479
gtcctggagg	caggatcatg	tgggtgattc	ttggcagtc	gcagtctgtg	gagcttttgc	539
agggtgattt	gccgctgcag	tcaccacccc	tctagacgtg	gcgaagacaa	gaattatgct	599
ggcaaaggct	ggctccagca	ctgetgatgg	gaatgtgctc	tctgtcctgc	atggggctctg	659
gcggtcacag	gggctggcag	gattatattgc	agggtgtcttc	cctcgaatgg	cagccatcag	719
tctgggaggt	ttcatctttc	tgggggctta	tgaccgaacg	cacagcttgc	tggttggaagt	779
tggcagaag	agtccttgaa	gcagagacaa	gcctcacctc	cacttctgtc	aagagagggg	839
cctgcagtgt	aaaccctctt	ccgctgagca	gctgtctgaa	ctataggccc	cagtgtctgaa	899
gaccagttgt	gctaagatac	cggcattggag	attgtgccat	ccgtgggtata	ggctggctgg	959
tatgaagtca	ttggcctgta	tgccagagag	ctaagagaag	aaaacggggg	ctgtggcagt	1019
actctgaaca	atttcctcag	aacctcttaa	taaataagtt	tggtaatgct	gaggccaggc	1079
cttttagagc	tttcatttga	tctgtatctg	atcttttcatt	tcctgccacc	tgatgggtgga	1139
ttcagcagaa	ggcaagatgg	ttataattct	aaaagaatag	cttgtttgtt	tgtttgtttg	1199
ggaaaaggag	acttggggaa	gagtttgtga	tgtgggtgtt	tctcccccta	gttaattcct	1259

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gttgtgtaag ggtaggcttt gttgaaaaag aaagaaagat tgaactacag gtgcatagca 1319
agcactcttt ctgggtaact aggctgctgg ttttaattac cctcagattt caccataaaa 1379
aacgcacaat tgtattattt tacagagatg tgtccagcgc cccctgtggt gtgtgagaga 1439
aagcagctgc aactcaagtg actagggtggg cccagctggc ttcgtgcagg agggcacggg 1499
gggtgagcca ttctcgccat tctcatgtca gactgaaagg agggcctggg ccagctttga 1559
aaaggcagga tgaaatggaa aggtcaccac acttagggat tttagacctt gactaacaag 1619
ctccaggtgt agaaaaattc aaaacaaaat gtcaggaatc tagcagtgtt gtctgccctg 1679
gagcaaacia acagtatgtg attttgcttc gcctattttt tttttctttt ttgggggaag 1739
ataattaaag gcagaatgac tgcgtttgta aaagaaggac caccaactat actgacattt 1799
ataaatgaac ctttattaaa gacacttcaa tgcaaaaaaa aaaaaaaaaa 1849

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<210> 11
<211> 565
<212> DNA
<213> Homo sapiens

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```

<220>
<221> CDS
<222> 55..468

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<220>
<221> sig_peptide
<222> 55..99
<223> Von Heijne matrix
      score 8.96936032049195
      seq FTTLLFLAAVAGA/LV

```

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<400> 11
attccccaga ccttctgcag attctgtggt tatactcact cctcatccca aaga atg      57
                                         Met
                                         -15
aaa ttt acc act ctc ctc ttc ttg gca gct gta gca ggg gcc ctg gtc      105
Lys Phe Thr Thr Leu Leu Phe Leu Ala Ala Val Ala Gly Ala Leu Val
                                         -10
                                         -5
                                         1
tat gct gaa gat gcc tcc tct gac tcg acg ggt gct gat cct gcc cag      153
Tyr Ala Glu Asp Ala Ser Ser Asp Ser Thr Gly Ala Asp Pro Ala Gln
      5
      10
      15
gaa gct ggg acc tct aag cct aat gaa gag atc tca ggt cca gca gaa      201
Glu Ala Gly Thr Ser Lys Pro Asn Glu Glu Ile Ser Gly Pro Ala Glu
      20
      25
      30
cca gct tca ccc cca gag aca acc aca aca gcc cag gag act tcg gcg      249
Pro Ala Ser Pro Pro Glu Thr Thr Thr Thr Ala Gln Glu Thr Ser Ala
      35
      40
      45
      50
gca gca gtt cag ggg aca gcc aag gtc acc tca agc agg cag gaa cta      297
Ala Ala Val Gln Gly Thr Ala Lys Val Thr Ser Ser Arg Gln Glu Leu
      55
      60
      65
aac ccc ctg aaa tcc ata gtg gag aaa agt atc tta cta aca gaa caa      345
Asn Pro Leu Lys Ser Ile Val Glu Lys Ser Ile Leu Leu Thr Glu Gln
      70
      75
      80
gcc ctt gca aaa gca gga aaa gga atg cac gga ggc gtg cca ggt gga      393
Ala Leu Ala Lys Ala Gly Lys Gly Met His Gly Gly Val Pro Gly Gly
      85
      90
      95
aaa caa ttc atc gaa aat gga agt gaa ttt gca caa aaa tta ctg aag      441
Lys Gln Phe Ile Glu Asn Gly Ser Glu Phe Ala Gln Lys Leu Leu Lys
      100
      105
      110
aaa ttc agt cta tta aaa cca tgg gca tgagaagctg aataatggga      488
Lys Phe Ser Leu Leu Lys Pro Trp Ala
115
120

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tcattggact taaagcctta aatacccttg tagcccagag ctattaaaac gaaagcatcc 548
 aaaaaaaaaa aaaaaaa 565

<210> 12
 <211> 1663
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> 152..475

<220>
 <221> sig_peptide
 <222> 152..244
 <223> Von Heijne matrix
 score 10.0910253445132
 seq LVLLLVTRSPVNA/CL

<400> 12
 atgtgtctgc tgccgccatt gtgcggcgct ggtccctca gagggttcct gctgctgccg 60
 gtgccttgga cctccccct cgcttctcgt tctactgccc caggagcccg gcgggtccgg 120
 gactcccgtc cgtgccggtg cgggcgcggg c atg tgg ctg tgg gag gac cag 172
 Met Trp Leu Trp Glu Asp Gln
 -30 -25
 ggc ggc ctc ctg ggc cct ttc tcc ttc ctg ctg cta gtg ctg ctg ctg 220
 Gly Gly Leu Leu Gly Pro Phe Ser Phe Leu Leu Leu Val Leu Leu Leu
 -20 -15 -10
 gtg acg cgg agc ccg gtc aat gcc tgc ctc ctc acc ggc agc ctc ttc 268
 Val Thr Arg Ser Pro Val Asn Ala Cys Leu Leu Thr Gly Ser Leu Phe
 -5 1 5
 gtt cta ctg cgc gtc ttc agc ttt gag ccg gtg ccc tct tgc agg gcc 316
 Val Leu Leu Arg Val Phe Ser Phe Glu Pro Val Pro Ser Cys Arg Ala
 10 15 20
 ctg cag gtg ctc aag ccc cgg gac cgc att tct gcc atc gcc cac cgt 364
 Leu Gln Val Leu Lys Pro Arg Asp Arg Ile Ser Ala Ile Ala His Arg
 25 30 35 40
 ggc ggc agc aam sag gcg ccc gag aac acg ctg gcg gcc att cgg cag 412
 Gly Gly Ser Xaa Xaa Ala Pro Glu Asn Thr Leu Ala Ala Ile Arg Gln
 45 50 55
 cta aga atg gag caa cag gcg tgg agt tgg aca ttg agt tta ctt ctg 460
 Leu Arg Met Glu Gln Gln Ala Trp Ser Trp Thr Leu Ser Leu Leu Leu
 60 65 70
 acg gga ttc ctg tct taatgcacga taacacagta gataggacga ctgatgggac 515
 Thr Gly Phe Leu Ser
 75
 tgggcgattg tgtgatttga catttgaaca aattaggaag ctgaatcctg cagcaaacca 575
 cagactcagg aatgatttcc ctgatgaaaa gatccctacc ctaagggaag ctgttgacga 635
 gtgcctaaac cataacctca caatcttctt tgatgtcaaa ggccatgcac acaaggctac 695
 tgaggctcta aagaaaatgt atatggaatt tcctcaactg tataataata gtgtgggtctg 755
 ttctttcttg ccagaagtta tctacaaggt aacattcggg atttttcttg tacatattag 815
 atgagacaaa cagatcggga tgtaataaca gcattaactc acagaccttg gagcctaagc 875
 catacaggag atgggaaacc acgctatgat actttctgga aacattttat atttgttatg 935
 atggacattt tgctcgattg gagcatgcat aatatcttgt ggtacctgtg tgggaatttca 995
 gctttcctca tgcaaaagga ttttgtatcc ccggcctact tgaagaagtg gtcagctaaa 1055
 ggaatccagg ttgttggttg gactgttaat acctttgatg aaaagagtta ctacgaatcc 1115
 catcttggtt ccagctatat cactgacagc atggtagaag actgcgaacc tcacttctag 1175
 actttcacgg tgggacgaaa cgggttcaga aactgccagg ggcctcatag aggatattca 1235

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aaataccctt tgtgctagcc caggccctgg ggaatcaggt gactcacaca aatgcaatag 1295
ttggtcactg catttttacc tgaaccaaag ctaaaccggg tgttgccacc atgcaccatg 1355
gcatgccaga gttcaacact gttgctcttg aaaatctggg tctgaaaaaa cgcacaagag 1415
cccctgccct gccctagctg aggcacacag ggagaccag tgaggataag cacagattga 1475
attgtacaat ttgcagatgc agatgtaaat gcatgggaca tgcataataa ctcagagttg 1535
acattttaaa acttgccaca cttatttcaa atatttgtac tcagctatgt taacatgtac 1595
tgtagacatc aaacttgtgg ccatactaata aaaattatta aaaggagcac taaaaaaaaa 1655
aaaaaaaaa 1663

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```

<210> 13
<211> 744
<212> DNA
<213> Homo sapiens

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<220>
<221> CDS
<222> 112..552

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<220>
<221> sig_peptide
<222> 112..183
<223> Von Heijne matrix
      score 11.7298925418815
      seq FVLGLGLTPPTLA/QD

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<400> 13
tcacaactgg aacccatctc caggaacaaa cagctggaac ccatctcccg ttgaagggaa 60
actgccagat ttttgtaaga ttcttctctc tgggagcctg tggttgaaga g atg gtg 117
                                     Met Val
atg ggc ctg ggc gtt ttg ttg ttg gtc ttc gtg ctg ggt ctg ggt ctg 165
Met Gly Leu Gly Val Leu Leu Leu Val Phe Val Leu Gly Leu Gly Leu
      -20                                -15                                -10
acc cca ccg acc ctg gct cag gat aac tcc agg tac aca cac ttc ctg 213
Thr Pro Pro Thr Leu Ala Gln Asp Asn Ser Arg Tyr Thr His Phe Leu
      -5                                1                                5                                10
acc cag cac tat gat gcc aaa cca cag ggc cgg gat gac aga tac tgt 261
Thr Gln His Tyr Asp Ala Lys Pro Gln Gly Arg Asp Asp Arg Tyr Cys
      15                                20                                25
gaa agc atc atg agg aga cgg ggc ctg acc tca ccc tgc aaa gac atc 309
Glu Ser Ile Met Arg Arg Arg Gly Leu Thr Ser Pro Cys Lys Asp Ile
      30                                35                                40
aac aca ttt att cat ggc aac aag cgc acg atc aag gcc atc tgt gaa 357
Asn Thr Phe Ile His Gly Asn Lys Arg Thr Ile Lys Ala Ile Cys Glu
      45                                50                                55
aac aag aat gga aac cct cac aga gaa aac cta aga ata agc aag tct 405
Asn Lys Asn Gly Asn Pro His Arg Glu Asn Leu Arg Ile Ser Lys Ser
      60                                65                                70
tct ttc cag gtc acc act tgc aag cta cat gga ggt tcc ccc tgg cct 453
Ser Phe Gln Val Thr Thr Cys Lys Leu His Gly Gly Ser Pro Trp Pro
      75                                80                                85                                90
cca tgc cag tac cga gcc aca gcg ggg ttc aga aac gtt gtt gtt gct 501
Pro Cys Gln Tyr Arg Ala Thr Ala Gly Phe Arg Asn Val Val Val Ala
      95                                100                                105
tgt gaa aat ggc tta cct gtc cac ttg gat cag tca att ttc cgt cgt 549
Cys Glu Asn Gly Leu Pro Val His Leu Asp Gln Ser Ile Phe Arg Arg
      110                                115                                120
ccg taaccagcgg gccctgggtc aagtgtgtggc tctgtgtgtcc ttgccttcca 602
Pro

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tttccctctt gcaccagaa cagtgggtggc aacattcatt gccaaaggcc caaagaaaga 662
gctacctgga ccttttgttt tctgtttgac aacatgttta ataaataaaa atgtcttgat 722
atcagcaaaa aaaaaaaaaa aa 744

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<210> 14
<211> 1759
<212> DNA
<213> Homo sapiens

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<220>
<221> CDS
<222> 101..1243

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<220>
<221> sig_peptide
<222> 101..199
<223> Von Heijne matrix
      score 3.57142340200611
      seq FLCLGMALCPRQA/TR

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<400> 14
gtagagtgtc gaaggtcctg ccaacggctc tcttggcgtc tcaacgttcg gatcagcagc 60
ttttttccat tctctctctc cacttcttca gtgagcagcc atg agt tgg act gtg 115
                               Met Ser Trp Thr Val
                               -30
cct gtt gtg cgg gcc agc cag aga gtg agc tcg gtg gga gcg aat ttc 163
Pro Val Val Arg Ala Ser Gln Arg Val Ser Ser Val Gly Ala Asn Phe
                               -25                               -20                               -15
cta tgc ctg ggg atg gcc ctg tgt ccg cgt caa gca acg cgc atc ccg 211
Leu Cys Leu Gly Met Ala Leu Cys Pro Arg Gln Ala Thr Arg Ile Pro
                               -10                               -5                               1
ctc aac ggc acc tgg ctc ttc acc ccc gtg agc aag atg gcg act gtg 259
Leu Asn Gly Thr Trp Leu Phe Thr Pro Val Ser Lys Met Ala Thr Val
5                               10                               15                               20
aag agt gag ctt att gag cgt ttc act tcc gag aag ccc gtt cat cac 307
Lys Ser Glu Leu Ile Glu Arg Phe Thr Ser Glu Lys Pro Val His His
                               25                               30                               35
agt aag gtc tcc atc ata gga act gga tcg gtg ggc atg gcc tgc gct 355
Ser Lys Val Ser Ile Ile Gly Thr Gly Ser Val Gly Met Ala Cys Ala
                               40                               45                               50
atc agc atc tta tta aaa ggc ttg agt gat gaa ctt gcc ctt gtg gat 403
Ile Ser Ile Leu Leu Lys Gly Leu Ser Asp Glu Leu Ala Leu Val Asp
                               55                               60                               65
ctt gat gaa gac aaa ctg aag ggt gag acg atg gat ctt caa cat ggc 451
Leu Asp Glu Asp Lys Leu Lys Gly Glu Thr Met Asp Leu Gln His Gly
70                               75                               80
agc cct ttc acg aaa atg cca aat att gtt tgt agc aaa gat tac ttt 499
Ser Pro Phe Thr Lys Met Pro Asn Ile Val Cys Ser Lys Asp Tyr Phe
85                               90                               95                               100
gtc aca gca aac tcc aac cta gtg att atc aca gca ggt gca cgc caa 547
Val Thr Ala Asn Ser Asn Leu Val Ile Ile Thr Ala Gly Ala Arg Gln
                               105                               110                               115
gaa aag gga gaa acg cgc ctt aat tta gtc cag cga aat gtg gcc atc 595
Glu Lys Gly Glu Thr Arg Leu Asn Leu Val Gln Arg Asn Val Ala Ile
120                               125                               130
ttc aag tta atg att tcc agt att gtc cag tac agc ccc cac tgc aaa 643
Phe Lys Leu Met Ile Ser Ser Ile Val Gln Tyr Ser Pro His Cys Lys
135                               140                               145

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Lys Leu Ser Ala Phe Pro Lys Asn Arg Ile Ile Gly Ser Gly Cys Asn	
165 170 175 180	
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Leu Asp Thr Ala Arg Phe Arg Phe Leu Ile Gly Gln Lys Leu Gly Ile	
185 190 195	
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His Ser Glu Ser Cys His Gly Trp Ile Leu Gly Glu His Gly Asp Ser	
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Ser Val Pro Val Trp Ser Gly Val Asn Ile Ala Gly Val Pro Leu Lys	
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gat ctg aac tct gat ata gga act gat aaa gat cct gag caa tgg aaa	931
Asp Leu Asn Ser Asp Ile Gly Thr Asp Lys Asp Pro Glu Gln Trp Lys	
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aat gtc cac aaa gaa gtg act gca act gcc tat gag att att aaa atg	979
Asn Val His Lys Glu Val Thr Ala Thr Ala Tyr Glu Ile Ile Lys Met	
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Lys Gly Tyr Thr Ser Trp Ala Ile Gly Leu Ser Val Ala Asp Leu Thr	
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Glu Ser Ile Leu Lys Asn Leu Arg Arg Ile His Pro Val Ser Thr Ile	
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Ile Lys Gly Leu Tyr Gly Ile Asp Glu Glu Val Phe Leu Ser Ile Pro	
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Cys Ile Leu Gly Glu Asn Gly Ile Thr Asn Leu Ile Lys Ile Lys Leu	
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Thr Pro Glu Glu Glu Ala His Leu Lys Lys Ser Ala Lys Thr Leu Trp	
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Glu Ile Gln Asn Lys Leu Lys Leu	
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                                     Met Ser Trp Thr Val
                                     -30
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Pro Val Val Arg Ala Ser Gln Arg Met Ser Ser Val Gly Ala Asn Phe
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Leu Cys Leu Gly Met Ala Leu Cys Leu Arg Gln Ala Thr Arg Ile Pro
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5      10      15      20
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Lys Ser Glu Leu Ile Glu Arg Phe Thr Ser Glu Lys Pro Val His His
      25      30      35
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Ser Lys Val Ser Ile Ile Gly Thr Gly Ser Val Gly Met Ala Cys Ala
      40      45      50
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Ile Ser Ile Leu Leu Lys Gly Leu Ser Asp Glu Leu Ala Leu Val Asp
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Leu Asp Glu Asp Lys Leu Lys Gly Glu Thr Met Asp Leu Gln His Gly
      70      75      80
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Ser Pro Phe Thr Lys Met Pro Ile Leu Phe Val Ala Lys Ile Thr Leu
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Ser Gln Gln Thr Pro Thr
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 Ile Lys Gln Tyr Val Phe Thr Thr Gln Asn Pro Asn Gly Thr Glu Ser
 55 60 65
 gaa ata tct gtg aga gcc aca act gac ctg aat ttt gct cta aaa aac 346
 Glu Ile Ser Val Arg Ala Thr Thr Asp Leu Asn Phe Ala Leu Lys Asn
 70 75 80
 gga tca acc cca aac gtg cct gca ttt tgg aca atg tta gct aaa gct 394
 Gly Ser Thr Pro Asn Val Pro Ala Phe Trp Thr Met Leu Ala Lys Ala
 85 90 95
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 Ile Asn Gly Thr Ala Val Val Met Asp Asp Lys Asp Gln Leu Phe His
 100 105 110
 cca att cca gag tct gat gtg aat gct aca cag gga gaa aat cag cca 490
 Pro Ile Pro Glu Ser Asp Val Asn Ala Thr Gln Gly Glu Asn Gln Pro
 115 120 125 130
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 Asp Leu Glu Asp Leu Lys Ile Lys Ile Met Leu Gly Ile Ser Leu Met
 135 140 145
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 Thr Leu Leu Leu Phe Val Val Leu Leu Ala Phe Cys Ser Ala Thr Leu
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 Tyr Lys Leu Arg His Leu Ser Tyr Lys Ser Cys Glu Ser Gln Tyr Ser
 165 170 175
 gtc aac cca gag ctg gcc acg atg tct tac ttt cat cca tca gaa ggt 682

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Gly	Thr	Thr	Ser	Ser	Asp	Met	Arg	Arg	Ser	Gly	Thr	Arg	Thr	Ser	Glu		
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Ser	Lys	Ile	Met	Thr	Asp	Ile	Ile	Ser	Ile	Gly	Ser	Asp	Asn	Glu	Met		
			230					235					240				
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His	Glu	Asn	Asp	Glu	Ser	Val	Thr	Arg									
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	-20		-15		-10												
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Phe Pro Pro	Glu Ile Thr	Ala Ser Glu	Tyr Glu Ser	Thr Glu	Leu Ser												
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gcc acg acc	ttt tca act	caa agc ccc	ttg caa aaa	tta ttt	gct aga											207	
Ala Thr Thr	Phe Ser Thr	Gln Ser Pro	Leu Gln Lys	Leu Phe	Ala Arg												
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Lys Met Lys	Ile Leu Gly	Thr Ile Gln	Ile Leu Phe	Gly Ile	Met Thr												
	30		35		40												
ttt tct ttt	gga gtt atc	ttc ctt ttc	act ttg tta	aaa cca	tat cca											303	
Phe Ser Phe	Gly Val Ile	Phe Leu Phe	Thr Leu Leu	Lys Pro	Tyr Pro												
	45		50		55												
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Arg Phe Pro	Phe Ile Phe	Leu Ser Gly	Tyr Pro Phe	Trp Gly	Ser Val												
	60		65		70												
ttg ttc att	aat tct gga	gcc ttc cta	att gca gtg	aaa aga	aaa acc											399	
Leu Phe Ile	Asn Ser Gly	Ala Phe Leu	Ile Ala Val	Lys Arg	Lys Thr												
	75		80		85												
aca gaa act	ctg ata ata	ttg agc cga	ata atg aat	ttt ctt	agt gcc											447	
Thr Glu Thr	Leu Ile Ile	Leu Ser Arg	Ile Met Asn	Phe Leu	Ser Ala												

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90          95          100          105
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          110          115          120
gat caa aac tac att tgt ggt tat tct cac caa aat agt cag tgt aag      543
Asp Gln Asn Tyr Ile Cys Gly Tyr Ser His Gln Asn Ser Gln Cys Lys

          125          130          135
gct gtt act gtc ctg ttc ttg gga att ttg att aca ttg atg act ttc      591
Ala Val Thr Val Leu Phe Leu Gly Ile Leu Ile Thr Leu Met Thr Phe

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agc att att gaa tta ttc att tct ctg cct ttc tca att ttg ggg tgc      639
Ser Ile Ile Glu Leu Phe Ile Ser Leu Pro Phe Ser Ile Leu Gly Cys

          155          160          165
cac tca gag gat tgt gat tgt gaa caa tgt tgt tgactagcac tgtgagaata      692
His Ser Glu Asp Cys Asp Cys Glu Gln Cys Cys

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                        Met Ala Thr Ala Gln Leu Gln
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agg act ccc atg agt gca ctg gta ttt ccc aat aag ata tca act gaa      162
Arg Thr Pro Met Ser Ala Leu Val Phe Pro Asn Lys Ile Ser Thr Glu
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His Gln Ser Leu Val Leu Val Lys Arg Leu Leu Ala Val Ser Val Ser
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Cys Ile Thr Tyr Leu Arg Gly Ile Phe Pro Glu Cys Ala Tyr Gly Thr
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Arg Tyr Leu Asp Asp Leu Cys Val Lys Ile Leu Arg Glu Asp Lys Asn
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      35          40          45
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Ala Leu Gln Lys Lys Tyr Leu Arg Met Val Val Leu Ala Val Tyr Thr
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Leu	Leu	Ile	Arg	Lys	Ile	Tyr	Ile	Leu	Met	Gln	Asn	Leu	Gly	Pro	Leu	
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Arg	Met	Glu	Asn	Ile	Asp	Ser	Thr	Ile	Leu	Ser	Pro	Lys	Gln	Ile	Lys	
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Gln	Glu	Lys	Asn	Pro	Ala	Ser	Ser	Glu	Leu	Glu	Glu	Pro	Ser	Leu	Val	
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Met	Ala	Asn	Gly	Asn	Gln	Pro	Val	Lys	Ser	Ser	Lys	Glu	Asn	Arg	Lys	
305				310						315				320		
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Ser	Ser	Gln	Glu	Ser	Val	Pro	Lys	Arg	Arg	Lys	Phe	Ser	Glu	Pro	Lys	
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Glu	His	Ile														
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                                         Met Ala Leu Glu Val
                                         -15
ttg atg ctc ctc gct gtc ttg att tgg acc ggt gct gag aac ctc cat 104
Leu Met Leu Leu Ala Val Leu Ile Trp Thr Gly Ala Glu Asn Leu His
      -10      -5      1
gtg aaa ata agt tgc tct ctg gac tgg ttg atg gtc tca gtt atc cca 152
Val Lys Ile Ser Cys Ser Leu Asp Trp Leu Met Val Ser Val Ile Pro
5      10      15      20
gtt gca gaa agc aga aat ctg tat ata ttt gcg gat gaa tta cat ctg 200
Val Ala Glu Ser Arg Asn Leu Tyr Ile Phe Ala Asp Glu Leu His Leu
      25      30      35
gga atg ggc tgc cct gca aat cgg ata cat aca tat gta tat gag ttt 248
Gly Met Gly Cys Pro Ala Asn Arg Ile His Thr Tyr Val Tyr Glu Phe
      40      45      50
ata tat ctt gtt cgt gat tgt ggc atc agg aca agg gta gtt tct gag 296
Ile Tyr Leu Val Arg Asp Cys Gly Ile Arg Thr Arg Val Val Ser Glu
      55      60      65
gaa act ctc ctt ttt caa acc gag ctg tac ttt acc cca agg aat ata 344
Glu Thr Leu Leu Phe Gln Thr Glu Leu Tyr Phe Thr Pro Arg Asn Ile
      70      75      80
gat cat gac cct cag gaa atc cat ttg gag tgt tcc acc tct agg aaa 392
Asp His Asp Pro Gln Glu Ile His Leu Glu Cys Ser Thr Ser Arg Lys
85      90      95      100
tca gtg tgg ctt aca cca gtt tct act gag aat gaa ata aaa ttg gat 440
Ser Val Trp Leu Thr Pro Val Ser Thr Glu Asn Glu Ile Lys Leu Asp
      105      110      115
cct agt cct ttt att gct gac ttt cag aca aca gca gaa gag tta gga 488
Pro Ser Pro Phe Ile Ala Asp Phe Gln Thr Thr Ala Glu Glu Leu Gly
      120      125      130
tta tta tct tct agt cca aac ttg ctc tgagctaaag gagaaatgga 535
Leu Leu Ser Ser Ser Pro Asn Leu Leu

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135 140
aacttgaagc tgggtgttatg tatttttgcag gaaaacagtt tcatttttttc atagcaaaaa 595
tatagttggg gtatatctct ccttaagtct ctggtttcta aaaaccctac ttcagtaaag 655
gtcctgatta gttgattagc gaaaaaaaaa aaaaaa 691

<210> 20
<211> 1138
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> 271..969

<220>
<221> sig_peptide
<222> 271..366
<223> Von Heijne matrix
score 5.6680378526706
seq WMGLACFRSLAAS/SP

<220>
<221> misc_feature
<222> 989
<223> n=a, g, c or t

<400> 20
aaaaaccttt caagtgcctc ctcctttcct taaagtcttt tataggggtc cccttcttgg 60
ccatctccat cctgtgagtc aggactgaaa gggcacagac aggtcactgc cagcattgtt 120
ggggcaagcc tgcaagcacg catcactggg gatctgacat gacaatggcc gcctgcccc 180
tctgagggtc acaggactta cccagtgagg aagcagctaa gcaggctctga ccagccgacc 240
tggacctggc caagggctct gtcacccctc atg gcc acc ccg cca ttc cgg ctg 294
Met Ala Thr Pro Pro Phe Arg Leu
-30 -25
ata agg aag atg ttt tcc ttc aag gtg agc aga tgg atg ggg ctt gcc 342
Ile Arg Lys Met Phe Ser Phe Lys Val Ser Arg Trp Met Gly Leu Ala
-20 -15 -10
tgc ttc cgg tcc ctg gcg gca tcc tct ccc agt att cgc cag aag aaa 390
Cys Phe Arg Ser Leu Ala Ala Ser Ser Pro Ser Ile Arg Gln Lys Lys
-5 1 5
cta atg cac aag ctg cag gag gaa aag gct ttt cgc gaa gag atg aaa 438
Leu Met His Lys Leu Gln Glu Glu Lys Ala Phe Arg Glu Glu Met Lys
10 15 20
att ttt cgt gaa aaa ata gag gac ttc agg gaa gag atg tgg act ttc 486
Ile Phe Arg Glu Lys Ile Glu Asp Phe Arg Glu Glu Met Trp Thr Phe
25 30 35 40
cga ggc aag atc cat gct ttc cgg ggc cag atc ctg ggt ttt tgg gaa 534
Arg Gly Lys Ile His Ala Phe Arg Gly Gln Ile Leu Gly Phe Trp Glu
45 50 55
gag gag aga cct ttc tgg gaa gag gag aaa acc ttc tgg aaa gag gaa 582
Glu Glu Arg Pro Phe Trp Glu Glu Lys Thr Phe Trp Lys Glu Glu
60 65 70
aaa tcc ttc tgg gaa atg gaa aag tct ttc agg gag gaa gag aaa act 630
Lys Ser Phe Trp Glu Met Glu Lys Ser Phe Arg Glu Glu Glu Lys Thr
75 80 85
ttc tgg aaa aag tac cgc act ttc tgg aag gag gat aag gcc ttc tgg 678
Phe Trp Lys Lys Tyr Arg Thr Phe Trp Lys Glu Asp Lys Ala Phe Trp
90 95 100

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aaa gag gac aat gcc tta tgg gaa aga gac cgg aac ctt ctt cag gag      726
Lys Glu Asp Asn Ala Leu Trp Glu Arg Asp Arg Asn Leu Leu Gln Glu
105                      110                      115                      120
gac aag gcc ctg tgg gag gaa gaa aag gcc ctg tgg gta gag gaa aga      774
Asp Lys Ala Leu Trp Glu Glu Glu Lys Ala Leu Trp Val Glu Glu Arg
                      125                      130                      135
gcc ctc ctt gag ggg gag aaa gcc ctg tgg gaa gat aaa acg tcc ctc      822
Ala Leu Leu Glu Gly Glu Lys Ala Leu Trp Glu Asp Lys Thr Ser Leu
                      140                      145                      150
tgg gag gaa gag aat gcc ctc tgg gag gaa gag agg gcc ttc tgg atg      870
Trp Glu Glu Glu Asn Ala Leu Trp Glu Glu Glu Arg Ala Phe Trp Met
                      155                      160                      165
gag aac aat ggc cac att gcc gga gag cag atg ctc gaa gat ggg ccc      918
Glu Asn Asn Gly His Ile Ala Gly Glu Gln Met Leu Glu Asp Gly Pro
                      170                      175                      180
cac aac gcc aac aga ggg cag cgc ttg ctg gcc ttc tcc cga ggc agg      966
His Asn Ala Asn Arg Gly Gln Arg Leu Leu Ala Phe Ser Arg Gly Arg
185                      190                      195                      200
gcg tagccagcat gcaggtgcan gggccctgtg gtccagactc ccctggggtg      1019
Ala
ggattcaagt ccaggggtgag cccatgtgct ggagaaaata cacactcatt ggtctccttg      1079
ctttgaaaga tccaataaag tcttgaggca aggtttggaa aaccaaaaaa aaaaaaaa      1138

<210> 21
<211> 468
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> 76..276

<220>
<221> sig_peptide
<222> 76..135
<223> Von Heijne matrix
      score 5.21332530399231
      seq SPVFLVFPPEITA/SE

<400> 21
agcacaagaa aagaacatgg tctagactga agtaccact aaatcatctc ctttcaaatt      60
atcaccgaca ccatac atg gat tca agc acc gca cac agt ccg gtg ttt ctg      111
                      Met Asp Ser Ser Thr Ala His Ser Pro Val Phe Leu
                      -20                      -15                      -10
gta ttt cct cca gaa atc act gct tca gaa tat gag tcc aca gaa ctt      159
Val Phe Pro Pro Glu Ile Thr Ala Ser Glu Tyr Glu Ser Thr Glu Leu
                      -5                      1                      5
tca gcc acg acc ttt tca act caa agc ccc ttg caa aaa tta ttt gct      207
Ser Ala Thr Thr Phe Ser Thr Gln Ser Pro Leu Gln Lys Leu Phe Ala
10                      15                      20
aga aaa atg aaa atc tta ggg gat atc cat tct ggg gct ctg ttt tgt      255
Arg Lys Met Lys Ile Leu Gly Asp Ile His Ser Gly Ala Leu Phe Cys
25                      30                      35                      40
tca tta att ctg gag cct tcc taattgcagt gaaaagaaaa accacagaaa      306
Ser Leu Ile Leu Glu Pro Ser
                      45
ctctgggaat tttgattaca ttgatgactt tcagcattat tgaattattc atttctctgc      366
ctttctcaat tttggggtgc cactcagagg attgtgattg tgaacaatgt tgttgactag      426

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cactgtgaga ataaagatgt gttaaaataa aaaaaaaaaa aa

468

<210> 22
<211> 720
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> 6..287

<220>
<221> sig_peptide
<222> 6..80
<223> Von Heijne matrix
score 4.17710408129886
seq ISLSHLFLDLSRS/LW

<400> 22
atttgc atg tgc ttc tta gtc tcg ttt aac ttg ccg att cat ata tcc ctg 50
Met Cys Phe Leu Val Ser Phe Asn Leu Pro Ile His Ile Ser Leu
-25 -20 -15
tct cat ttg ttc tta gat ttg tca cga agc ctc tgg ttt ttg gct tgt 98
Ser His Leu Phe Leu Asp Leu Ser Arg Ser Leu Trp Phe Leu Ala Cys
-10 -5 1 5
cct ggt ttg aac ttg gtg tat ctg gct ctt gac tca ttt tct gac ctc 146
Pro Gly Leu Asn Leu Val Tyr Leu Ala Leu Asp Ser Phe Ser Asp Leu
10 15 20
aga cca tcc tta aat ctg ctt ttc tac ttt gta cca ggc ttt ggc gtc 194
Arg Pro Ser Leu Asn Leu Leu Phe Tyr Phe Val Pro Gly Phe Gly Val
25 30 35
tcc aag tac ctg acc tca gct caa cct gtc ttg ggt ttt ctt ctc ctc 242
Ser Lys Tyr Leu Thr Ser Ala Gln Pro Val Leu Gly Phe Leu Leu Leu
40 45 50
cct gac att gac aac cca gcc ctc cta ggc aca gag aga tgg agc 287
Pro Asp Ile Asp Asn Pro Ala Leu Leu Gly Thr Glu Arg Trp Ser
55 60 65
tgagtgtggt tttcctgaaa taaagcttgc attatgagag ggaataaaca gaagaaaaaa 347
atagtaagta aaatcttgct tgccctctcag taaaataaag ctctattttt cgtttttttt 407
ttttccaact tcctgtacaa aaaagggaaa acttttagctt ttgggggaaa tttggagcta 467
gcctgttggt actgttgagc ttagtgtatc tataactata tattattcca caatatctta 527
aatactttat aaagatattt tcataaatta cagcaatcct ggcttttagat gattgatggc 587
cattttttaa caattaaagc taatttctag ctttttatga gtttggtatt aagcacagta 647
gtttcttaga aagtcctccag ggaatgcatt ttgcaaaata aaaatcagct aatgacccaa 707
aaaaaaaaaa aaa 720

<210> 23
<211> 727
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> 171..692

<220>
<221> sig_peptide
<222> 171..227

<223> Von Heijne matrix
 score 4.17573075349936
 seq LLLGQRCSLKVSG/QE

<400> 23
 attgtgacat caccgtgcac tagccaatgg ctgcctgcct aagctgggtc cctgggtctcc 60
 tgggactact agccctttgt tgatagggag aagccaacat ctcccgagg accccctaata 120
 cttcagggca gctcccagag catggatccc tctgattcc actcagcccg atg ttc 176
 Met Phe
 ctc aca gtc aag ctg ctc ctg ggc cag aga tgc agt ctg aag gtg tca 224
 Leu Thr Val Lys Leu Leu Leu Gly Gln Arg Cys Ser Leu Lys Val Ser
 -15 -10 -5
 ggg caa gag agt gta gcc acg ctg aag aga ctg gtg tcc agg cgg ctg 272
 Gly Gln Glu Ser Val Ala Thr Leu Lys Arg Leu Val Ser Arg Arg Leu
 1 5 10 15
 aag gtg cct gag gag cag cag cac ctg ctt ttc cgt ggc cag ctc ctg 320
 Lys Val Pro Glu Glu Gln Gln His Leu Leu Phe Arg Gly Gln Leu Leu
 20 25 30
 gag gat gac aag cac ctc tct gac tac tgc att ggg ccc aat gcc tct 368
 Glu Asp Asp Lys His Leu Ser Asp Tyr Cys Ile Gly Pro Asn Ala Ser
 35 40 45
 atc aat gtc atc atg cag ccc ttg gag aag atg gcg cta aag gag gcc 416
 Ile Asn Val Ile Met Gln Pro Leu Glu Lys Met Ala Leu Lys Glu Ala
 50 55 60
 cac cag ccg cag acc cag ccc ctg tgg cac cag ctg gga ctg gtc cta 464
 His Gln Pro Gln Thr Gln Pro Leu Trp His Gln Leu Gly Leu Val Leu
 65 70 75
 gct aaa cac ttt gaa cca cag gat gcc aag gcc gtg ctg cag ctg cta 512
 Ala Lys His Phe Glu Pro Gln Asp Ala Lys Ala Val Leu Gln Leu Leu
 80 85 90 95
 agg cag gag cac gag gag cgc ctg cag aag ata agc ctg gag cac ctg 560
 Arg Gln Glu His Glu Glu Arg Leu Gln Lys Ile Ser Leu Glu His Leu
 100 105 110
 gag cag ctg gcc cag tac ctc ctg gca gag gag cct cac gtg gag cca 608
 Glu Gln Leu Ala Gln Tyr Leu Leu Ala Glu Glu Pro His Val Glu Pro
 115 120 125
 gct gga gag agg gag ctt gag gcg aag gca cgg cct cag agc tcc tgt 656
 Ala Gly Glu Arg Glu Leu Glu Ala Lys Ala Arg Pro Gln Ser Ser Cys
 130 135 140
 gac atg gag gag aag gag gag gca gca gct gat cag taaacggggcc 702
 Asp Met Glu Glu Lys Glu Glu Ala Ala Ala Asp Gln
 145 150 155
 atcctaccg aaaaaaaaaa aaaaa 727

<210> 24
 <211> 470
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> 137..454

<220>
 <221> sig_peptide
 <222> 137..187
 <223> Von Heijne matrix
 score 10.7019149919754

seq VLMLLAVLIWTGA/EN

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<400> 24
atcctgtgaa ctacccaaaa ggaggaaaac gaacgcagct gagcatggga tgccatataa    60
aaatcactta aaccagtcgc cactccttgt ttcctgagtt gtcctgtgct ggaggtctgc    120
tcagacgaag gtctcc atg gcg tta gaa gtc ttg atg ctc ctc gct gtc ttg    172
          Met Ala Leu Glu Val Leu Met Leu Leu Ala Val Leu
                -15                      -10
att tgg acc ggt gct gag aac ctc cat gtg aaa ata agt tgc tct ctg    220
Ile Trp Thr Gly Ala Glu Asn Leu His Val Lys Ile Ser Cys Ser Leu
-5                      1                      5                      10
gac tgg ttg atg gtc tca gtt atc cca gtt gca gaa agc aga aat ctg    268
Asp Trp Leu Met Val Ser Val Ile Pro Val Ala Glu Ser Arg Asn Leu
          15                      20                      25
tat ata ttt gcg gat gaa tta cat ctg gga atg ggc tgc cct gca aat    316
Tyr Ile Phe Ala Asp Glu Leu His Leu Gly Met Gly Cys Pro Ala Asn
          30                      35                      40
cgg ata cat aca tat gta tat gag ttt ata tat ctt gtt cgt gat tgt    364
Arg Ile His Thr Tyr Val Tyr Glu Phe Ile Tyr Leu Val Arg Asp Cys
          45                      50                      55
ggc atc agg aca agg gta aga aca gtg att gtc tgt aaa aaa tac tgc    412
Gly Ile Arg Thr Arg Val Arg Thr Val Ile Val Cys Lys Lys Tyr Cys
60                      65                      70                      75
atg ttt tgt cag act ttt atg cct agt att aaa att gtc ttt    454
Met Phe Cys Gln Thr Phe Met Pro Ser Ile Lys Ile Val Phe
          80                      85
taaaaaaaaa aaaaaa    470

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<210> 25
<211> 987
<212> DNA
<213> Homo sapiens

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<220>
<221> CDS
<222> 238..609

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<220>
<221> sig_peptide
<222> 238..291
<223> Von Heijne matrix
      score 10.0374888212272
      seq LLLLVMALPPGTT/GV

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<400> 25
attccattca cagactcttg ttgggcagca gccacccgct cacctccatc cccaggactt    60
agagggacgc agggcggttg gaacagagga cactccaggc gctgaccctg ggaggccagg    120
accagggcca aagtcccgta ggcaagagga gtcctcagag gtccttcatt cagcggttcc    180
gggaggtctg ggaagcccac ggctggctg gggcagggtc aacgccgcca ggccgcc    237
atg gtc ctg tgc tgg ctg ctg ctt ctg gtg atg gct ctg ccc cca ggc    285
Met Val Leu Cys Trp Leu Leu Leu Leu Val Met Ala Leu Pro Pro Gly
          -15                      -10                      -5
acg acg ggc gtc aag gac tgc gtc ttc tgt gag ctc acc gac tcc atg    333
Thr Thr Gly Val Lys Asp Cys Val Phe Cys Glu Leu Thr Asp Ser Met
          1                      5                      10
cag tgt cct ggt acc tac atg cac tgt ggc gat gag gag gac tgc ttc    381
Gln Cys Pro Gly Thr Tyr Met His Cys Gly Asp Asp Glu Asp Cys Phe
15                      20                      25                      30

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[illegible]

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<210> 26
<211> 908
<212> DNA
<213> Homo sapiens
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<220>  
<221> CDS  
<222> 80..862
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<220>
<221> sig_peptide
<222> 80..127
<223> Von Heijne matrix
score 3.66725851505537
seq FSLLSISGPPISS/SA
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<400> 26																	
gaatgtttat cctctggaca aaccagccag cctctccaga gcaggcgtgt gatctctgta																	60
ccccgcagt ggtcagaat atg gag aac ttc tca ctc ctc agc atc tct gga																	112
Met Glu Asn Phe Ser Leu Leu Ser Ile Ser Gly																	
-15 -10																	
cct cca atc tct tcc tcc gcc ctg agt gct ttt ccc gac att atg ttc																	160
Pro Pro Ile Ser Ser Ser Ala Leu Ser Ala Phe Pro Asp Ile Met Phe																	
-5 1 5 10																	
tct cgt gcc acc agc ctg cca gac att gca aag aca gca gta ccc act																	208
Ser Arg Ala Thr Ser Leu Pro Asp Ile Ala Lys Thr Ala Val Pro Thr																	
15 20 25																	
gag gca tcc agc cca gct cag gcc ctg cca ccc cag tac caa agc atc																	256
Glu Ala Ser Ser Pro Ala Gln Ala Leu Pro Pro Gln Tyr Gln Ser Ile																	
30 35 40																	
att gtc agg caa ggg ata cag aac aca gtg ctc tca cca gac tgc agc																	304
Ile Val Arg Gln Gly Ile Gln Asn Thr Val Leu Ser Pro Asp Cys Ser																	
45 50 55																	
ttg ggg gac acc cag cac gga gag aag ctg agg cgg aac tgc act atc																	352
Leu Gly Asp Thr Gln His Gly Glu Lys Leu Arg Arg Asn Cys Thr Ile																	

Cys	Cys	Leu	Cys	Ala	Leu	Leu	Ser	Asn	Phe	Cys	Pro	Ser	Thr	Thr	Val	
-15					-10					-5					1	
aaa	gga	gac	gtc	gtg	act	tcc	ttc	ttt	cgt	gct	gac	tat	gac	tta	gcc	208
Lys	Gly	Asp	Val	Val	Thr	Ser	Phe	Phe	Arg	Ala	Asp	Tyr	Asp	Leu	Ala	
		5						10				15				
agt	agg	tct	gca	gat	cag	tcc	tcc	cag	aaa	gtg	aag	ttg	cgc	atg	ttc	256
Ser	Arg	Ser	Ala	Asp	Gln	Ser	Ser	Gln	Lys	Val	Lys	Leu	Arg	Met	Phe	
		20					25				30					
act	ggg	cgt	ctt	ccc	atc	ggc	ccc	ttc	gcc	agt	gtg	ggg	aac	gcg	gcg	304
Thr	Gly	Arg	Leu	Pro	Ile	Gly	Pro	Phe	Ala	Ser	Val	Gly	Asn	Ala	Ala	
	35					40					45					
gag	ctg	tgagccggcg	actcgggtcc	ctgaggtctg	gattctttct	ccgctactga										360
Glu	Leu															
50																
gacacggcgg	acacacacaa	acacagaacc	acacagccag	ttccaggagc	ccagtaatgg											420
agagcccca	aaagaagaac	cagcagctga	aagtcgggat	cctacacctg	ggcagcagac											480
agaagaagat	caggatacag	ctgagatccc	agtgcgcgac	atggaagggtg	atctgcaaga											540
gctgcatcag	tcaaacaccg	gggataaatc	tggatttggg	ttccggcgctc	aagggtgaaga											600
taatacctaa	agaggaacac	tgtaaaatgc	cagaagcagg	tgaagagcaa	ccacaagttt											660
aaatgaagac	aagctgaaac	aacgcaagct	ggttttatat	tagatatttg	acttaaaacta											720
tctcaataaa	gttttgcagc	tttcaccaa	aaaaaaaaaa	aa												762

<210> 28
 <211> 1102
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> 310..906

<220>
 <221> sig_peptide
 <222> 310..357
 <223> Von Heijne matrix
 score 11.0931109030915
 seq FPLLLSLGLVLA/EA

<400> 28																
atacagtgac	ctagagcagg	catgggtggg	tcacaggctt	tggagagcac	tctctgtcct											60
gatcttttca	gttgagagac	ttcagctgtt	cattgctcat	ttggacttag	ttcaagggtca											120
tgtcaaagaa	gaagggtgcac	ttacgctagt	tgtagctct	gtcttttgta	accatcaagt											180
tccatgcgat	tgatcagatt	taggaggggg	cggtggggga	taatcaattt	tgggtgtcac											240
caggtaaaca	gagccctcag	catctgaata	gaaactgaac	aggaacagaa	gagattcact											300
acatctgag	atg gag acc	ttt cct ctg	ctg ctg ctc	agc ctg ggc	ctg gtt											351
	Met Glu Thr	Phe Pro Leu	Leu Leu Leu	Ser Leu Gly	Leu Val											
	-15		-10		-5											
ctt gca gaa	gca tca gaa	agc aca atg	aag ata att	aaa gaa gaa	ttt											399
Leu Ala Glu	Ala Ser Glu	Ser Thr Met	Lys Ile Ile	Lys Glu Glu	Phe											
	1		5		10											
aca gac gaa	gag atg caa	tat gac atg	gca aaa agt	ggc caa gaa	aaa											447
Thr Asp Glu	Glu Met Gln	Tyr Asp Met	Ala Lys Ser	Gly Gln Glu	Lys											
	15		20		25											
cag acc att	gag ata tta	atg aac ccg	atc ctg tta	gtt aaa aat	acc											495
Gln Thr Ile	Glu Ile Leu	Met Asn Pro	Ile Leu Leu	Val Lys Asn	Thr											
	35		40		45											
agc ctc agc	atg tcc aag	gat gat atg	tct tcc aca	tta ctg aca	ttc											543
Ser Leu Ser	Met Ser Lys	Asp Asp Met	Ser Ser Thr	Leu Leu Thr	Phe											

	50		55		60	
aga agt tta cat tat aat gac ccc aag gga aac agt tcg ggt aat gac						591
Arg Ser Leu His Tyr Asn Asp Pro Lys Gly Asn Ser Ser Gly Asn Asp						
65		70		75		
aaa gag tgt tgc aat gac atg aca gtc tgg aga aaa gtt tca gaa gca						639
Lys Glu Cys Cys Asn Asp Met Thr Val Trp Arg Lys Val Ser Glu Ala						
80		85		90		
aac gga tcg tgc aag tgg agc aat aac ttc atc cgc agc tcc aca gaa						687
Asn Gly Ser Cys Lys Trp Ser Asn Asn Phe Ile Arg Ser Ser Thr Glu						
95		100		105		110
gtg atg cgc agg gtc cac agg gcc ccc agc tgc aag ttt gta cag aat						735
Val Met Arg Arg Val His Arg Ala Pro Ser Cys Lys Phe Val Gln Asn						
115		120		125		
cct ggc ata agc tgc tgt gag agc cta gaa ctg gaa aat aca gtg tgc						783
Pro Gly Ile Ser Cys Cys Glu Ser Leu Glu Leu Glu Asn Thr Val Cys						
130		135		140		
cag ttc act aca ggc aaa caa ttc ccc agg tgc caa tac cat agt gtt						831
Gln Phe Thr Thr Gly Lys Gln Phe Pro Arg Cys Gln Tyr His Ser Val						
145		150		155		
acc tca tta gag aag ata ttg aca gtg ctg aca ggt cat tct ctg atg						879
Thr Ser Leu Glu Lys Ile Leu Thr Val Leu Thr Gly His Ser Leu Met						
160		165		170		
agc tgg tta gtt tgt ggc tct aag ttg taaatccac agagctttag						926
Ser Trp Leu Val Cys Gly Ser Lys Leu						
175		180				
gactaggggtc ttactaaaga aggacctctt cttgttcatt cttgtttaaa cctttcctta						986
atatctactc ttttagcacta tagtgaactc ctgattattt attctaactg gaggagtga						1046
aaatccaaaa ttgtggataa ttcaattaaa agttatgact gaaaaaaaaa aaaaaa						1102

<210> 29

<211> 436

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> 24..287

<220>

<221> sig_peptide

<222> 24..131

<223> Von Heijne matrix

score 3.79790641648006

seq ILMRDFSPSGIFG/AF

<400> 29

acagcggaca ccaggactcc aaa atg gcg tca gtt gta cca gtg aag gac aag	53
Met Ala Ser Val Val Pro Val Lys Asp Lys	

-35

-30

aaa ctt ctg gag gtc aaa ctg ggg gag ctg cca agc tgg atc ttg atg	101
Lys Leu Leu Glu Val Lys Leu Gly Glu Leu Pro Ser Trp Ile Leu Met	

-25

-20

-15

cgg gac ttc agt cct agt ggc att ttc gga gcg ttt caa aga ggt tac	149
Arg Asp Phe Ser Pro Ser Gly Ile Phe Gly Ala Phe Gln Arg Gly Tyr	

-10

-5

1

5

tac cgg tac tac aac aag tac atc aat gtg aag aag ggg agc atc tcg	197
Tyr Arg Tyr Tyr Asn Lys Tyr Ile Asn Val Lys Lys Gly Ser Ile Ser	

10

15

20

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ggg att acc atg gtg ctg gca tgc tac gtg ctc ttt agc tac tcc ttt      245
Gly Ile Thr Met Val Leu Ala Cys Tyr Val Leu Phe Ser Tyr Ser Phe
      25              30              35
tcc tac aag cat ctc aag cac gag cgg ctc cgc aaa tac cac      287
Ser Tyr Lys His Leu Lys His Glu Arg Leu Arg Lys Tyr His
      40              45              50
tgaagaggac acactctgca cccccccacc ccacgacctt ggccccgagcc cctccgtgag      347
gaacacaatc tcaatcggtg ctgaatcctt tcatatccta ataggaatta acctccaaat      407
aaaacatgac tggtaaaaaa aaaaaaaaaa      436

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gggaatctag g atg ggg gcc ttg gcc aga gcc ctg ccg tcc ata ctg ctg      170
      Met Gly Ala Leu Ala Arg Ala Leu Pro Ser Ile Leu Leu
      -25              -20              -15
gca ttg ctg ctt acg tcc acc cca gag gct ctg ggt gcc aac ccc ggc      218
Ala Leu Leu Leu Thr Ser Thr Pro Glu Ala Leu Gly Ala Asn Pro Gly
      -10              -5              1
ttg gtc gcc agg atc acc gac aag gga ctg cag tat gcg gcc cag gag      266
Leu Val Ala Arg Ile Thr Asp Lys Gly Leu Gln Tyr Ala Ala Gln Glu
      5              10              15              20
ggg cta ttg gct ctg cag agt gag ctg ctc agg atc acg ctg cct gac      314
Gly Leu Leu Ala Leu Gln Ser Glu Leu Leu Arg Ile Thr Leu Pro Asp
      25              30              35
ttc acc ggg gac ttg agg atc ccc cac gtc ggc cgt ggg cgc tat gag      362
Phe Thr Gly Asp Leu Arg Ile Pro His Val Gly Arg Gly Arg Tyr Glu
      40              45              50
ttc cac agc ctg aac atc cac agc tgt gag ctg ctt cac tct gcg ctg      410
Phe His Ser Leu Asn Ile His Ser Cys Glu Leu Leu His Ser Ala Leu
      55              60              65
agg cct gtc cct ggc cag ggc ctg agt ctc agc atc tcc gac tcc tcc      458
Arg Pro Val Pro Gly Gln Gly Leu Ser Leu Ser Ile Ser Asp Ser Ser
      70              75              80
atc cgg gtc cag ggc agg tgg aag gtg cgc aag tca ttc ttc aaa cta      506
Ile Arg Val Gln Gly Arg Trp Lys Val Arg Lys Ser Phe Phe Lys Leu
      85              90              95              100
cag ggc tcc ttt gat gtc agt gtc aag ggc atc agc att tcg gtc aac      554
Gln Gly Ser Phe Asp Val Ser Val Lys Gly Ile Ser Ile Ser Val Asn
      105              110              115
ctc ctg ttg ggc agc gat tcc tcc ggg agg ccc aca gtt act gcc tcc      602
Leu Leu Leu Gly Ser Asp Ser Ser Gly Arg Pro Thr Val Thr Ala Ser

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ggg ctg cag atc cat aag gac ttc ctg ttc ttg ggt gcc aat gtc caa      1562
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      440                      445                      450
tac atg aga gtt tgaggacaag aaagatgaag cttggagggtc acagctggat      1614
Tyr Met Arg Val
      455
ctgcttggtg catttccagc tgtgcagcac gtctcagaga ttcttgaaga atgaagacat      1674
ttctgctctc agctccgggg gtgaggtgtg cctggcctct gcctccaccc tcctcctctt      1734
caccaggtgc atgcatgccc tctctgagtc tggactttgc ttccctcca ggagggacca      1794
ccctccctga ctggcctggg atatctttac aagcaggcac tgtatttttt tattcgccat      1854
ctgatcccca tgcctagcag agtgctggca cttagtaggt cctcaataaa tattttattaa      1914
atgatgacaa aaaaaaaaaa aaaa      1938

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tgctctctgt cgccgggaac tggcgaggta gttccttcgc ggtggagaga cctgga atg      119
                                Met
gcc aaa tat caa ggt gaa gtt caa agt ttg aaa ctg gat gat gat tca      167
Ala Lys Tyr Gln Gly Glu Val Gln Ser Leu Lys Leu Asp Asp Asp Ser
      -40                      -35                      -30
gtt ata gaa gga gta agc gac caa gta ctt gtg gca gtt gtg gtc agt      215
Val Ile Glu Gly Val Ser Asp Gln Val Leu Val Ala Val Val Val Ser
      -25                      -20                      -15
ttc gct ttg att gct acc ctg gta tat gca ctt ttc aga aat gta cat      263
Phe Ala Leu Ile Ala Thr Leu Val Tyr Ala Leu Phe Arg Asn Val His
      -10                      -5                      1                      5
caa aac att cac cca gaa aac cag gag cta gta agg gta ctt cga gaa      311
Gln Asn Ile His Pro Glu Asn Gln Glu Leu Val Arg Val Leu Arg Glu
      10                      15                      20
cag ctt caa aca gaa cag gat gca cct gct gcc act cga cag cag ttc      359
Gln Leu Gln Thr Glu Gln Asp Ala Pro Ala Ala Thr Arg Gln Gln Phe
      25                      30                      35
tac act gac atg tac tgt ccc atc tgc ctg cac caa gcc tcc ttc ccg      407
Tyr Thr Asp Met Tyr Cys Pro Ile Cys Leu His Gln Ala Ser Phe Pro
      40                      45                      50
gtg gag acc aac tgt gga cat ctt ttt tgt ggt gcc tgc att att gct      455
Val Glu Thr Asn Cys Gly His Leu Phe Cys Gly Ala Cys Ile Ile Ala
      55                      60                      65                      70
tac tgg cga tat ggt tca tgg ctt ggg gca atc agt tgt cca atc tgt      503
Tyr Trp Arg Tyr Gly Ser Trp Leu Gly Ala Ile Ser Cys Pro Ile Cys
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aga caa acg aga cat ggc cac att gca ttg tcc aga aca gct      545

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 acgtctcttc ggagagcgcg cac atg gcg act cag gcg cac tcc ctc agc tac 173
 Met Ala Thr Gln Ala His Ser Leu Ser Tyr
 -25 -20
 gca ggg tgc aac ttc ttg tgc caa cgt ctg gtc ctg tct acc ctg agc 221
 Ala Gly Cys Asn Phe Leu Cys Gln Arg Leu Val Leu Ser Thr Leu Ser
 -15 -10 -5
 ggg cgc ccc gtc aaa atc cga aag att cgg gcc aga gac gac aac ccg 269
 Gly Arg Pro Val Lys Ile Arg Lys Ile Arg Ala Arg Asp Asp Asn Pro
 1 5 10 15
 ggc ctc cga gat ttt gaa gcc agc ttc ata agg cta ttg gac aaa ata 317
 Gly Leu Arg Asp Phe Glu Ala Ser Phe Ile Arg Leu Leu Asp Lys Ile
 20 30
 acg aat ggt tct cga att gaa ata aac caa aca gga aca acc tta tat 365
 Thr Asn Gly Ser Arg Ile Glu Ile Asn Gln Thr Gly Thr Thr Leu Tyr
 35 40 45
 tat cag cct ggc ctc ctg tat ggt gga tct gtg gaa cat gac tgt agc 413
 Tyr Gln Pro Gly Leu Leu Tyr Gly Gly Ser Val Glu His Asp Cys Ser
 50 55 60
 gtc ctt cgt ggc att ggg tat tac ctg gag agt ctt ctt tgc ttg gct 461
 Val Leu Arg Gly Ile Gly Tyr Leu Glu Ser Leu Leu Cys Leu Ala
 65 70 75
 cca ttt atg aag cac ccg tta aaa ata gtt cta cga gga gtg acc aat 509
 Pro Phe Met Lys His Pro Leu Lys Ile Val Leu Arg Gly Val Thr Asn
 80 85 90 95
 gat cag att gac cct tca gtt gat gtt ctt aag gca aca gca ctc cct 557
 Asp Gln Ile Asp Pro Ser Val Asp Val Leu Lys Ala Thr Ala Leu Pro
 100 105 110
 ttg ttg aaa caa ttt ggg att gat ggt gaa tca ttt gaa ctg aag att 605
 Leu Leu Lys Gln Phe Gly Ile Asp Gly Glu Ser Phe Glu Leu Lys Ile
 115 120 125
 gtg cga cgg gga atg cct ccc gga gga gga ggc gaa gtg gtt ttc tca 653
 Val Arg Arg Gly Met Pro Pro Gly Gly Gly Gly Glu Val Val Phe Ser
 130 135 140
 tgt cct gtg agg aag gtc ttg aag ccc att caa ctc aca gat cca gga 701
 Cys Pro Val Arg Lys Val Leu Lys Pro Ile Gln Leu Thr Asp Pro Gly
 145 150 155
 aaa atc aaa cgt att aga gga atg gcg tac tct gta cgt gtg tca cct 749
 Lys Ile Lys Arg Ile Arg Gly Met Ala Tyr Ser Val Arg Val Ser Pro
 160 165 170 175
 cag atg gcg aac cgg att gtg gat tct gca agg agc atc ctc aac aag 797

Gln Met Ala Asn Arg Ile Val Asp Ser Ala Arg Ser Ile Leu Asn Lys	
180 185 190	
ttc ata cct gat atc tat att tac aca gat cac att aaa gga gtc aac	845
Phe Ile Pro Asp Ile Tyr Ile Tyr Thr Asp His Ile Lys Gly Val Asn	
195 200 205	
tct ggg aag tct ccg ggc ttt ggg ttg tca ctg gtt gct gag acc acc	893
Ser Gly Lys Ser Pro Gly Phe Gly Leu Ser Leu Val Ala Glu Thr Thr	
210 215 220	
agt ggc acc ttc ctc agt gct gaa ctg gcc tcc aac ccc cag ggc cag	941
Ser Gly Thr Phe Leu Ser Ala Glu Leu Ala Ser Asn Pro Gln Gly Gln	
225 230 235	
gga gca gca gta ctt cca gag gac ctt ggc agg aac tgt gcc cgg ctg	989
Gly Ala Ala Val Leu Pro Glu Asp Leu Gly Arg Asn Cys Ala Arg Leu	
240 245 250 255	
ctg ctg gag gaa atc tac agg ggt gga tgc gta gac tcg acc aac caa	1037
Leu Leu Glu Glu Ile Tyr Arg Gly Gly Cys Val Asp Ser Thr Asn Gln	
260 265 270	
agc ctg gcg cta cta ctc atg acc ctt gga cag cag gat gtt tcc aaa	1085
Ser Leu Ala Leu Leu Leu Met Thr Leu Gly Gln Gln Asp Val Ser Lys	
275 280 285	
gtc ctg cta ggc cct ctc tct ccc tac acg ata gaa ttt ttg cgg cat	1133
Val Leu Leu Gly Pro Leu Ser Pro Tyr Thr Ile Glu Phe Leu Arg His	
290 295 300	
ttg aag agc ttt ttc cag att atg ttt aaa att gaa acc aag cca tgt	1181
Leu Lys Ser Phe Phe Gln Ile Met Phe Lys Ile Glu Thr Lys Pro Cys	
305 310 315	
ggt gaa gaa ctc aag ggt ggg gat aaa gtg ctg atg acc tgt gtt ggc	1229
Gly Glu Glu Leu Lys Gly Gly Asp Lys Val Leu Met Thr Cys Val Gly	
320 325 330 335	
att ggt ttc tcc aac ctt agc agg acc ctc aag tgataaccat cacaagataa	1282
Ile Gly Phe Ser Asn Leu Ser Arg Thr Leu Lys	
340 345	
ggccccagtg cctacagaca aagcagaagc tgccacggac accaatggga ccaagtccaa	1342
atggattaat ccaggacaga atagccactt gcttaatttt ctgtgaagaa atatcaatat	1402
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gggattaaat gagataatat gagtggcagc tcttcatgag tcttgcagtg ctaagcaa	1762
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acacggacac ggatcttcat ctgggttcatt gtatttataat gtgagggatg gatggctgcg	1882
gggctccaag taagttattg ggatgttttt atattccagg tgtgctgtac gttcttattt	1942
tatttttcaca atagctctgt gatgtaagt ctatctccat gagaaaattc ataaagggtg	2002
ttttgttcat ttgaaatgta taatgtaaag acattaaatc tcctcattta aggaaaaaaa	2062
aaaaaaaaa	2072

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 <213> Homo sapiens

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<222> 35..109
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 seq AVTSLLSPTPATA/LA

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 ctg agg acc cgg aca gcc gtt aca tcc ttg cta agc ccc act ccg gct 103
 Leu Arg Thr Arg Thr Ala Val Thr Ser Leu Leu Ser Pro Thr Pro Ala
 -15 -10 -5
 aca gct ctt gct gtc aga tac gca tcc aag aag tcg ggt ggt agc tcc 151
 Thr Ala Leu Ala Val Arg Tyr Ala Ser Lys Lys Ser Gly Gly Ser Ser
 1 5 10
 aaa aac ctc ggt gga aag tca tca ggc aga cgc caa ggc att aag aaa 199
 Lys Asn Leu Gly Gly Lys Ser Ser Gly Arg Arg Gln Gly Ile Lys Lys
 15 20 25 30
 atg gaa ggt cac tat gtt cat gct ggg aac atc att gca aca cag cgc 247
 Met Glu Gly His Tyr Val His Ala Gly Asn Ile Ile Ala Thr Gln Arg
 35 40 45
 cat ttc cgc tgg cac cca ggt gcc cat gtg agt tgc tcc gtt gct gcc 295
 His Phe Arg Trp His Pro Gly Ala His Val Ser Cys Ser Val Ala Ala
 50 55 60
 ccc ctt ttt cct ttt cta ggt tgacctctcc ttgccctaa gcatggtaat 346
 Pro Leu Phe Pro Phe Leu Gly
 65
 aacagttgca tgtattgagt gcttaccaaa tggcaagcat tgtgccaaaa aaaaaaaaaa 406
 aaa 409

<210> 35
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<220>
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 score 6.51720597568932
 seq LAVILTLLGLAIL/AI

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 acacccaagt tcatattgct cagaaacagt gaacttgagt ttttcatttt accttgatct 120
 ctctctgaca aagaaatcca gatgatgcga gacctgatga agacaatata tggaaa atg 179
 Met
 -20
 aca gtc ttg gaa ata act ttg gct gtc atc ctg act cta ctg gga ctt 227
 Thr Val Leu Glu Ile Thr Leu Ala Val Ile Leu Thr Leu Leu Gly Leu
 -15 -10 -5
 gcc atc ctg gct att ttg tta aca aga tgg gca cga cgt aag caa agt 275
 Ala Ile Leu Ala Ile Leu Leu Thr Arg Trp Ala Arg Lys Gln Ser
 1 5 10

gaa atg tat atc tcc aga tac agt tca gaa caa agt gct aga ctt ctg	323
Glu Met Tyr Ile Ser Arg Tyr Ser Ser Glu Gln Ser Ala Arg Leu Leu	
15 20 25	
gac tat gag gat ggt aga gga tcc cga cat gca tat tca aca caa agt	371
Asp Tyr Glu Asp Gly Arg Gly Ser Arg His Ala Tyr Ser Thr Gln Ser	
30 35 40 45	
gag aga tcc aaa aga gat tac aca cca tca acc aac tct cta gca ctg	419
Glu Arg Ser Lys Arg Asp Tyr Thr Pro Ser Thr Asn Ser Leu Ala Leu	
50 55 60	
tct cga tca agt att gct tta cct caa gga tcc atg agt agt ata aaa	467
Ser Arg Ser Ser Ile Ala Leu Pro Gln Gly Ser Met Ser Ser Ile Lys	
65 70 75	
tgt tta caa aca act gaa gaa cct cct tcc aga act gca gga gcc atg	515
Cys Leu Gln Thr Thr Glu Glu Pro Pro Ser Arg Thr Ala Gly Ala Met	
80 85 90	
atg caa ttc aca gcc cct att ccc gga gct aca gga cct atc aag ctc	563
Met Gln Phe Thr Ala Pro Ile Pro Gly Ala Thr Gly Pro Ile Lys Leu	
95 100 105	
tct caa aaa acc att gtg caa act cta gga cct att gta caa tat cct	611
Ser Gln Lys Thr Ile Val Gln Thr Leu Gly Pro Ile Val Gln Tyr Pro	
110 115 120 125	
gga tcc aat ggg agg ata aac ata agc cag ctc acc tca gag gat ctc	659
Gly Ser Asn Gly Arg Ile Asn Ile Ser Gln Leu Thr Ser Glu Asp Leu	
130 135 140	
act ggg gct aaa gga agg gtc aca tct ggt cca cag ttc cct aat agc	707
Thr Gly Ala Lys Gly Arg Val Thr Ser Gly Pro Gln Phe Pro Asn Ser	
145 150 155	
cac cat gtg cca gag aat cta cat gga tac atg aat tcc ctt tcc ctt	755
His His Val Pro Glu Asn Leu His Gly Tyr Met Asn Ser Leu Ser Leu	
160 165 170	
ttc tcc cct gct tgactccctc tcccttatgt gtaaacaatt taaaaaatatg	807
Phe Ser Pro Ala	
175	
atagtgtata aatgaaaaaa aaaaaaaaaa	836

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<211> 1323

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<221> CDS

<222> 208..1239

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<222> 208..294

<223> Von Heijne matrix

score 5.73027134157378

seq GLVLICVCSKTHS/LK

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gctgctgttt gaattatctg tgaatgttg gaagaggaat gccagagctg cgggctgaaa	180
attaccaaac caagagaaat ctgcagg atg gac ttt ctg gtc ctc ttc ttg ttc	234
Met Asp Phe Leu Val Leu Phe Leu Phe	

-25

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Tyr	Leu	Ala	Ser	Val	Leu	Met	Gly	Leu	Val	Leu	Ile	Cys	Val	Cys	Ser	
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aaa	acc	cat	agc	ttg	aaa	ggc	ctg	gcc	agg	gga	gga	gca	cag	ata	ttt	330
Lys	Thr	His	Ser	Leu	Lys	Gly	Leu	Ala	Arg	Gly	Gly	Ala	Gln	Ile	Phe	
			1				5					10				
tcc	tgt	ata	att	cca	gaa	tgt	ctt	cag	aga	gcc	gtg	cat	gga	ttg	ctt	378
Ser	Cys	Ile	Ile	Pro	Glu	Cys	Leu	Gln	Arg	Ala	Val	His	Gly	Leu	Leu	
	15						20					25				
cat	tac	ctt	ttc	cat	acg	aga	aac	cac	acc	ttc	att	gtc	ctg	cac	ctg	426
His	Tyr	Leu	Phe	His	Thr	Arg	Asn	His	Thr	Phe	Ile	Val	Leu	His	Leu	
	30					35					40					
gtc	ttg	caa	ggg	atg	gtt	tat	act	gag	tac	acc	tgg	gaa	gta	ttt	ggc	474
Val	Leu	Gln	Gly	Met	Val	Tyr	Thr	Glu	Tyr	Thr	Trp	Glu	Val	Phe	Gly	
45					50					55					60	
tac	tgt	cag	gag	ctg	gag	ttg	tcc	ttg	cat	tac	ctt	ctt	ctg	ccc	tat	522
Tyr	Cys	Gln	Glu	Leu	Glu	Leu	Ser	Leu	His	Tyr	Leu	Leu	Leu	Pro	Tyr	
			65						70					75		
ctg	ctg	cta	ggt	gta	aac	ctg	ttt	ttt	ttc	acc	ctg	act	tgt	gga	acc	570
Leu	Leu	Leu	Gly	Val	Asn	Leu	Phe	Phe	Phe	Thr	Leu	Thr	Cys	Gly	Thr	
			80					85					90			
aat	cct	ggc	att	ata	aca	aaa	gca	aat	gaa	tta	tta	ttt	ctt	cat	gtt	618
Asn	Pro	Gly	Ile	Ile	Thr	Lys	Ala	Asn	Glu	Leu	Leu	Phe	Leu	His	Val	
	95						100					105				
tat	gaa	ttt	gat	gaa	gtg	atg	ttt	cca	aag	aac	gtg	agg	tgc	tct	act	666
Tyr	Glu	Phe	Asp	Glu	Val	Met	Phe	Pro	Lys	Asn	Val	Arg	Cys	Ser	Thr	
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tgt	gat	tta	agg	aaa	cca	gct	cga	tcc	aag	cac	tgc	agt	gtg	tgt	aac	714
Cys	Asp	Leu	Arg	Lys	Pro	Ala	Arg	Ser	Lys	His	Cys	Ser	Val	Cys	Asn	
125					130					135					140	
tgg	tgt	gtg	cac	cgt	ttc	gac	cat	cac	tgt	gtt	tgg	gtg	aac	aac	tgc	762
Trp	Cys	Val	His	Arg	Phe	Asp	His	His	Cys	Val	Trp	Val	Asn	Asn	Cys	
				145					150					155		
atc	ggg	gcc	tgg	aac	atc	agg	tac	ttc	ctc	atc	tac	gtc	ttg	acc	ttg	810
Ile	Gly	Ala	Trp	Asn	Ile	Arg	Tyr	Phe	Leu	Ile	Tyr	Val	Leu	Thr	Leu	
			160					165					170			
acg	gcc	tcg	gct	gcc	acc	gtc	gcc	att	gtg	agc	acc	act	ttt	ctg	gtc	858
Thr	Ala	Ser	Ala	Ala	Thr	Val	Ala	Ile	Val	Ser	Thr	Thr	Phe	Leu	Val	
			175				180					185				
cac	ttg	gtg	gtg	atg	tca	gat	tta	tac	cag	gag	act	tac	atc	gat	gac	906
His	Leu	Val	Val	Met	Ser	Asp	Leu	Tyr	Gln	Glu	Thr	Tyr	Ile	Asp	Asp	
	190				195					200						
ctt	gga	cac	ctc	cat	gtt	atg	gac	acg	gtc	ttt	ctt	att	cag	tac	ctg	954
Leu	Gly	His	Leu	His	Val	Met	Asp	Thr	Val	Phe	Leu	Ile	Gln	Tyr	Leu	
205					210					215					220	
ttc	ctg	act	ttt	cca	cgg	att	gtc	ttc	atg	ctg	ggc	ttt	gtc	gtg	gtt	1002
Phe	Leu	Thr	Phe	Pro	Arg	Ile	Val	Phe	Met	Leu	Gly	Phe	Val	Val	Val	
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Cys	Gln	Arg	Cys	Pro	Leu	Val	Ala	Trp	Pro	Pro	Ser	Ala	Glu	Pro	Gln	
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Phe	Ile	His	Arg	Tyr	Tyr	Arg	Arg	Ser	Pro	His	Arg	Pro	Leu	Ala	Gly		
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Ala Arg Leu Ala His Ile Ala Val Gly Ala Phe Cys Leu Gly Ala Thr	
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Leu Gly Thr Ala Phe Leu Thr Glu Thr Lys Leu Ile His Phe Leu Arg	
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His	Met	Phe	Val	Lys	Leu	Lys	Val	Ile	Ala	Glu	Ser	Leu	Ser	Val	Ile	
		120					125					130				
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Leu	Lys	Ser	Val	Leu	Thr	Ala	Phe	Leu	Val	Leu	Trp	Leu	Pro	His	Trp	
	135					140					145					
gga	ttg	tac	att	ttc	tct	ttg	gcc	cag	ctt	ttc	tat	acc	aca	gtt	ctg	634
Gly	Leu	Tyr	Ile	Phe	Ser	Leu	Ala	Gln	Leu	Phe	Tyr	Thr	Thr	Val	Leu	
150				155					160						165	
gly	ctc	tgc	tat	gtt	att	tat	ttc	aca	aag	tta	ctg	ggg	tcc	cca	gaa	682
Val	Leu	Cys	Tyr	Val	Ile	Tyr	Phe	Thr	Lys	Leu	Leu	Gly	Ser	Pro	Glu	
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tca	acc	aag	ctt	caa	act	ctt	cct	gtc	tcc	aga	ata	aca	gat	ctg	tta	730
Ser	Thr	Lys	Leu	Gln	Thr	Leu	Pro	Val	Ser	Arg	Ile	Thr	Asp	Leu	Leu	
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ccc	aat	att	aca	aga	aat	gga	gcg	ttt	ata	aac	tgg	aaa	gag	gct	aaa	778
Pro	Asn	Ile	Thr	Arg	Asn	Gly	Ala	Phe	Ile	Asn	Trp	Lys	Glu	Ala	Lys	
	200					205					210					
ctg	act	tgg	agt	ttt	ttc	aaa	cag	tct	ttc	ttg	aaa	cag	att	ttg	aca	826
Leu	Thr	Trp	Ser	Phe	Phe	Lys	Gln	Ser	Phe	Leu	Lys	Gln	Ile	Leu	Thr	
	215					220					225					
gaa	ggc	gag	cga	tat	gtg	atg	aca	ttt	ttg	aat	gta	ttg	aac	ttt	ggg	874
Glu	Gly	Glu	Arg	Tyr	Val	Met	Thr	Phe	Leu	Asn	Val	Leu	Asn	Phe	Gly	
230				235					240					245		
gat	cag	ggg	gtg	tat	gat	ata	gtg	aat	aat	ctt	ggc	tcc	ctt	gtg	gcc	922
Asp	Gln	Gly	Val	Tyr	Asp	Ile	Val	Asn	Asn	Leu	Gly	Ser	Leu	Val	Ala	
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Arg	Leu	Ile	Phe	Gln	Pro	Ile	Glu	Glu	Ser	Phe	Tyr	Ile	Phe	Phe	Ala	
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Lys	Val	Leu	Glu	Arg	Gly	Lys	Asp	Ala	Thr	Leu	Gln	Lys	Gln	Glu	Asp	
	280					285					290					
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Val	Ala	Val	Ala	Ala	Ala	Val	Leu	Glu	Ser	Leu	Leu	Lys	Leu	Ala	Leu	
	295					300					305					
ctg	gcc	ggc	ctg	acc	atc	act	gtt	ttt	ggc	ttt	gcc	tat	tct	cag	ctg	1114
Leu	Ala	Gly	Leu	Thr	Ile	Thr	Val	Phe	Gly	Phe	Ala	Tyr	Ser	Gln	Leu	
	310				315				320					325		
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Ala	Leu	Asp	Ile	Asn	Gly	Gly	Thr	Met	Leu	Ser	Ser	Gly	Ser	Gly	Pro	
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gtt	ttg	ctg	cgt	tcc	tac	tgt	ctc	tat	gtt	ctc	ctg	ctt	gcc	atc	aat	1210
Val	Leu	Leu	Arg	Ser	Tyr	Cys	Leu	Tyr	Val	Leu	Leu	Leu	Ala	Ile	Asn	
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gga	gtg	aca	gag	tgt	ttc	aca	ttt	gct	gcc	atg	agc	aaa	gag	gag	gtc	1258
Gly	Val	Thr	Glu	Cys	Phe	Thr	Phe	Ala	Ala	Met	Ser	Lys	Glu	Glu	Val	
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gac	agg	tac	aat	ttt	gtg	atg	ctg	gcc	ctg	tcc	tcc	tca	ttc	ctg	gtg	1306


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 375                               380                               385
tta tcc tat ctc ttg acc cgt tgg tgt ggc agc gtg ggc ttc atc ttg      1354
Leu Ser Tyr Leu Leu Thr Arg Trp Cys Gly Ser Val Gly Phe Ile Leu
390                               395                               400                               405
gcc aac tgc ttt aac atg ggc att cgg atc acg cag agc ctt tgc ttc      1402
Ala Asn Cys Phe Asn Met Gly Ile Arg Ile Thr Gln Ser Leu Cys Phe
                               410                               415                               420
atc cac cgc tac tac cga agg agc ccc cac agg ccc ctg gct ggc ctg      1450
Ile His Arg Tyr Tyr Arg Arg Ser Pro His Arg Pro Leu Ala Gly Leu
                               425                               430                               435
cac cta tcg cca gtc ctg ctc ggg aca ttt gcc ctc agt ggt ggg gtt      1498
His Leu Ser Pro Val Leu Leu Gly Thr Phe Ala Leu Ser Gly Gly Val
                               440                               445                               450
act gct gtt tcg gag gta ttc ctc tgc tgt gag cag ggc tgg cca gcc      1546
Thr Ala Val Ser Glu Val Phe Leu Cys Cys Glu Gln Gly Trp Pro Ala
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aga ctg gca cac att gct gtg ggg gcc ttc tgt ctg gga gca act ctc      1594
Arg Leu Ala His Ile Ala Val Gly Ala Phe Cys Leu Gly Ala Thr Leu
470                               475                               480                               485
ggg aca gca ttc ctc aca gag acc aag ctg atc cat ttc ctc agg act      1642
Gly Thr Ala Phe Leu Thr Glu Thr Lys Leu Ile His Phe Leu Arg Thr
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cag tta ggt gtg ccc aga cgc act gac aaa atg acg tgacttcagg      1688
Gln Leu Gly Val Pro Arg Arg Thr Asp Lys Met Thr
                               505                               510
gaagcctgga cacccgaggc acctggacca gctatgggta gttctgtggg tggaacacat      1748
tctgtgtaag agcccccactg agggctctgc agcggagtga cagcaacccc agagatgagg      1808
caccagagag tgccactgca tgagacacct gtgaccattc gaagtctgaa atgcgggggg      1868
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atg ggc aca cag gag ggc tgg tgc ctg ctg ctc tgc ctg gct cta tct      166
Met Gly Thr Gln Glu Gly Trp Cys Leu Leu Leu Cys Leu Ala Leu Ser
-20                               -15                               -10
gga gca gca gaa acc aag ccc cac cca gca gag ggg cag tgg cgg gca      214
Gly Ala Ala Glu Thr Lys Pro His Pro Ala Glu Gly Gln Trp Arg Ala
-5                               1                               5                               10
gtg gac gtg gtc cta gac tgt ttc ctg gtg aag gac ggt gcg cac cgt      262

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Val	Asp	Val	Val	Leu	Asp	Cys	Phe	Leu	Val	Lys	Asp	Gly	Ala	His	Arg	
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Gly	Ala	Leu	Ala	Ser	Ser	Glu	Asp	Arg	Ala	Arg	Ala	Ser	Leu	Val	Leu	
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aag	cag	gtg	cca	gtg	ctg	gac	gat	ggc	tcc	ctg	gag	gac	ttc	acc	gat	358
Lys	Gln	Val	Pro	Val	Leu	Asp	Asp	Gly	Ser	Leu	Glu	Asp	Phe	Thr	Asp	
	45					50					55					
ttc	caa	ggg	ggc	aca	ctg	gcc	caa	gat	gac	cca	cct	att	atc	ttt	gag	406
Phe	Gln	Gly	Gly	Thr	Leu	Ala	Gln	Asp	Asp	Pro	Pro	Ile	Ile	Phe	Glu	
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gcc	tca	gtg	gac	ctg	gtc	cag	att	ccc	cag	gcc	gag	gcc	ttg	ctc	cat	454
Ala	Ser	Val	Asp	Leu	Val	Gln	Ile	Pro	Gln	Ala	Glu	Ala	Leu	Leu	His	
			80					85						90		
gct	gac	tgc	agt	ggg	aag	gag	gtg	acc	tgt	gag	atc	tcc	cgc	tac	ttt	502
Ala	Asp	Cys	Ser	Gly	Lys	Glu	Val	Thr	Cys	Glu	Ile	Ser	Arg	Tyr	Phe	
		95						100					105			
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Leu	Gln	Met	Thr	Glu	Thr	Thr	Val	Lys	Thr	Ala	Ala	Trp	Phe	Met	Ala	
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Asn	Val	Gln	Val	Ser	Gly	Gly	Gly	Pro	Ser	Ile	Ser	Leu	Val	Met	Lys	
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Thr	Pro	Arg	Val	Ala	Lys	Asn	Glu	Val	Leu	Trp	His	Pro	Thr	Leu	Asn	
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ttg	cca	ctg	agc	ccc	cag	ggg	act	gtg	cga	act	gca	gtg	gag	ttc	cag	694
Leu	Pro	Leu	Ser	Pro	Gln	Gly	Thr	Val	Arg	Thr	Ala	Val	Glu	Phe	Gln	
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gtg	atg	aca	cag	acc	caa	tcc	ctg	agc	ttc	ctg	ctg	ggg	tcc	tca	gcc	742
Val	Met	Thr	Gln	Thr	Gln	Ser	Leu	Ser	Phe	Leu	Leu	Gly	Ser	Ser	Ala	
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tcc	ttg	gac	tgt	ggc	ttc	tcc	atg	gca	ccg	ggc	ttg	gac	ctc	atc	agt	790
Ser	Leu	Asp	Cys	Gly	Phe	Ser	Met	Ala	Pro	Gly	Leu	Asp	Leu	Ile	Ser	
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Val	Glu	Trp	Arg	Leu	Gln	His	Lys	Gly	Arg	Gly	Gln	Leu	Val	Tyr	Ser	
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Trp	Thr	Ala	Gly	Gln	Gly	Gln	Ala	Val	Arg	Lys	Gly	Ala	Thr	Leu	Glu	
220					225			230							235	
cct	gca	caa	ctg	ggc	atg	gcc	agg	gat	gcc	tcc	ctc	acc	ctg	ccc	ggc	934
Pro	Ala	Gln	Leu	Gly	Met	Ala	Arg	Asp	Ala	Ser	Leu	Thr	Leu	Pro	Gly	
			240					245						250		
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Leu	Thr	Ile	Gln	Asp	Glu	Gly	Thr	Tyr	Ile	Cys	Gln	Ile	Thr	Thr	Ser	
		255					260						265			
ctg	tac	cga	gct	cag	cag	atc	atc	cag	ctc	aac	atc	caa	gct	tcc	cct	1030
Leu	Tyr	Arg	Ala	Gln	Gln	Ile	Ile	Gln	Leu	Asn	Ile	Gln	Ala	Ser	Pro	
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aaa	gta	cga	ctg	agc	ttg	gca	aac	gaa	gct	ctg	ctg	ccc	acc	ctc	atc	1078
Lys	Val	Arg	Leu	Ser	Leu	Ala	Asn	Glu	Ala	Leu	Leu	Pro	Thr	Leu	Ile	
	285					290					295					
tgc	gac	att	gct	ggc	tat	tac	cct	ctg	gat	gtg	gtg	gtg	acg	tgg	acc	1126
Cys	Asp	Ile	Ala	Gly	Tyr	Tyr	Pro	Leu	Asp	Val	Val	Val	Thr	Trp	Thr	
300					305			310							315	
cga	gag	gag	ctg	ggc	gga	tcc	cca	gcc	caa	gtc	tct	ggc	tcc	ttc		1174
Arg	Glu	Glu	Leu	Gly	Gly	Ser	Pro	Ala	Gln	Val	Ser	Gly	Ala	Ser	Phe	

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Ser Ser Leu Arg Gln Ser Val Ala Gly Thr Tyr Ser Ile Ser Ser Ser				
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Leu Thr Ala Glu Pro Gly Ser Ala Gly Ala Thr Tyr Thr Cys Gln Val				
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Thr His Ile Ser Leu Glu Glu Pro Leu Gly Ala Ser Thr Gln Val Val				
	365	370	375	
cca cca gag cgg aga aca gcc ttg gga gtc atc ttt gcc agc agt ctc				1366
Pro Pro Glu Arg Arg Thr Ala Leu Gly Val Ile Phe Ala Ser Ser Leu				
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ttc ctt ctt gca ctg atg ttc ctg ggg ctt cag aga cgg caa gca cct				1414
Phe Leu Leu Ala Leu Met Phe Leu Gly Leu Gln Arg Arg Gln Ala Pro				
	400	405	410	
aca gga ctt ggg ctg ctt cag gct gaa cgc tgg gag acc act tcc tgt				1462
Thr Gly Leu Gly Leu Leu Gln Ala Glu Arg Trp Glu Thr Thr Ser Cys				
	415	420	425	
gct gac aca cag agc tcc cat ctc cat gaa gac cgc aca gcg cgt gta				1510
Ala Asp Thr Gln Ser Ser His Leu His Glu Asp Arg Thr Ala Arg Val				
	430	435	440	
agc cag ccc agc tgacctaaag cgacatgaga ctactagaaa gaaacgacac				1562
Ser Gln Pro Ser				
	445			
ccttccccaa gccccacag ctactccaac ccaaacaaca accaagccag tttaatggta				1622
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ttcttccatg tgaagtgtg tcgggctctg ggctgacgag agaacacctg gtaaccaggt	300
tagccctctg tcagtcaccc agggcagggc agc atg gtg cgg att cag agg agg	354
	Met Val Arg Ile Gln Arg Arg
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Lys Leu Leu Ala Ser Cys Leu Cys Val Thr Ala Thr Val Phe Leu Leu	
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tgg	cct	tta	tct	aac	acc	agg	agc	agc	gag	cac	ata	aaa	gag	gtc	atg		546
Trp	Pro	Leu	Ser	Asn	Thr	Arg	Ser	Ser	Glu	His	Ile	Lys	Glu	Val	Met		
25					30					35					40		
ggt	gag	ctg	ggg	aag	ttt	gaa	agg	aag	gag	ttt	aaa	agt	tcc	agt	ttg		594
Val	Glu	Leu	Gly	Lys	Phe	Glu	Arg	Lys	Glu	Phe	Lys	Ser	Ser	Ser	Leu		
			45			50								55			
caa	gat	gga	cat	aca	aaa	atg	gag	gaa	gca	cct	acg	cat	ctt	aat	tca		642
Gln	Asp	Gly	His	Thr	Lys	Met	Glu	Glu	Ala	Pro	Thr	His	Leu	Asn	Ser		
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Phe	Leu	Lys	Lys	Glu	Gly	Leu	Thr	Phe	Asn	Arg	Lys	Arg	Lys	Trp	Glu		
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Leu	Asp	Ser	Tyr	Pro	Ile	Met	Leu	Trp	Trp	Ser	Pro	Leu	Thr	Gly	Glu		
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Asn	Arg	Thr	Tyr	Leu	His	His	His	Met	Thr	Lys	Ala	Phe	Leu	Phe	Tyr		
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Gly	Thr	Asp	Phe	Asn	Ile	Asp	Ser	Leu	Pro	Leu	Pro	Arg	Lys	Ala	His		
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His	Asp	Trp	Ala	Val	Phe	His	Glu	Glu	Ser	Pro	Lys	Asn	Asn	Tyr	Lys		
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Asp	Pro	Pro	Ser	Asp	Arg	Asp	Ser	Tyr	Val	Arg	Glu	Leu	Met	Thr	Tyr		
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Ile	Glu	Val	Asp	Ser	Tyr	Gly	Glu	Cys	Leu	Arg	Asn	Lys	Asp	Leu	Pro		
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cag	cag	ctg	aaa	aat	cca	gcc	tct	atg	gat	gcc	gat	ggc	ttt	tat	agg		1266
Gln	Gln	Leu	Lys	Asn	Pro	Ala	Ser	Met	Asp	Ala	Asp	Gly	Phe	Tyr	Arg		
	265				270					275					280		
atc	att	gca	cag	tat	aag	ttt	atc	cta	gct	ttt	gag	aat	gca	gtt	tgt		1314
Ile	Ile	Ala	Gln	Tyr	Lys	Phe	Ile	Leu	Ala	Phe	Glu	Asn	Ala	Val	Cys		
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gat	gac	tac	atc	act	gag	aag	ttc	tgg	agg	cca	ctg	aaa	ctg	ggg	gta		1362
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Val Pro Val Tyr Tyr Gly Ser Pro Ser Ile Thr Asp Trp Leu Pro Ser
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Asn Lys Ser Ala Ile Leu Val Ser Glu Phe Ser His Pro Arg Glu Leu
      330      335      340
gca agt tac atc aga cga ctg gat tct gat gac aga ttg tat gag gcc   1506
Ala Ser Tyr Ile Arg Arg Leu Asp Ser Asp Asp Arg Leu Tyr Glu Ala
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tat gta gaa tgg aag ctg aag ggt aga tct cta acc agc gac ttc   1551
Tyr Val Glu Trp Lys Leu Lys Gly Arg Ser Leu Thr Ser Asp Phe
      365      370      375
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      Met Gly Ile Gln Thr Ser Pro Val Leu Leu Ala Ser Leu
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Gly Val Gly Leu Val Thr Leu Leu Gly Leu Ala Val Gly Ser Tyr Leu
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Lys Tyr Leu Leu Arg Leu Leu Asp Lys Thr Thr Val Ser His Asn Thr
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Lys Arg Phe Arg Phe Ala Leu Pro Thr Ala His His Thr Leu Gly Leu
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Pro Val Gly Lys His Ile Tyr Leu Ser Thr Arg Ile Asp Gly Ser Leu
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gtc atc agg cca tac act cct gtc acc agt gat gag gat caa ggc tat   398

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 Met Gly Thr Gln Glu Gly
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 Trp Cys Leu Leu Leu Cys Leu Ala Leu Ser Gly Ala Ala Glu Thr Lys
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 Cys Phe Leu Ala Lys Asp Gly Ala His Arg Gly Ala Leu Ala Ser Ser
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 Glu Asp Arg Ala Arg Ala Ser Leu Val Leu Lys Gln Val Pro Val Leu
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 Asp Asp Gly Ser Leu Glu Asp Phe Thr Asp Phe Gln Gly Gly Thr Leu
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 Ala Gln Asp Asp Pro Pro Ile Ile Phe Glu Ala Ser Val Asp Leu Val
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Tyr Pro Leu Asp Val Val Val Thr Trp Thr Arg Glu Glu Leu Gly Gly		
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Lys Val Phe Trp Asp Leu Ala Ala Thr Arg Ala Val Phe Gly Val Gln						
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Ser Thr Ala Ala Gly Leu Trp Ala Leu Leu Gly Asp Pro Val Leu His						
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Thr Ala Thr Gly Phe Phe Cys Phe Glu Asn Val Ala Val His Leu Ser						
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aac ttg atc ttc cgg aca ttt gac ttg ttt ctg gtt atc cac cat ctc	614					
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Gly Gln Pro Tyr Arg Val Thr Leu Leu Glu Leu Pro Glu Ser Pro								
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Arg Gly Gly Arg Ile Ile Ser Thr Ser Ser Arg Ser Val Met Leu His								
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Tyr Arg Ser Asp Leu Leu Gln Met Leu Asp Thr Leu Val Phe Ser Ser								
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Ile Ile Glu Ile His Ser Lys Arg Ile Gln Leu Tyr Gly Ala Tyr Leu								
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Arg Ile His Ala His Phe Thr Gly Leu Arg Tyr Leu Leu Tyr Asn Phe								
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Trp Pro Arg His Arg Phe Ser Leu Val Asn Ile Arg Lys Arg Asp								
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aat tcc cgg aag gaa gtc caa cga agg atc tct gct cat cag cca ggg								1098
Asn Ser Arg Lys Glu Val Gln Arg Arg Ile Ser Ala His Gln Pro Gly								
	260			265		270		
cct gaa ggc cag gag gag tca act ccg caa tca gat gtt aca gag gat								1146
Pro Glu Gly Gln Glu Glu Ser Thr Pro Gln Ser Asp Val Thr Glu Asp								
	275			280		285		
ggt gag agc cct gaa gat ccc tca ggg aca gag ggt cag ctg tcc gag								1194
Gly Glu Ser Pro Glu Asp Pro Ser Gly Thr Glu Gly Gln Leu Ser Glu								
	290			295		300		305
gag gag aaa cca gat cag cag ccc ctg agc gga gaa gag gag cta gag								1242
Glu Glu Lys Pro Asp Gln Gln Pro Leu Ser Gly Glu Glu Glu Leu Glu								
	310			315		320		
cct gag gcc agt gat ggt tca ggc tcc tgg gaa gat gca gct ttg ctg								1290
Pro Glu Ala Ser Asp Gly Ser Gly Ser Trp Glu Asp Ala Ala Leu Leu								
	325			330		335		
acg gag gcc aac ctg cct gct cct gct cct gct tct gct tct gcc cct								1338
Thr Glu Ala Asn Leu Pro Ala Pro Ala Pro Ala Ser Ala Ser Ala Pro								
	340			345		350		
gtc cta gag act ctg ggc agc tct gaa cct gct ggg ggt gct ctc cga								1386
Val Leu Glu Thr Leu Gly Ser Ser Glu Pro Ala Gly Gly Ala Leu Arg								
	355			360		365		

<210> 49
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 <213> Homo sapiens

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 <222> 234..491

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 <222> 234..293
 <223> Von Heijne matrix
 score 4.85037394589162
 seq AVAGLPALGFTGA/GI

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 gtttactcgc tgctgtgccc atctatcagc aggetccggg ctgaagattg cttctcttct 60
 ctctccaag gtctagtac ggagcccgcg cgcggcgcca ccatgcggca gaaggcggta 120
 tcgttttct ctgctacctg ctgctcttca cttgcagtgg ggtggaggca ggtaagaaaa 180
 agtgcctgga gagctcggac agcggctccg ggttctggaa ggccctgacc ttc atg 236
 Met
 -20
 gcc gtc gga gga gga ctc gca gtc gcc ggg ctg ccc gcg ctg ggc ttc 284
 Ala Val Gly Gly Gly Leu Ala Val Ala Gly Leu Pro Ala Leu Gly Phe
 -15 -10 -5
 acc ggc gcc ggc atc gcg gcc aac tcg gtg gct gcc tcg ctg atg agc 332
 Thr Gly Ala Gly Ile Ala Ala Asn Ser Val Ala Ala Ser Leu Met Ser
 1 5 10
 tgg tct gcg atc ctg aat ggg ggc ggc gtg ccc gcc ggg ggg cta gtg 380
 Trp Ser Ala Ile Leu Asn Gly Gly Gly Val Pro Ala Gly Gly Leu Val
 15 20 25
 gcc acg ctg cag agc ctc ggg gct ggt ggc agc agc gtc gtc ata ggt 428
 Ala Thr Leu Gln Ser Leu Gly Ala Gly Gly Ser Ser Val Val Ile Gly
 30 35 40 45
 aat att ggt gcc ctg atg ggc tac gcc acc cac aag tat ctc gat agt 476
 Asn Ile Gly Ala Leu Met Gly Tyr Ala Thr His Lys Tyr Leu Asp Ser
 50 55 60
 gag gag gat gag gag tagccagcag ctcccagaac ctcttcttcc ttcttggcct 531
 Glu Glu Asp Glu Glu
 65
 aactcttcca gttaggatct agaactttgc cttttttttt tttttttttt tttttttgag 591
 atgggttctc actatattgt ccaggctaga gtgcagtggc tattcacaga tgcgaacata 651
 gtacactgca gcctccaact cctagcctca agtgatcctc ctgtctcaac ctcccaagta 711
 ggattacaag catgcgccga cgatgccag aatccagaac tttgtctatc actctcccca 771
 acaacctaga tgtgaaaaca gaataaactt caccagaaa gcaaaaaaaaa aaaaaaaaaa 831

<210> 50
 <211> 917
 <212> DNA
 <213> Homo sapiens

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 <222> 180..800

<220>
 <221> sig_peptide

<222> 180..248
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 score 14.6828672385356
 seq ILLLLWLIAPSRA/CT

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 acccttggct tctgcactga tgggtgggtgg atgagtaatg catccaggaa gcctggaggc 60
 ctgtgggtttc cgcaccccgct gccacccccg cccctagcgt ggacatttat cctctagcgc 120
 tcaggccctg cgcgccatgc cgcagatcca gcgcccagag agacaccaga gaaccacc 179
 atg gcc ccc ttt gag ccc ctg gct tct ggc atc ctg ttg ttg ctg tgg 227
 Met Ala Pro Phe Glu Pro Leu Ala Ser Gly Ile Leu Leu Leu Leu Trp
 -20 -15 -10
 ctg ata gcc ccc agc agg gcc tgc acc tgt gtc cca ccc cac cca cag 275
 Leu Ile Ala Pro Ser Arg Ala Cys Thr Cys Val Pro Pro His Pro Gln
 -5 1 5
 acg gcc ttc tgc aat tcc gac ctc gtc atc agg gcc aag ttc gtg ggg 323
 Thr Ala Phe Cys Asn Ser Asp Leu Val Ile Arg Ala Lys Phe Val Gly
 10 15 20 25
 aca cca gaa gtc aac cag acc acc tta tac cag cgt tat gag atc aag 371
 Thr Pro Glu Val Asn Gln Thr Thr Leu Tyr Gln Arg Tyr Glu Ile Lys
 30 35 40
 atg acc aag atg tat aaa ggg ttc caa gcc tta ggg gat gcc gct gac 419
 Met Thr Lys Met Tyr Lys Gly Phe Gln Ala Leu Gly Asp Ala Ala Asp
 45 50 55
 atc cgg ttc gtc tac acc ccc gcc atg gag agt gtc tgc gga tac ttc 467
 Ile Arg Phe Val Tyr Thr Pro Ala Met Glu Ser Val Cys Gly Tyr Phe
 60 65 70
 cac agg tcc cac aac cgc agc gag gag ttt ctc att gct gga aaa ctg 515
 His Arg Ser His Asn Arg Ser Glu Glu Phe Leu Ile Ala Gly Lys Leu
 75 80 85
 cag gat gga ctc ttg cac atc act acc tgc agt ttt gtg gct ccc tgg 563
 Gln Asp Gly Leu Leu His Ile Thr Thr Cys Ser Phe Val Ala Pro Trp
 90 95 100 105
 aac agc ctg agc tta gct cag cgc cgg ggc ttc acc aag acc tac act 611
 Asn Ser Leu Ser Leu Ala Gln Arg Arg Gly Phe Thr Lys Thr Tyr Thr
 110 115 120
 gtt ggc tgt gag gaa tgc aca gtg ttt ccc tgt tta tcc ttc ccc tgc 659
 Val Gly Cys Glu Glu Cys Thr Val Phe Pro Cys Leu Ser Phe Pro Cys
 125 130 135
 aaa ctg cag agt ggc act cat tgc ttg tgg acg gac cag ctc ctc caa 707
 Lys Leu Gln Ser Gly Thr His Cys Leu Trp Thr Asp Gln Leu Leu Gln
 140 145 150
 ggc tct gaa aag ggc ttc cag tcc cgt cac ctt gcc tgc ctg cct cgg 755
 Gly Ser Glu Lys Gly Phe Gln Ser Arg His Leu Ala Cys Leu Pro Arg
 155 160 165
 gag cca ggg ctg tgc acc tgg cag tcc ctg cgg tcc cag ata gcc 800
 Glu Pro Gly Leu Cys Thr Trp Gln Ser Leu Arg Ser Gln Ile Ala
 170 175 180
 tgaatcctgc ccggagtggg agctgaagcc tgcacagtgt ccaccctgtt cccactccca 860
 tctttcttcc ggacaatgaa ataaagagtt accaccacgc aaaaaaaaaa aaaaaaa 917

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 <211> 621
 <212> DNA
 <213> Homo sapiens

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<222> 140..472

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<221> sig_peptide

<222> 140..211

<223> Von Heijne matrix

score 8.44884907465122

seq FVVFSFLICAMA/GD

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ggagaagatg ctggaaattc agagtttccg ccagagaata tatgcctgaa ctaaaagagg 120

aagtggctca taggagaaa atg aaa tat gat tgt ccc ttc agt ggg aca tca 172

Met Lys Tyr Asp Cys Pro Phe Ser Gly Thr Ser

-20

-15

ttt gtg gtc ttc tct ctc ttt ttg atc tgt gca atg gct gga gat gta 220

Phe Val Val Phe Ser Leu Phe Leu Ile Cys Ala Met Ala Gly Asp Val

-10

-5

1

gtc tac gct gac atc aaa act gtt cgg act tcc ccg tta gaa ctc gcg 268

Val Tyr Ala Asp Ile Lys Thr Val Arg Thr Ser Pro Leu Glu Leu Ala

5

10

15

ttt cca ctt cag aga tct gtt tct ttc aac ttt tct act gtc cat aaa 316

Phe Pro Leu Gln Arg Ser Val Ser Phe Asn Phe Ser Thr Val His Lys

20

25

30

35

tca tgt cct gcc aaa gac tgg aag gtg cat aag gga aaa tgt tac tgg 364

Ser Cys Pro Ala Lys Asp Trp Lys Val His Lys Gly Lys Cys Tyr Trp

40

45

50

att gct gaa act aag aaa tct tgg aac aaa agt caa aat gac tgt gcc 412

Ile Ala Glu Thr Lys Lys Ser Trp Asn Lys Ser Gln Asn Asp Cys Ala

55

60

ata aac aat tca tat ctc atg gtg att caa gac att act gct atg gtg 460

Ile Asn Asn Ser Tyr Leu Met Val Ile Gln Asp Ile Thr Ala Met Val

70

75

80

aga ttt aac att tagaggtgac agcatccccc acactggcag ttaatttttt 512

Arg Phe Asn Ile

85

gtctacaaac ttggcaaaag tctgtgaaaa gaagtttcaa cttcatgtgt tattaactat 572

acaaatatta gttgaatgaa ttgttgaatt acaaaaaaaaa aaaaaaaaaa 621

<210> 52

<211> 673

<212> DNA

<213> Homo sapiens

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<221> CDS

<222> 68..484

<220>

<221> sig_peptide

<222> 68..112

<223> Von Heijne matrix

score 4.93618539864455

seq AVVFVFSLLDCCA/LI

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ctatcagggg tgggtcgggg catccgagcg ggtttgacgg aaggagcggc ggcgacggag 60

gaggagg atg gag gcg gtg gtg ttc gtc ttc tct ctc ctc gat tgt tgc 109

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      Met Glu Ala Val Val Phe Val Phe Ser Leu Leu Asp Cys Cys
      -15          -10          -5
gcg ctc atc ttc ctc tcg gtc tac ttc ata att aca ttg tct gat tta      157
Ala Leu Ile Phe Leu Ser Val Tyr Phe Ile Ile Thr Leu Ser Asp Leu
  1          5          10          15
gaa tgt gat tac att aat gct aga tca tgt tgc tca aaa tta aac aag      205
Glu Cys Asp Tyr Ile Asn Ala Arg Ser Cys Cys Ser Lys Leu Asn Lys
      20          25          30
tgg gta att cca gaa ttg att ggc cat acc att gtc act gta tta ctg      253
Trp Val Ile Pro Glu Leu Ile Gly His Thr Ile Val Thr Val Leu Leu
      35          40          45
ctc atg tca ttg cac tgg ttc atc ttc ctt ctc aac tta cct gtt gcc      301
Leu Met Ser Leu His Trp Phe Ile Phe Leu Leu Asn Leu Pro Val Ala
      50          55          60
act tgg aat ata tat cga tac att atg gtg ccg agt ggt aac atg gga      349
Thr Trp Asn Ile Tyr Arg Tyr Ile Met Val Pro Ser Gly Asn Met Gly
      65          70          75
gtg ttt gat cca aca gaa ata cac aat cga ggg cag ctg aag lca cac      397
Val Phe Asp Pro Thr Glu Ile His Asn Arg Gly Gln Leu Lys Ser His
      80          85          90          95
atg aaa gaa gcc atg atc aag ctt ggt ttc cac ttg ctc tgc ttc ttc      445
Met Lys Glu Ala Met Ile Lys Leu Gly Phe His Leu Leu Cys Phe Phe
      100          105          110
atg tat ctt tat agt atg atc tta gct ttg ata aat gac tgaagctgga      494
Met Tyr Leu Tyr Ser Met Ile Leu Ala Leu Ile Asn Asp
      115          120
gaagccgtgg ttgaagtcag cctacactac agtgcacagt tgaggagcca gagacttctt      554
aaatcatcct tagaaccgtg accatagcag tatatatattt cctcttgga caaaaaacta      614
tttttgctgt atttttacca tataaagtat ttaaaaaaca cgaaaaaaaa aaaaaaaaaa      673

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<210> 53
 <211> 897
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> 38..517

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 <221> sig_peptide
 <222> 38..118
 <223> Von Heijne matrix
 score 7.20400999800742
 seq VLWLSGLSEPGAA/RQ

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agattgggac agtcgccagg gatggctgag cgtgaag atg cag cgg gtg tcc ggg      55
      Met Gln Arg Val Ser Gly
      -25
ctg ctc tcc tgg acg ctg agc aga gtc ctg tgg ctc tcc ggc ctc tct      103
Leu Leu Ser Trp Thr Leu Ser Arg Val Leu Trp Leu Ser Gly Leu Ser
      -20          -15          -10
gag ccg gga gct gcc cgg cag ccc cgg atc atg gaa gag aaa gcg cta      151
Glu Pro Gly Ala Ala Arg Gln Pro Arg Ile Met Glu Glu Lys Ala Leu
      -5          1          5          10
gag gtt tat gat ttg att aga act atc cgg gac cca gaa aag ccc aat      199
Glu Val Tyr Asp Leu Ile Arg Thr Ile Arg Asp Pro Glu Lys Pro Asn

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      15      20      25
act tta gaa gaa ctg gaa gtg gtc tcg gaa agt tgt gtg gaa gtt cag      247
Thr Leu Glu Glu Leu Glu Val Val Ser Glu Ser Cys Val Glu Val Gln
      30      35      40
gag ata aat gaa gaa gaa tat ctg gtt att atc agg ttc acg cca aca      295
Glu Ile Asn Glu Glu Glu Tyr Leu Val Ile Ile Arg Phe Thr Pro Thr
      45      50      55
gta cct cat tgc tct ttg gcg act ctt att ggg ctg tgc tta aga gta      343
Val Pro His Cys Ser Leu Ala Thr Leu Ile Gly Leu Cys Leu Arg Val
      60      65      70      75
aaa ctt cag cga tgt tta cca ttt aaa cat aag ttg gaa atc tac att      391
Lys Leu Gln Arg Cys Leu Pro Phe Lys His Lys Leu Glu Ile Tyr Ile
      80      85      90
tct gaa gga acc cac tca aca gaa gaa gac atc aat aag cag ata aat      439
Ser Glu Gly Thr His Ser Thr Glu Glu Asp Ile Asn Lys Gln Ile Asn
      95      100      105
gac aaa gag cga gtg gca gct gca atg gaa aac ccc aac tta cgg gaa      487
Asp Lys Glu Arg Val Ala Ala Ala Met Clu Asn Pro Asn Leu Arg Glu
      110      115      120
att gtg gaa cag tgt gtc ctt gaa cct gac tgatagctgt ttttaagagcc      537
Ile Val Glu Gln Cys Val Leu Glu Pro Asp
      125      130
actggcctgt aattgtttga tatatttgta actcttttgta taatgtcaga gactcatggt      597
taatacatag gtgatttgta cctcagagca ttttttaaag gattctttcc aagcgagatt      657
taattataag gtagtaccta atttgttcaa tgtataacat tctcaggatt tgtaacactt      717
aaatgatcag acagaataat attttctagt tattatgtgt aagatgagtt gctatttttc      777
tgatgctcat tctgatacaa ctatttttctg tgtcaaatat ctactgtgcc caaatgtact      837
caattttaat cattactctg taaaataaat aagcagatga ttcttataaa aaaaaaaaaa      897

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<210> 54
 <211> 1101
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> 92..634

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 <221> sig_peptide
 <222> 92..139
 <223> Von Heijne matrix
 score 7.36306712986597
 seq FLLLTCLFITGTS/VS

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ttccagtgtt tctggcagtt ggtccagaag g atg cct cca ttc ctg ctt ctc      112
                               Met Pro Pro Phe Leu Leu Leu
                               -15                               -10
acc tgc ctc ttc atc aca ggc acc tcc gtg tca ccc gtg gcc cta gat      160
Thr Cys Leu Phe Ile Thr Gly Thr Ser Val Ser Pro Val Ala Leu Asp
                               -5                               1                               5
cct tgt tct gct tac atc agc ctg aat gag ccc tgg agg aac act gac      208
Pro Cys Ser Ala Tyr Ile Ser Leu Asn Glu Pro Trp Arg Asn Thr Asp
                               10                               15                               20
cac cag ttg gat gag tct caa ggt cct cct cta tgt gac aac cat gtg      256
His Gln Leu Asp Glu Ser Gln Gly Pro Pro Leu Cys Asp Asn His Val

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25	30	35	
aat ggg gag tgg tac cac ttc acg ggc atg gcg gga gat gcc atg cct			304
Asn Gly Glu Trp Tyr His Phe Thr Gly Met Ala Gly Asp Ala Met Pro			
40	45	50	55
acc ttc tgc ata cca gaa aac cac tgt gga acc cac gca cct gtc tgg			352
Thr Phe Cys Ile Pro Glu Asn His Cys Gly Thr His Ala Pro Val Trp			
	60	65	70
ctc aat ggc agc cac ccc cta gaa ggc gac ggc att gtg caa cgc cag			400
Leu Asn Gly Ser His Pro Leu Glu Gly Asp Gly Ile Val Gln Arg Gln			
	75	80	85
gct tgt gcc agc ttc aat ggg aac tgc tgt ctc tgg aac acc acg gtg			448
Ala Cys Ala Ser Phe Asn Gly Asn Cys Cys Leu Trp Asn Thr Thr Val			
	90	95	100
gaa gtc aag gct tgc cct gga ggc tac tat gtg tat cgt ctg acc aag			496
Glu Val Lys Ala Cys Pro Gly Gly Tyr Tyr Val Tyr Arg Leu Thr Lys			
	105	110	115
ccc agc gtc tgc ttc cac gtc tac tgt ggt cgt gag tac ctt ccc tgt			544
Pro Ser Val Cys Phe His Val Tyr Cys Gly Arg Glu Tyr Leu Pro Cys			
	120	125	130
gct ctt ttt ctc cac caa caa ggc cac agg tgg agt cca aaa gtg ccc			592
Ala Leu Phe Leu His Gln Gln Gly His Arg Trp Ser Pro Lys Val Pro			
	140	145	150
aat tat agg ata tgc agt tac agt ggc aac tat atc tca atc			634
Asn Tyr Arg Ile Cys Ser Tyr Ser Gly Asn Tyr Ile Ser Ile			
	155	160	165
tgaacaacat tgatgtgggg ctaaagatac tctgatttct gagatctctt cttagaactt			694
ctgaaaaatt cctgaagaaa tagaagggga aaggagctat gactttgatc agttcttttt			754
aattttgtct gaattccatt caaacaaaac attagaaaat gaaacattgg gccaggcgca			814
gtggctcatg cctgtaatcc cagcactttg ggaggctgag gcgggtggat cacaagatca			874
ggagttaaag accagcctgg ccaatatggt gaaaccctgt ctctactaga aatacaaaaa			934
ttagacaggc gtggtggcag gcaactgtaa ccccagctac ccgggaggct gaggcaggag			994
aattgcttga acccgggagg tggacgttgc ggtcaggcga aaatcgtgcc attgcactcc			1054
agcctgggtg acagagtgag actctgattc aaaaaaaaaa aaaaaaa			1101

<210> 55
 <211> 1047
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> 27..767

<220>
 <221> sig_peptide
 <222> 27..80
 <223> Von Heijne matrix
 score 8.96664802487992
 seq LFCLAVLAASSFS/KA

<400> 55	
agcagaggcc ctacaccac cgaggc atg ggg ctc cct ggg ctg ttc tgc ttg	53
Met Gly Leu Pro Gly Leu Phe Cys Leu	
-15	-10
gcc gtg ctg gct gcc agc agc ttc tcc aag gca cgg gag gaa gaa att	101
Ala Val Leu Ala Ala Ser Ser Phe Ser Lys Ala Arg Glu Glu Glu Ile	
-5	1
acc cct gtg gtc tcc att gcc tac aaa gtc ctg gaa gtt ttc ccc aaa	149

Thr	Pro	Val	Val	Ser	Ile	Ala	Tyr	Lys	Val	Leu	Glu	Val	Phe	Pro	Lys	
		10					15					20				
ggc	cgc	tgg	gtg	ctc	ata	acc	tgc	tgt	gca	ccc	cag	cca	cca	ccg	ccc	197
Gly	Arg	Trp	Val	Leu	Ile	Thr	Cys	Cys	Ala	Pro	Gln	Pro	Pro	Pro	Pro	
	25					30					35					
atc	acc	tat	tcc	ctc	tgt	gga	acc	aag	aac	atc	aag	gtg	gcc	aag	aag	245
Ile	Thr	Tyr	Ser	Leu	Cys	Gly	Thr	Lys	Asn	Ile	Lys	Val	Ala	Lys	Lys	
	40				45					50					55	
gtg	gtg	aag	acc	cac	gag	ccg	gcc	tcc	ttc	aac	ctc	aac	gtc	aca	ctc	293
Val	Val	Lys	Thr	His	Glu	Pro	Ala	Ser	Phe	Asn	Leu	Asn	Val	Thr	Leu	
				60					65					70		
aag	tcc	agt	cca	gac	ctg	ctc	acc	tac	ttc	tgc	cgg	gcg	tcc	tcc	acc	341
Lys	Ser	Ser	Pro	Asp	Leu	Leu	Thr	Tyr	Phe	Cys	Arg	Ala	Ser	Ser	Thr	
			75					80					85			
tca	ggc	gcc	cat	gtg	gac	agt	gcc	agg	cta	cag	atg	cac	tgg	gag	ctg	389
Ser	Gly	Ala	His	Val	Asp	Ser	Ala	Arg	Leu	Gln	Met	His	Trp	Glu	Leu	
		90					95					100				
tgg	tcc	aag	cca	gtg	tct	gag	ctg	cgg	gcc	aac	ttc	act	ctg	cag	gac	437
Trp	Ser	Lys	Pro	Val	Ser	Glu	Leu	Arg	Ala	Asn	Phe	Thr	Leu	Gln	Asp	
		105				110					115					
aga	ggg	gca	ggc	ccc	agg	gtg	gag	atg	atc	tgc	cag	gcg	tcc	tcg	ggc	485
Arg	Gly	Ala	Gly	Pro	Arg	Val	Glu	Met	Ile	Cys	Gln	Ala	Ser	Ser	Gly	
	120				125					130					135	
agc	cca	cct	atc	acc	aac	agc	ctg	atc	ggg	aag	gat	ggg	cag	gtc	cac	533
Ser	Pro	Pro	Ile	Thr	Asn	Ser	Leu	Ile	Gly	Lys	Asp	Gly	Gln	Val	His	
				140					145					150		
ctg	cag	cag	aga	cca	tgc	cac	agg	cag	cct	gcc	aac	ttc	tcc	ttc	ctg	581
Leu	Gln	Gln	Arg	Pro	Cys	His	Arg	Gln	Pro	Ala	Asn	Phe	Ser	Phe	Leu	
			155					160					165			
ccg	agc	cag	aca	tcg	gac	tgg	ttc	tgg	tgc	cag	gct	gca	aac	aac	gcc	629
Pro	Ser	Gln	Thr	Ser	Asp	Trp	Phe	Trp	Cys	Gln	Ala	Ala	Asn	Asn	Ala	
		170					175					180				
aat	gtc	cag	cac	agc	gcc	ctc	aca	gtg	gtg	ccc	cca	gga	ggg	ttg	ccc	677
Asn	Val	Gln	His	Ser	Ala	Leu	Thr	Val	Val	Pro	Pro	Gly	Gly	Leu	Pro	
		185				190					195					
agg	gca	ccc	acc	atc	gtg	ctg	gtt	ggc	agc	ctt	gcc	tcc	act	gcg	gcc	725
Arg	Ala	Pro	Thr	Ile	Val	Leu	Val	Gly	Ser	Leu	Ala	Ser	Thr	Ala	Ala	
	200				205					210					215	
atc	acc	tcc	agg	atg	ctg	ggc	tgg	acc	acg	tgg	gcc	agg	tgg			767
Ile	Thr	Ser	Arg	Met	Leu	Gly	Trp	Thr	Thr	Trp	Ala	Arg	Trp			
				220					225							
tgaccagaag	atggaggact	ggcaggggtcc	cctggagagc	cccataccttg	ccttgccgct											827
ctacaggagc	acccgcgcgtc	tgagtgaaga	ggagtttggg	gggttcagga	tagggaatgg											887
ggaggtcaga	ggacgcaaag	cagcagccat	gtagaatgaa	ccgtccagag	agccaagcac											947
ggcagaggac	tgcaggccat	cagcgtgcac	tggtcgtatt	tggagttcat	gcaaaatgag											1007
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<210> 56
 <211> 925
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> 4..399

<220>
 <221> sig_peptide

<222> 4..126
 <223> Von Heijne matrix
 score 4.34454795165846
 seq RVVSWLFSIVVFG/SI

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 Met Glu Gly Gly Ala Tyr Gly Ala Gly Lys Ala Gly Gly Ala Phe
 -40 -35 -30
 gac ccc tac acc ctg gtc cgg cag ccg cac acc atc ctg cgc gtc gtg 96
 Asp Pro Tyr Thr Leu Val Arg Gln Pro His Thr Ile Leu Arg Val Val
 -25 -20 -15
 tct tgg ctg ttc tcc ata gtg gtg ttc ggc tcc atc gtg aac gag ggc 144
 Ser Trp Leu Phe Ser Ile Val Val Phe Gly Ser Ile Val Asn Glu Gly
 -10 -5 1 5
 tac ctc aac agc gcc tcc gag ggg gag cag ttc tgc atc tac aac cgc 192
 Tyr Leu Asn Ser Ala Ser Glu Gly Glu Gln Phe Cys Ile Tyr Asn Arg
 10 15 20
 aac ccc aac gcc tgc agc tat ggc gtg gcc gtg ggc gtg ctc gcc ttc 240
 Asn Pro Asn Ala Cys Ser Tyr Gly Val Ala Val Gly Val Leu Ala Phe
 25 30 35
 ctc acc tgc ctg ctg tac ctg gcc ctg gac gtg tac ttc ccg cag atc 288
 Leu Thr Cys Leu Leu Tyr Leu Ala Leu Asp Val Tyr Phe Pro Gln Ile
 40 45 50
 agc agc gtc aag gac cgc aag aaa gcc gtc ctg tcc gac atc ggt gtc 336
 Ser Ser Val Lys Asp Arg Lys Lys Ala Val Leu Ser Asp Ile Gly Val
 55 60 65 70
 tcg ggt gag ccc cac cca gca ggt acc ccc tgc aca gag tct aca gag 384
 Ser Gly Glu Pro His Pro Ala Gly Thr Pro Cys Thr Glu Ser Thr Glu
 75 80 85
 ggc tgt ccc ggg cca taggaggcgg ctgccaccct tcttcccatg tttcagatga 439
 Gly Cys Pro Gly Pro
 90
 gggaaatgag ccttctgggc tttcctctggg ttctgtgggat tctgtctacct ggccaaccag 499
 tggcaggtct ccaagcccaa ggacaaccca ctgaacgaag ggacggacgc agcccgggcc 559
 gccatcgccct tctccttttt ctccatcttc acctggagcc tgaccgcagc cctggccgtg 619
 cggagattca aggacctaag cttccaggag gagtacagca cactgttccc tgcttcggca 679
 cagccgtagg cctcccggc ttgcagaggc cggcagccct gtatcaccac tggcagtgag 739
 gtggcaggag cagcctagtg ccagaaatgt ccaagatgcc agggcatgca gggcagtgga 799
 aggctggcctt gaggaaccaa ttcaggttct ccaactgactc attcattcct tcaccgcctc 859
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 aaaaaa 925

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 <213> Homo sapiens

<220>
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 <222> 127..879

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 <222> 127..198
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 score 5.38660866264012
 seq ALCSVCSMSVLRA/YP

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agtctaggat cctcacacca gctacttgca agggagaagg aaaaggccag taaggcctgg      60
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ggcacg atg ttg ggg gcc cgc ctc agg ctc tgg gtc tgt gcc ttg tgc      168
      Met Leu Gly Ala Arg Leu Arg Leu Trp Val Cys Ala Leu Cys
      -20                               -15
agc gtc tgc agc atg agc gtc ctc aga gcc tat ccc aat gcc tcc cca      216
Ser Val Cys Ser Met Ser Val Leu Arg Ala Tyr Pro Asn Ala Ser Pro
-10                               -5                               1                               5
ctg ctc ggc tcc agc tgg ggt ggc ctg atc cac ctg tac aca gcc aca      264
Leu Leu Gly Ser Ser Trp Gly Gly Leu Ile His Leu Tyr Thr Ala Thr
      10                               15                               20
gcc agg aac agc tac cac ctg cag atc cac aag aat ggc cat gtg gat      312
Ala Arg Asn Ser Tyr His Leu Gln Ile His Lys Asn Gly His Val Asp
      25                               30                               35
ggc gca ccc cat cag acc atc tac agt gcc ctg atg atc aga tca gag      360
Gly Ala Pro His Gln Thr Ile Tyr Ser Ala Leu Met Ile Arg Ser Glu
      40                               45                               50
gat gct ggc ttt gtg gtg att aca ggt gtg atg agc aga aga tac ctc      408
Asp Ala Gly Phe Val Val Ile Thr Gly Val Met Ser Arg Arg Tyr Leu
      55                               60                               65                               70
tgc atg gat ttc aga ggc aac att ttt gga tca cac tat ttc gac ccg      456
Cys Met Asp Phe Arg Gly Asn Ile Phe Gly Ser His Tyr Phe Asp Pro
      75                               80                               85
gag aac tgc agg ttc caa cac cag acg ctg gaa aac ggg tac gac gtc      504
Glu Asn Cys Arg Phe Gln His Gln Thr Leu Glu Asn Gly Tyr Asp Val
      90                               95                               100
tac cac tct cct cag tat cac ttc ctg gtc agt ctg ggc cgg gcg aag      552
Tyr His Ser Pro Gln Tyr His Phe Leu Val Ser Leu Gly Arg Ala Lys
      105                               110                               115
aga gcc ttc ctg cca ggc atg aac cca ccc ccg tac tcc cag ttc ctg      600
Arg Ala Phe Leu Pro Gly Met Asn Pro Pro Pro Tyr Ser Gln Phe Leu
      120                               125                               130
tcc cgg agg aac gag atc ccc cta att cac ttc aac acc ccc ata cca      648
Ser Arg Arg Asn Glu Ile Pro Leu Ile His Phe Asn Thr Pro Ile Pro
      135                               140                               145                               150
cgg cgg cac acc cgg agc gcc gag gac gac tcg gag cgg gac ccc ctg      696
Arg Arg His Thr Arg Ser Ala Glu Asp Asp Ser Glu Arg Asp Pro Leu
      155                               160                               165
aac gtg ctg aag ccc cgg gcc cgg atg acc ccg gcc ccg gcc tcc tgt      744
Asn Val Leu Lys Pro Arg Ala Arg Met Thr Pro Ala Pro Ala Ser Cys
      170                               175                               180
tca cag gag ctc ccg agc gcc gag gac aac agc ccg atg gcc agt gac      792
Ser Gln Glu Leu Pro Ser Ala Glu Asp Asn Ser Pro Met Ala Ser Asp
      185                               190                               195
cca tta ggg gtg gtc agg ggc ggt cga gtg aac acg cac gct ggg gga      840
Pro Leu Gly Val Val Arg Gly Gly Arg Val Asn Thr His Ala Gly Gly
      200                               205                               210
acg ggc ccg gaa ggc tgc cgc ccc ttc gcc aag ttc atc tagggctcgct      889
Thr Gly Pro Glu Gly Cys Arg Pro Phe Ala Lys Phe Ile
      215                               220                               225
ggaagggcac cctctttaac ccatccctca gcaaagcag ctcttcccaa ggaccaggtc      949
ccttgacgtt ccgaggatgg gaaagggtgac aggggcatgt atggaatttg ctgcttctct      1009
gggggtccctt ccacaggagg tctgtgaga accaaccttt gagggcccaag tcatgggggtt      1069
tcaccgcctt cctcactcca tatagaacac ctttcccaat aggaaacccc aacaggtaaa      1129
ctagaaattt ccccttcatt aaggtagaga gaagggtct ctccaacat atttctcttc      1189
cttgtgcctc tctcttttat cacttttaag catgaaaaaa aaaaaaaaaa a      1240

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<210> 58
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 <212> DNA
 <213> Homo sapiens

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 <221> CDS
 <222> 156..566

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 <221> sig_peptide
 <222> 156..221
 <223> Von Heijne matrix
 score 5.67458379966095
 seq LVSMAGRVCLCQG/SA

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cctcactcct ggcgtctgag tctctggcgt agccc atg ctg agt ggg cgg ctg      173
                                Met Leu Ser Gly Arg Leu
                                -20
gtc ctg ggt ctg gtc tcc atg gct ggc cgc gtt tgt ttg tgc cag ggc      221
Val Leu Gly Leu Val Ser Met Ala Gly Arg Val Cys Leu Cys Gln Gly
-15 -10 -5
agc gcg gga tcc ggg gcc atc ggt ccg gtg gag gcc gcc att cgc acg      269
Ser Ala Gly Ser Gly Ala Ile Gly Pro Val Glu Ala Ala Ile Arg Thr
1 5 10 15
aag ttg gag gag gcc ctg agc ccc gag gtg cta gag ctt cgc aac gag      317
Lys Leu Glu Glu Ala Leu Ser Pro Glu Val Leu Glu Leu Arg Asn Glu
20 25 30
agc ggt ggc cac gcg gtc ccg cca ggc agt gag act cac ttc cgc gtg      365
Ser Gly Gly His Ala Val Pro Pro Gly Ser Glu Thr His Phe Arg Val
35 40 45
gct gtg gtg agc tct cgt ttc gag gga ctg agc ccc cta caa cga cac      413
Ala Val Val Ser Ser Arg Phe Glu Gly Leu Ser Pro Leu Gln Arg His
50 55 60
cgg ctg gtc cac gca gcg ctg gcc gag gag ctg gga ggt ccg gtc cat      461
Arg Leu Val His Ala Ala Leu Ala Glu Glu Leu Gly Gly Pro Val His
65 70 75 80
gcg ctg gcc atc cag gca cgg acc ccc gcc cag tgg aga gag aac tct      509
Ala Leu Ala Ile Gln Ala Arg Thr Pro Ala Gln Trp Arg Glu Asn Ser
85 90 95
cag ctg gac act agc ccc cca tgc ctg ggt ggg aac aag aaa act cta      557
Gln Leu Asp Thr Ser Pro Pro Cys Leu Gly Gly Asn Lys Lys Thr Leu
100 105 110
gga acc ccc tgaaccccaa gagagggagg accaggatcc gaatgggctg      606
Gly Thr Pro
115
ggtgagcacg aattaccgag gccttccctt tgatacagtc caggatttgt aagggatgaa      666
gacctctggg cccattctg ttgggggtcca tacatactct ccgaagatag caacttgctt      726
caggtcaaag tgaaccgag aaaagagaag aatcactcac tactgctctt gccctggact      786
attcaggaag ggcagcccg atgttccatg ttaaactctg acagaattgc accagacctg      846
atgagttgga aacaatccta tacattaaaa gaaattacac taacacacacac aacacacac      902

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<210> 59
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<212> DNA
<213> Homo sapiens

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<221> CDS
<222> 35..1657

<220>
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<222> 35..118
<223> Von Heijne matrix
score 3.75144398608723
seq SGLLLQVLFRLIT/FV

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Met Gly Ser Gln Glu Val Leu
-25
ggc cac gcg gcc cgg ctg gcc tcc tcc ggt ctc ctc ctg cag gtg ttg 103
Gly His Ala Ala Arg Leu Ala Ser Ser Gly Leu Leu Leu Gln Val Leu
-20 -15 -10
ttt cgg ttg atc acc ttt gtc ttg aat gca ttt att ctt cgc ttc ctg 151
Phe Arg Leu Ile Thr Phe Val Leu Asn Ala Phe Ile Leu Arg Phe Leu
-5 1 5 10
tca aag gaa atc gtt ggc gta gta aat gta aga cta acg ctg ctt tac 199
Ser Lys Glu Ile Val Gly Val Val Asn Val Arg Leu Thr Leu Leu Tyr
15 20 25
tca acc acc ctc ttc ctg gcc aga gag gcc ttc cgc aga gca tgt ctc 247
Ser Thr Thr Leu Phe Leu Ala Arg Glu Ala Phe Arg Arg Ala Cys Leu
30 35 40
agt ggg ggc acc cag cga gac tgg agc cag acc ctc aac ctg ctg tgg 295
Ser Gly Gly Thr Gln Arg Asp Trp Ser Gln Thr Leu Asn Leu Leu Trp
45 50 55
cta aca gtc ccc ctg ggt gtg ttt tgg tcc tta ttc ctg ggc tgg atc 343
Leu Thr Val Pro Leu Gly Val Phe Trp Ser Leu Phe Leu Gly Trp Ile
60 65 70 75
tgg ttg cag ctg ctt gaa gtg cct gat cct aat gtt gtc cct cac tat 391
Trp Leu Gln Leu Leu Glu Val Pro Asp Pro Asn Val Val Pro His Tyr
80 85 90
gca act gga gtg gtg ctg ttt ggt ctc tcg gca gtg gtg gag ctt cta 439
Ala Thr Gly Val Val Leu Phe Gly Leu Ser Ala Val Val Glu Leu Leu
95 100 105
gga gag ccc ttt tgg gtc ttg gca caa gca cat atg ttt gtg aag ctc 487
Gly Glu Pro Phe Trp Val Leu Ala Gln Ala His Met Phe Val Lys Leu
110 115 120
aag gtg att gca gag agc ctg tcg gta att ctt aag agc gtt ctg aca 535
Lys Val Ile Ala Glu Ser Leu Ser Val Ile Leu Lys Ser Val Leu Thr
125 130 135
gct ttt ctc gtg ctg tgg ttg cct cac tgg gga ttg tac att ttc tct 583
Ala Phe Leu Val Leu Trp Leu Pro His Trp Gly Leu Tyr Ile Phe Ser
140 145 150 155
ttg gcc cag ctt ttc tat acc aca gtt ctg gtg ctc tgc tat gtt att 631
Leu Ala Gln Leu Phe Tyr Thr Thr Val Leu Val Leu Cys Tyr Val Ile
160 165 170
tat ttc aca aag tta ctg ggt tcc cca gaa tca acc aag ctt caa act 679
Tyr Phe Thr Lys Leu Leu Gly Ser Pro Glu Ser Thr Lys Leu Gln Thr
175 180 185
ctt cct gtc tcc aga ata aca gat ctg tta ccc aat att aca aga aat 727

495 500 505
 cgc act gac aaa atg aca tgacttcagg gaagcctgga cacccgaggc 1687
 Arg Thr Asp Lys Met Thr
 510
 acctggacca gctatgggta gttctgtggg tggaacacat tctgtgtaag agccccactg 1747
 agggctctgc agcggagtga cagcaacccc agagatgagg caccagagag tgccactgca 1807
 tgagacacct gtgaccattc gaagtctgaa atgcgggggg ggagtttcat ttttaagtga 1867
 agacaaaaag ccctttaaaa ataatagttt tttatcattt tatagtaatc agcattttct 1927
 cttttactaa tatactcatt ccttttgaaa aaaaaaaaaa aa 1969

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 <213> Homo sapiens

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 <222> 77..937

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 <222> 77..127
 <223> Von Heijne matrix
 score 3.74817238048175
 seq RIVSAALLAFVQT/HL

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 gaggagaaga gagagc atg gag ctg gag agg atc gtc agt gca gcc ctc ctt 112
 Met Glu Leu Glu Arg Ile Val Ser Ala Ala Leu Leu
 -15 -10
 gcc ttt gtc cag aca cac ctc ccg gag gcc gac ctc agt ggc ttg gat 160
 Ala Phe Val Gln Thr His Leu Pro Glu Ala Asp Leu Ser Gly Leu Asp
 -5 1 5 10
 gag gtc atc ttc tcc tat gtg ctt ggg gtc ctg gag gac ctg ggc ccc 208
 Glu Val Ile Phe Ser Tyr Val Leu Gly Val Leu Glu Asp Leu Gly Pro
 15 20 25
 tcg ggc cca tca gag gag aac ttc gat atg gag gct ttc act gag atg 256
 Ser Gly Pro Ser Glu Glu Asn Phe Asp Met Glu Ala Phe Thr Glu Met
 30 35 40
 atg gag gcc tat gtg cct ggc ttc gcc cac atc ccc agg ggc aca ata 304
 Met Glu Ala Tyr Val Pro Gly Phe Ala His Ile Pro Arg Gly Thr Ile
 45 50 55
 ggg gac atg atg cag aag ctc tca ggg cag ctg agc gat gcc agg aac 352
 Gly Asp Met Met Gln Lys Leu Ser Gly Gln Leu Ser Asp Ala Arg Asn
 60 65 70 75
 aaa gag aac ctg caa ccg cag agc tct ggt gtc caa ggt cag gtg ccc 400
 Lys Glu Asn Leu Gln Pro Gln Ser Ser Gly Val Gln Gly Gln Val Pro
 80 85 90
 atc tcc cca gag ccc ctg cag cgg ccc gaa atg ctc aaa gaa gag act 448
 Ile Ser Pro Glu Pro Leu Gln Arg Pro Glu Met Leu Lys Glu Glu Thr
 95 100 105
 agg tct tcg gct gct gct gct gca gac acc caa gat gag gca act ggc 496
 Arg Ser Ser Ala Ala Ala Ala Ala Asp Thr Gln Asp Glu Ala Thr Gly
 110 115 120
 gct gag gag gag ctt ctg cca ggg gtg gat gta ctc ctg gag gtg ttc 544
 Ala Glu Glu Glu Leu Leu Pro Gly Val Asp Val Leu Leu Glu Val Phe
 125 130 135

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cct acc tgt tgc gtg gag cag gcc cag tgg gtg ctg gcc aaa gct cgg      592
Pro Thr Cys Ser Val Glu Gln Ala Gln Trp Val Leu Ala Lys Ala Arg
140          145          150          155
ggg gac ttg gaa gaa gct gtg cag atg ctg gta gag gga aag gaa gag      640
Gly Asp Leu Glu Glu Ala Val Gln Met Leu Val Glu Gly Lys Glu Glu
          160          165          170
ggg cct gca gcc tgg gag ggc ccc aac cag gac ctg ccc aga cgc ctc      688
Gly Pro Ala Ala Trp Glu Gly Pro Asn Gln Asp Leu Pro Arg Arg Leu
          175          180          185
aga ggc ccc caa aag gat gag ctg aag tcc ttc atc ctg cag aag tac      736
Arg Gly Pro Gln Lys Asp Glu Leu Lys Ser Phe Ile Leu Gln Lys Tyr
          190          195          200
atg atg gtg gat agc gca gag gat cag aag att cac cgg ccc atg gct      784
Met Met Val Asp Ser Ala Glu Asp Gln Lys Ile His Arg Pro Met Ala
          205          210          215
ccc aag gag gcc ccc aag aag ctg atc cga tac atc gac aac cag gta      832
Pro Lys Glu Ala Pro Lys Lys Leu Ile Arg Tyr Ile Asp Asn Gln Val
          220          225          230          235
gtg agc acc aaa ggg gag cga ttc aaa gat gtg cgg aac cct gag gcc      880
Val Ser Thr Lys Gly Glu Arg Phe Lys Asp Val Arg Asn Pro Glu Ala
          240          245          250
gag gag atg aag gcc aca tac atc aac ctc aag cca gcc aga aag tac      928
Glu Glu Met Lys Ala Thr Tyr Ile Asn Leu Lys Pro Ala Arg Lys Tyr
          255          260          265
cgc ttc cat tgaggcactc gccggactct gcccgagcct tctaggctca      977
Arg Phe His
          270
gatcccagag ggatgcagga gccctataacc cctacacagg ggccccctaa ctctgtccc      1037
ccttctctac tcctttgtc catagtgtta acctactctc ggagctgcct ccatgggcac      1097
agtaaagggtg gcccaaggaa aaaaaaaaaa aaaaa      1132

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<212> DNA
<213> Homo sapiens

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<221> CDS
<222> 9..503

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<221> sig_peptide
<222> 9..113
<223> Von Heijne matrix
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      seq LLPLVLLPPLAAA/AA

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tgccaggg atg atg cgc tgc tgc cgc cgc cgc tgc tgc tgc cgg caa cca      50
      Met Met Arg Cys Cys Arg Arg Arg Cys Cys Cys Arg Gln Pro
      -35          -30          -25
ccc cat gcc ctg agg ccg ttg ctg ttg ctg ccc ctc ctt tta cct      98
Pro His Ala Leu Arg Pro Leu Leu Leu Leu Pro Leu Val Leu Leu Pro
      -20          -15          -10
ccc ctg gca gca gct gca gcg ggc cca aac cga tgt gac acc ata tac      146
Pro Leu Ala Ala Ala Ala Ala Gly Pro Asn Arg Cys Asp Thr Ile Tyr
      -5          1          5          10
cag ggc ttc gcc gag tgt ctc atc cgc ttg ggg gac agc atg ggc cgc      194

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Gln	Gly	Phe	Ala	Glu	Cys	Leu	Ile	Arg	Leu	Gly	Asp	Ser	Met	Gly	Arg	
			15					20					25			
gga	ggc	gag	ctg	gag	acc	atc	tgc	agg	tct	tgg	aat	tac	ttc	cat	gcc	242
Gly	Gly	Glu	Leu	Glu	Thr	Ile	Cys	Arg	Ser	Trp	Asn	Tyr	Phe	His	Ala	
		30					35				40					
tgt	gcc	tct	cag	gtc	ctg	tca	ggc	tgt	ccg	gag	gag	gca	gct	gca	gtg	290
Cys	Ala	Ser	Gln	Val	Leu	Ser	Gly	Cys	Pro	Glu	Glu	Ala	Ala	Ala	Val	
	45					50				55						
tgg	gaa	tca	cta	cag	caa	gaa	gct	cgc	cag	gcc	ccc	cgt	ccg	aat	aac	338
Trp	Glu	Ser	Leu	Gln	Gln	Glu	Ala	Arg	Gln	Ala	Pro	Arg	Pro	Asn	Asn	
60					65				70					75		
ttg	cac	act	ctg	tgc	ggg	gcc	ccg	gtg	cat	ggt	cgg	gag	cgc	ggc	aca	386
Leu	His	Thr	Leu	Cys	Gly	Ala	Pro	Val	His	Val	Arg	Glu	Arg	Gly	Thr	
			80				85						90			
ggc	tcc	gaa	acc	aac	cag	gag	acg	ctg	cgg	gct	aca	gcg	cct	gca	ctc	434
Gly	Ser	Glu	Thr	Asn	Gln	Glu	Thr	Leu	Arg	Ala	Thr	Ala	Pro	Ala	Leu	
		95					100				105					
ccc	atg	gcc	cct	ggg	ccc	cca	ctg	ctg	ggg	gct	gct	ctg	gct	ctg	gcc	482
Pro	Met	Ala	Pro	Ala	Pro	Pro	Leu	Leu	Ala	Ala	Ala	Leu	Ala	Leu	Ala	
	110						115				120					
tac	ctc	ctg	agg	cct	ctg	gcc	tagcttggtg	gggtgggtag	cagcgcccg							533
Tyr	Leu	Leu	Arg	Pro	Leu	Ala										
	125					130										
acctccagcc	ctgctctggc	gggtggttg	gc	caggtctgc	agagcgcagc	agggcttttc										593
attaaaggta	tttatatttg	caaaaaaaaa	aaaaaaaa													631

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 <213> Homo sapiens

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 score 5.38058532480537
 seq AVTSLLSPTPATA/LA

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	Met	Ala	Ser	Val	Val	Leu	Ala	Leu	Arg	Thr	Arg					
	-25				-20						-15					
aca	gcc	ggt	aca	tcc	ttg	cta	agc	ccc	act	ccg	gct	aca	gct	ctt	gct	101
Thr	Ala	Val	Thr	Ser	Leu	Leu	Ser	Pro	Thr	Pro	Ala	Thr	Ala	Leu	Ala	
			-10				-5							1		
gtc	aga	tac	gca	tcc	aag	aag	tcg	ggg	ggg	agc	tcc	aaa	aac	ctc	ggg	149
Val	Arg	Tyr	Ala	Ser	Lys	Lys	Ser	Gly	Gly	Ser	Ser	Lys	Asn	Leu	Gly	
	5					10					15					
gga	aag	tca	tca	ggc	aga	cgc	caa	ggc	att	aag	aaa	atg	gaa	ggg	cac	197
Gly	Lys	Ser	Ser	Gly	Arg	Arg	Gln	Gly	Ile	Lys	Lys	Met	Glu	Gly	His	
	20				25				30							
tat	ggt	cat	gct	ggg	aac	atc	att	gca	aca	cag	cgc	cat	ttc	cgc	tgg	245
Tyr	Val	His	Ala	Gly	Asn	Ile	Ile	Ala	Thr	Gln	Arg	His	Phe	Arg	Trp	
35					40				45						50	

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cac cca ggt gcc cat gtg ggt gtt ggg aag aat aaa tgt ctg tat gcc      293
His Pro Gly Ala His Val Gly Val Gly Lys Asn Lys Cys Leu Tyr Ala
                    55                                60                                65
ctg gaa gag ggg ata gtc cgc tac act aag gag gtc tac gtg cct cat      341
Leu Glu Glu Gly Ile Val Arg Tyr Thr Lys Glu Val Tyr Val Pro His
                    70                                75                                80
ccc aga aac acg gag gct gtg gat ctg atc acc agg ctg ccc aag ggt      389
Pro Arg Asn Thr Glu Ala Val Asp Leu Ile Thr Arg Leu Pro Lys Gly
                    85                                90                                95
gct gtg ctc tac aag act ttt gtc cac gtg gtt cct gcc aag cct gag      437
Ala Val Leu Tyr Lys Thr Phe Val His Val Val Pro Ala Lys Pro Glu
                    100                               105                               110
ggc acc ttc aaa ctg gta gct atg ctt tgatgtcctg ttgaggccat      484
Gly Thr Phe Lys Leu Val Ala Met Leu
                    115                               120
cggacagaga ctggagccca ggtgacagga gatggtgata ccagaagtca aggggtgggg      544
tggcgacacg gcctcccag gaagaggtct gcttgatggt gactctgcag gagactctga      604
agtgactgct gggaaaccct ttgggaqacc tgacctgggg ccaaaaataa agtgagccag      664
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<211> 1442
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
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<220>
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<222> 178..279
<223> Von Heijne matrix
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      seq FLCLLSALLLTEG/KK

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gcagagatac agaggcagag gaaaagggca ctcctatgtg acctgttctt agagcaagac      120
aatcaccatc tgaattccag aagccctggt catggttggg gatattttct cgactgc      177
atg gaa tca gaa aga agc aaa agg atg gga aat gcc tgc att ccc ctg      225
Met Glu Ser Glu Arg Ser Lys Arg Met Gly Asn Ala Cys Ile Pro Leu
                    -30                                -25                                -20
aaa aga att gct tat ttc cta tgt ctc tta tct gcg ctt ttg ctg act      273
Lys Arg Ile Ala Tyr Phe Leu Cys Leu Leu Ser Ala Leu Leu Thr
                    -15                                -10                                -5
gag ggg aag aaa cca gcg aag cca aaa tgc cct gcc gtg tgt act tgt      321
Glu Gly Lys Lys Pro Ala Lys Pro Lys Cys Pro Ala Val Cys Thr Cys
                    1                                5                                10
acc aaa gat aat gct tta tgt gag aat gcc aga tcc att cca cgc acc      369
Thr Lys Asp Asn Ala Leu Cys Glu Asn Ala Arg Ser Ile Pro Arg Thr
                    15                                20                                25                                30
gtt cct cct gat gtt atc tca tta tcc ttt gtg aga tct ggt ttt act      417
Val Pro Pro Asp Val Ile Ser Leu Ser Phe Val Arg Ser Gly Phe Thr
                    35                                40                                45
gaa atc tca gaa ggg agt ttt tta ttc acg cca tcg ctg cag ctc ttg      465
Glu Ile Ser Glu Gly Ser Phe Leu Phe Thr Pro Ser Leu Gln Leu Leu
                    50                                55                                60

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tta ttc aca tcg aac tcc ttt gat gtg atc agt gat gat gct ttt att      513
Leu Phe Thr Ser Asn Ser Phe Asp Val Ile Ser Asp Asp Ala Phe Ile
      65      70      75

ggg ctt cca cat cta gag tat tta ttc ata gaa aac aac aac atc aag      561
Gly Leu Pro His Leu Glu Tyr Leu Phe Ile Glu Asn Asn Asn Ile Lys
      80      85      90

tca att tca aga cat act ttc cgg gga cta aag tca tta att cac ttg      609
Ser Ile Ser Arg His Thr Phe Arg Gly Leu Lys Ser Leu Ile His Leu
      95      100      105      110

agc ctt gca aac aac aat ctc cag aca ctc cca aaa gat att ttc aaa      657
Ser Leu Ala Asn Asn Asn Leu Gln Thr Leu Pro Lys Asp Ile Phe Lys
      115      120      125

ggc ctg gat tct tta aca aat gtg gac ctg agg ggt aat tca ttt aat      705
Gly Leu Asp Ser Leu Thr Asn Val Asp Leu Arg Gly Asn Ser Phe Asn
      130      135      140

tgt gac tgt aaa ctg aaa tgg cta gtg gaa tgg ctt ggc cac acc aat      753
Cys Asp Cys Lys Leu Lys Trp Leu Val Glu Trp Leu Gly His Thr Asn
      145      150      155

gca act gtt gaa gac atc tac tgc gaa ggc ccc cca gaa tac aag aag      801
Ala Thr Val Glu Asp Ile Tyr Cys Glu Gly Pro Pro Glu Tyr Lys Lys
      160      165      170

cgc aaa atc aat agt ctc tcc tcg aag gat ttc gat tgc atc att aca      849
Arg Lys Ile Asn Ser Leu Ser Ser Lys Asp Phe Asp Cys Ile Ile Thr
      175      180      185      190

gaa ttt gca aag tct caa gac ctg cct tat caa tca ttg tcc ata gac      897
Glu Phe Ala Lys Ser Gln Asp Leu Pro Tyr Gln Ser Leu Ser Ile Asp
      195      200      205

act ttt tct tat ttg aat gat gag tat gta gtc atc gct cag cct ttt      945
Thr Phe Ser Tyr Leu Asn Asp Glu Tyr Val Val Ile Ala Gln Pro Phe
      210      215      220

act gga aaa tgc att ttc ctt gaa tgg gac cat gtg gaa aag acc ttc      993
Thr Gly Lys Cys Ile Phe Leu Glu Trp Asp His Val Glu Lys Thr Phe
      225      230      235

cgg aat tat gac aac att aca gtt tta agg gaa ata cac aga ttt aca      1041
Arg Asn Tyr Asp Asn Ile Thr Val Leu Arg Glu Ile His Arg Phe Thr
      240      245      250

aac atg tca tagttgactt aagcgcacga gacaccaa tctgtggctg      1090
Asn Met Ser
255

ccatcagaaa ttttctacag tacatgaccc ggatgaactc aatgcatgat gactcttctt      1150
atcacacttg caaatgaatg cctttcaaac attgagactg ctagaaccaa gcactaccag      1210
tatctccatc cttaactgtc cagtccagtg atgtgggaag ttacctttta taagacaaaa      1270
tttaattgtg taactgttct ttgcagtga gatgtgtaaa taagcgttta atgggtatctg      1330
ttactccaaa aagaaatatt aatatgtact ttccattta tttattcatg tgtacagaaa      1390
caactgccaa ataaaatggt tacattttct ttcagaaaaa aaaaaaaaaa aa      1442

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<210> 64
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 <222> 32..178

<223> Von Heijne matrix
 score 4.30837886795471
 seq LMVELLKVFFVEA/AV

<400> 64

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                               -45
tcc ggc ttc cgg aag gag ctg gtg agc agg ctg ctg cac ctg cac ttc      100
Ser Gly Phe Arg Lys Glu Leu Val Ser Arg Leu Leu His Leu His Phe
-40 -35 -30
aag gat gac aag acc aaa gtg agc ggg gac gcg ctg cag ctc atg gtg      148
Lys Asp Asp Lys Thr Lys Val Ser Gly Asp Ala Leu Gln Leu Met Val
-25 -20 -15
gag ttg ctg aag gtc ttc gtt gtg gaa gca gca gtc cgc ggc gtg cgg      196
Glu Leu Leu Lys Val Phe Val Val Glu Ala Ala Val Arg Gly Val Arg
-10 -5 1 5
cag gcc cag gca gaa gac gcg ctc cgt gtg gac gtg gac cag ctg gag      244
Gln Ala Gln Ala Glu Asp Ala Leu Arg Val Asp Val Asp Gln Leu Glu
10 15 20
aag gtg ctt ccg cag ctg ctc ctg gac ttc tagggatctc agccgtggct      294
Lys Val Leu Pro Gln Leu Leu Leu Asp Phe
25 30
gaggccaccc ccagaggagc ccctggtcca cagaagcagg ccttggtgtt ccagcggcct      354
ctgataagag gcaggggaagg acctgaagga tttggagttg attcaaacaa gatctctggg      414
agtctccagc ctgtgcagaa ggggcaggac tgcagtgcac tgcgggcctt ggagtgtcca      474
gtggggacac tgggtgtgga aggggcagca cctggggagt cctgcctct cctccctggg      534
acaatagtgt gcatgccacc cggggtccta caggcagggt ctgggaaagg cctggccagc      594
aggtagcctg tgtgtttgac aaacagcagc tggcagcgct gcctcctgcc cacattcctg      654
ccacccgaca tcaaagctgg cgtgtgacct ttccagccat gcgatattcc ccttgggaaga      714
tgcttcccca ggctataaat ttgttctcac aaagcaacat caataaatca aaactgtctc      774
tctcaaaaaa aaaaaaaaaa a      795

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<210> 65
 <211> 1236

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> 222..920

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<221> sig_peptide

<222> 222..311

<223> Von Heijne matrix
 score 4.35083245061594
 seq VAHALSLPAESYG/ND

<400> 65

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agtactccac ctctgcgcct gtgcggggag ggtaaggcgg ggccagcaac ttcctcagct      120
ggagggagag cgcacgggtg agccgccagt tgagaaggac tctgatccgg ctcagctttc      180
caatcagctg cggaaggagc cacgctttcg ggggttgcaa g atg gcg gcc acc agt      236
                               Met Ala Ala Thr Ser
                               -30
gga act gat gag ccg gtt tcc ggg gag ttg gtg tct gtg gca cat gcg      284
Gly Thr Asp Glu Pro Val Ser Gly Glu Leu Val Ser Val Ala His Ala

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<220>
<221> sig_peptide
<222> 101..160
<223> Von Heijne matrix
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      seq LFLCYLLLFTCSG/VE

<400> 66
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cctccaaggt ctagtgacgg agcccgcgcg cggcgccacc atg cgg cag aag gcg 115
                                   Met Arg Gln Lys Ala
                                   -20
gta tcg ctt ttc ttg tgc tac ctg ctg ctc ttc act tgc agt ggg gtg 163
Val Ser Leu Phe Leu Cys Tyr Leu Leu Leu Phe Thr Cys Ser Gly Val
-15                                     -10                                     -5                                     1
gag gca ggt aag aaa aag tgc tcg gag agc tcg gac agc ggc tcc ggg 211
Glu Ala Gly Lys Lys Lys Cys Ser Glu Ser Ser Asp Ser Gly Ser Gly
      5                                     10                                     15
ttc tgg aag gcc ctg acc ttc atg gcc gtc gga gga gga ctc gca gtc 259
Phe Trp Lys Ala Leu Thr Phe Met Ala Val Gly Gly Gly Leu Ala Val
      20                                     25                                     30
gcc ggg ctg ccc gcg ctg ggc ttc acc ggc gcc ggc atc gcg gcc aac 307
Ala Gly Leu Pro Ala Leu Gly Phe Thr Gly Ala Gly Ile Ala Ala Asn
      35                                     40                                     45
tcg gtg gct gcc tcg ctg atg agc tgg tct gcg atc ctg aat ggg ggc 355
Ser Val Ala Ala Ser Leu Met Ser Trp Ser Ala Ile Leu Asn Gly Gly
      50                                     55                                     60                                     65
tagtggccac gctgcagagc ctccggggctg gtggcagcag cgtcgtcata ggtaatatgt 415
gtgccctgat gggctacgcc acccacaagt atctcgatag tgaggaggat gaggagtagc 475
cagcagctcc cagaacctct tcttccttct tggcctaact ctccagtta ggatctagaa 535
ctttgccttt tttttttttt tttttttttt ttgagatggg ttctcactat attgtccagg 595
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cctcaagtga tcctcctgtc tcaacctccc aagtaggatt acaagcatgc gccgacgatg 715
cccaraatcc araactttgt ctatcactct ccccaacaac ctagatgtga aaacagaata 775
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aaaaaaaaaa rrraaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaa 881

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<211> 524
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<222> 173..301
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catttcctgg gccaagttgg gaccgggacg gcctcaccat gatgaaacgg gcagctgctg 120
ctgcagtggg aggagccctg gcagtggggg ctgtgccgtg gtgctcagtg cc atg ggc 178
                                   Met Gly

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ttc act ggg gca gga atc gcc gcg tcc tcc ata gca gcc aag atg atg      226
Phe Thr Gly Ala Gly Ile Ala Ala Ser Ser Ile Ala Ala Lys Met Met
    -40          -35          -30
tcc gca gca gcc att gcc aac ggg ggt ggt gtt tct gcg ggg agc ctg      274
Ser Ala Ala Ala Ile Ala Asn Gly Gly Gly Val Ser Ala Gly Ser Leu
    -25          -20          -15          -10
gtg gct act ctg cag tcc gtg ggg gca gct gga ctc tcc aca tca tcc      322
Val Ala Thr Leu Gln Ser Val Gly Ala Ala Gly Leu Ser Thr Ser Ser
          -5          1          5
aac atc ctc ctg gcc tct gtt ggg tca gtg ttg ggg gcc tgc ttg ggg      370
Asn Ile Leu Leu Ala Ser Val Gly Ser Val Leu Gly Ala Cys Leu Gly
          10          15          20
aat tca cct tct tct tct ctc cca gct gaa ccc gag gct aaa gaa gat      418
Asn Ser Pro Ser Ser Ser Leu Pro Ala Glu Pro Glu Ala Lys Glu Asp
          25          30          35
gag gca aga gaa aat gta ccc caa ggt gaa cct cca aaa ccc cca ctc      466
Glu Ala Arg Glu Asn Val Pro Gln Gly Glu Pro Pro Lys Pro Pro Leu
    40          45          50          55
aag tca gag aaa cat gag gaa taaaggtcac atgcagatgc aaaaaaaaaa      517
Lys Ser Glu Lys His Glu Glu
          60
aaaaaaa      524

<210> 68
<211> 1472
<212> DNA
<213> Homo sapiens

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gaatcagctg caggtctctg ttttgaaaaa gcagagatac agaggcagag gaaaaggggtg      120
gactcctatg tgacctgttc ttagagcaag acaatcacca tctgaattcc agaagccctg      180
ttcatgggtg gggatatttt ctgcactgc atg gaa tca gaa aga agc aaa agg      233
                                Met Glu Ser Glu Arg Ser Lys Arg
                                -30
atg gga aat gcc tgc att ccc ctg aaa aga att gct tat ttc cta tgt      281
Met Gly Asn Ala Cys Ile Pro Leu Lys Arg Ile Ala Tyr Phe Leu Cys
    -25          -20          -15
ctc tta tct gcg ctt ttg ctg act gag ggg aag aaa cca gcg aag cca      329
Leu Leu Ser Ala Leu Leu Leu Thr Glu Gly Lys Lys Pro Ala Lys Pro
    -10          -5          1          5
aaa tgc cct gcc gtg tgt act tgt acc aaa gat aat gct tta tgt gag      377
Lys Cys Pro Ala Val Cys Thr Cys Thr Lys Asp Asn Ala Leu Cys Glu
          10          15          20
aat gcc aga tcc att cca cgc acc gtt cct cct gat gtt atc tca tta      425
Asn Ala Arg Ser Ile Pro Arg Thr Val Pro Pro Asp Val Ile Ser Leu
          25          30          35

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tcc ttt gtg aga tct gtt ttt act gaa atc tca gaa ggg agt ttt tta 473
Ser Phe Val Arg Ser Val Phe Thr Glu Ile Ser Glu Gly Ser Phe Leu
40 45 50
ttc acg cca tcg ctg cag ctc ttg tta ttc aca tcg aac tcc ttt gat 521
Phe Thr Pro Ser Leu Gln Leu Leu Leu Phe Thr Ser Asn Ser Phe Asp
55 60 65 70
gtg atc agt gat gat gct ttt att ggt ctt cca cat cta gag tat tta 569
Val Ile Ser Asp Asp Ala Phe Ile Gly Leu Pro His Leu Glu Tyr Leu
75 80 85
ttc ata gaa aac aac aac atc aag tca att tca aga cat act ttc cgg 617
Phe Ile Glu Asn Asn Asn Ile Lys Ser Ile Ser Arg His Thr Phe Arg
90 95 100
gga cta aag tca tta att cac ttg agc ctt gca aac aac aat ctc cag 665
Gly Leu Lys Ser Leu Ile His Leu Ser Leu Ala Asn Asn Asn Leu Gln
105 110 115
aca ctc cca aaa gat att ttc aaa ggc ctg gat tct tta aca aat gtg 713
Thr Leu Pro Lys Asp Ile Phe Lys Gly Leu Asp Ser Leu Thr Asn Val
120 125 130
gac ctg agg ggt aat tca ttt aat tgt gac tgt aaa ctg aaa tgg cta 761
Asp Leu Arg Gly Asn Ser Phe Asn Cys Asp Cys Lys Leu Lys Trp Leu
135 140 145 150
gtg gaa tgg ctt ggc cac acc aat gca act gtt gaa gac atc tac tgc 809
Val Glu Trp Leu Gly His Thr Asn Ala Thr Val Glu Asp Ile Tyr Cys
155 160 165
gaa ggc ccc cca gaa tac aag aag cgc aaa atc aat agt ctc tcc tcg 857
Glu Gly Pro Pro Glu Tyr Lys Lys Arg Lys Ile Asn Ser Leu Ser Ser
170 175 180
aag gat ttc gat tgc atc att aca gaa ttt gca aag tct caa gac ctg 905
Lys Asp Phe Asp Cys Ile Ile Thr Glu Phe Ala Lys Ser Gln Asp Leu
185 190 195
cct tat caa tca ttg tcc ata gac act ttt tct tat ttg aat gat gag 953
Pro Tyr Gln Ser Leu Ser Ile Asp Thr Phe Ser Tyr Leu Asn Asp Glu
200 205 210
tat gta gtc atc gct cag cct ttt act gga aaa tgc att ttc ctt gaa 1001
Tyr Val Val Ile Ala Gln Pro Phe Thr Gly Lys Cys Ile Phe Leu Glu
215 220 225 230
tgg gac cat gtg gaa aag acc ttc cgg aat tat gac aac att aca gtt 1049
Trp Asp His Val Glu Lys Thr Phe Arg Asn Tyr Asp Asn Ile Thr Val
235 240 245
tta agg gaa ata cac aga ttt aca aac atg tca tagttgactt aagcgcatga 1102
Leu Arg Glu Ile His Arg Phe Thr Asn Met Ser
250 255
gacaccaaatt tctgtggctg ccacacagaaa ttttctacag tacatgaccc ggatgaactc 1162
aatgcatgat gactcttctt atcacacttg caaatgaatg cctttcaaac attgagactg 1222
ctagaaccaa gcactaccag tatctccatc cttaactgtc cagtccagtg atgtgggaag 1282
ttacctttta taagacaaaa tttaattgtg taactgttct ttgcagtgaa gatgtgtaaa 1342
taagcgttta atggtatctg ttactccaaa aagaaatatt aatatgtact tttccattta 1402
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 <213> Homo sapiens

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 <222> 172..255
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 seq XVLLEPFVHQVGG/HS

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 caagccaagg agccaagacg agagggacac acggacaaac aacagacaga agacgtactg 120
 gccgctggac tccgctgcct ccccatctc cccgccatct gcgcccggag g atg agc 177
 Met Ser
 cca gcc ttc agg gcc atg gat gtg gag ccc cgc gcc aaa ggc gtc ctt 225
 Pro Ala Phe Arg Ala Met Asp Val Glu Pro Arg Ala Lys Gly Val Leu
 -25 -20 -15
 ctg gag ccc ttt gtc cac cag gtc ggg ggg cac tca tgc gtg ctc cgc 273
 Leu Glu Pro Phe Val His Gln Val Gly Gly His Ser Cys Val Leu Arg
 -10 -5 1 5
 ttc aat gag aca acc ctg tgc aag ccc ctg gtc cca agg gaa cat cag 321
 Phe Asn Glu Thr Thr Leu Cys Lys Pro Leu Val Pro Arg Glu His Gln
 10 15 20
 ttc tac gag acc ctc cct gct gag atg cgc aaa ttc act ccc cag tac 369
 Phe Tyr Glu Thr Leu Pro Ala Glu Met Arg Lys Phe Thr Pro Gln Tyr
 25 30 35
 aaa ggt gtg gta tct gtg cgc ttt gaa gaa gat gaa gac agg aac ttg 417
 Lys Gly Val Val Ser Val Arg Phe Glu Glu Asp Glu Asp Arg Asn Leu
 40 45 50
 tgt cta ata gca tat cca ttg aaa ggg gac cat gga att gtg gac att 465
 Cys Leu Ile Ala Tyr Pro Leu Lys Gly Asp His Gly Ile Val Asp Ile
 55 60 65 70
 gta gat aat tca gac tgt gaa cca aaa agt aag ctc cta agg tgg aca 513
 Val Asp Asn Ser Asp Cys Glu Pro Lys Ser Lys Leu Leu Arg Trp Thr
 75 80 85
 aca aac aaa aaa cat cat gtc tta gaa aca gaa aag acc cct aag gac 561
 Thr Asn Lys Lys His His Val Leu Glu Thr Glu Lys Thr Pro Lys Asp
 90 95 100
 tgg gtg cgt cag cac cgt aaa gag gag aaa atg aag agc cat aag tta 609
 Trp Val Arg Gln His Arg Lys Glu Glu Lys Met Lys Ser His Lys Leu
 105 110 115
 gaa gaa gaa ttt gag tgg cta aag aaa tct gaa gtc ttg tac tac act 657
 Glu Glu Glu Phe Glu Trp Leu Lys Lys Ser Glu Val Leu Tyr Tyr Thr
 120 125 130
 gta gag aag aag ggg aat ata agt tcc cag ctt aaa cac tat aac cct 705
 Val Glu Lys Lys Gly Asn Ile Ser Ser Gln Leu Lys His Tyr Asn Pro
 135 140 145 150
 tgg agc atg aaa tgt cac cag caa cag tta cag aga atg aag gag aat 753
 Trp Ser Met Lys Cys His Gln Gln Gln Leu Gln Arg Met Lys Glu Asn
 155 160 165
 gca aag cat cgg aac cag tac aaa ttt atc tta ctg gaa aac ctg act 801
 Ala Lys His Arg Asn Gln Tyr Lys Phe Ile Leu Leu Glu Asn Leu Thr
 170 175 180
 tcc cgc tat gag gtg cct tgt gtc ctt gac ctc aag atg ggc aca cga 849
 Ser Arg Tyr Glu Val Pro Cys Val Leu Asp Leu Lys Met Gly Thr Arg
 185 190 195
 caa cat ggt gat gat gct tca gag gag aag gca gcc aac cag atc cga 897
 Gln His Gly Asp Asp Ala Ser Glu Glu Lys Ala Ala Asn Gln Ile Arg
 200 205 210

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aaa tgt cag cag agc aca tct gca gtc att ggt gtg cgt gtg tgt ggc      945
Lys Cys Gln Gln Ser Thr Ser Ala Val Ile Gly Val Arg Val Cys Gly
215                220                225                230
atg cag gtg tac caa gca ggc agt ggg cag ctc atg ttc atg aac aag      993
Met Gln Val Tyr Gln Ala Gly Ser Gly Gln Leu Met Phe Met Asn Lys
                235                240                245
tac cat gga cgg aag cta tct atg cag ggc ttc aag gag gca ctt ttc      1041
Tyr His Gly Arg Lys Leu Ser Met Gln Gly Phe Lys Glu Ala Leu Phe
                250                255                260
cag ttc ttc cac aat ggg cgg tac ctg cgc cgt gaa ctc ctg ggc cct      1089
Gln Phe Phe His Asn Gly Arg Tyr Leu Arg Arg Glu Leu Leu Gly Pro
                265                270                275
gtg ctc aag aag ctg act gag ctc aag gca gtg ttg gag cga cag gag      1137
Val Leu Lys Lys Leu Thr Glu Leu Lys Ala Val Leu Glu Arg Gln Glu
                280                285                290
tcc tac cgc ttc tac tca agc tcc ctg ctg gtc att tat gat ggc aag      1185
Ser Tyr Arg Phe Tyr Ser Ser Ser Leu Leu Val Ile Tyr Asp Gly Lys
295                300                305                310
gag cgg ccc gaa gtg gtc ctg gac tca gat gct gag gat ttg gag gac      1233
Glu Arg Pro Glu Val Val Leu Asp Ser Asp Ala Glu Asp Leu Glu Asp
                315                320                325
ctg tca gag gaa tca gct gat gag tct gct ggt gcc tat gcc tac aaa      1281
Leu Ser Glu Glu Ser Ala Asp Glu Ser Ala Gly Ala Tyr Ala Tyr Lys
                330                335                340
ccc atc ggc gcc agc tct gta gat gtg cgc atg atc gac ttt gca cac      1329
Pro Ile Gly Ala Ser Ser Val Asp Val Arg Met Ile Asp Phe Ala His
                345                350                355
acc acc tgc agg ctg tat ggc gag gac acc gtg gtg cat gag ggc cag      1377
Thr Thr Cys Arg Leu Tyr Gly Glu Asp Thr Val Val His Glu Gly Gln
                360                365                370
gat gct ggc tat atc ttc ggg ctc cag agc ctg ata gac att gtc aca      1425
Asp Ala Gly Tyr Ile Phe Gly Leu Gln Ser Leu Ile Asp Ile Val Thr
375                380                385                390
gag ata agt gag gag agt ggg gag tgagcttgct agctgctcca gtacttgaga      1479
Glu Ile Ser Glu Glu Ser Gly Glu
                395
gcgactctgt gtcccaggca cagctgtgct gcgtcaggga ggaagccagt atggccaggt      1539
ggtggctcct gcagcctgga gctgatgtgc agtggcctct gtgagcccca gcctgagcca      1599
gtcccagctg tgcttggagt ctttatttat tttaactatt tcttcaacat tccacatttg      1659
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gaaaaaaaaa aaaaaaaaaa
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<210> 70

<211> 1637

<212> DNA

<213> Homo sapiens

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<222> 30..1427

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<221> sig_peptide

<222> 30..77

<223> Von Heijne matrix

score 3.71064775937629

seq YAAAAGVLAVES/RQ

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Met Gly Leu Tyr Ala Ala Ala Ala
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ggc gtg ttg gcc ggc gtg gag agc cgc cag ggc tct atc aag ggg ttg 101
Gly Val Leu Ala Gly Val Glu Ser Arg Gln Gly Ser Ile Lys Gly Leu
-5 1 5
gtg tac tcc agc aac ttc cag aac gtg aag cag ctg tac gcg ctg gtg 149
Val Tyr Ser Ser Asn Phe Gln Asn Val Lys Gln Leu Tyr Ala Leu Val
10 15 20
tgc gaa acg cag cgc tac tcc gcc gtg ctg gat gct gtg atc gcc agc 197
Cys Glu Thr Gln Arg Tyr Ser Ala Val Leu Asp Ala Val Ile Ala Ser
25 30 35 40
gcc ggc ctc ctc cgt gcg gag aag aag ctg cgg ccg cac ctg gcc aag 245
Ala Gly Leu Leu Arg Ala Glu Lys Lys Leu Arg Pro His Leu Ala Lys
45 50 55
gtg cta gtg tat gag ttg ttg ttg gga aag ggc ttt cga ggg ggt ggg 293
Val Leu Val Tyr Glu Leu Leu Leu Gly Lys Gly Phe Arg Gly Gly Gly
60 65 70
ggc cga tgg aag gct ctg ttg ggc cgg cac cag gcg agg ctc aag gct 341
Gly Arg Trp Lys Ala Leu Leu Gly Arg His Gln Ala Arg Leu Lys Ala
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gag ttg gct cgg ctc aag gtt cat cgg ggt gtg agc cgg aat gag gac 389
Glu Leu Ala Arg Leu Lys Val His Arg Gly Val Ser Arg Asn Glu Asp
90 95 100
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Leu Leu Glu Val Gly Ser Arg Pro Gly Pro Ala Ser Gln Leu Pro Arg
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Phe Val Arg Val Asn Thr Leu Lys Thr Cys Ser Asp Asp Val Val Asp
125 130 135
tat ttc aag aga caa ggt ttc tcc tat cag ggt cgg gct tcc agc ctc 533
Tyr Phe Lys Arg Gln Gly Phe Ser Tyr Gln Gly Arg Ala Ser Ser Leu
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Asp Asp Leu Arg Ala Leu Lys Gly Lys His Phe Leu Leu Asp Pro Leu
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Met Pro Glu Leu Leu Val Phe Pro Ala Gln Thr Asp Leu His Glu His
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cca ctg tac cgg gcc gga cac ctc att ctg cag gac agg gcc agc tgt 677
Pro Leu Tyr Arg Ala Gly His Leu Ile Leu Gln Asp Arg Ala Ser Cys
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Leu Pro Ala Met Leu Leu Asp Pro Pro Gly Ser His Val Ile Asp
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Ala Cys Ala Ala Pro Gly Asn Lys Thr Ser His Leu Ala Ala Leu Leu
220 225 230
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Lys Asn Gln Gly Lys Ile Phe Ala Phe Asp Leu Asp Ala Lys Arg Leu
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Val Arg Leu His Ala Leu Ala Gly Phe Gln Gln Arg Ala Leu Cys His
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aac ccg ggc gcc ttc agg cta gct ccc gcc ctg cct gcc tgg ccc cac      1205
Asn Pro Gly Ala Phe Arg Leu Ala Pro Ala Leu Pro Ala Trp Pro His
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Arg Gly Leu Ser Thr Phe Pro Gly Ala Glu His Cys Leu Arg Ala Ser
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cct gag acc aca ctc agc agt ggc ttc ttc gtt gct gta att gaa cgg      1301
Pro Glu Thr Thr Leu Ser Ser Gly Phe Phe Val Ala Val Ile Glu Arg
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gtc gag gtg cca agc tca gcc tca cag gcc aaa gca tca gca cca gaa      1349
Val Glu Val Pro Ser Ser Ala Ser Gln Ala Lys Ala Ser Ala Pro Glu
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cgc aca ccc agc cca gcc cca aag aga aag aag aga cag caa aga gcc      1397
Arg Thr Pro Ser Pro Ala Pro Lys Arg Lys Lys Arg Gln Gln Arg Ala
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Cys	Glu	Thr	Gln	Arg	Tyr	Ser	Ala	Val	Leu	Asp	Ala	Val	Ile	Ala	Ser	
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Gly	Arg	Trp	Lys	Ala	Leu	Leu	Gly	Arg	His	Gln	Ala	Arg	Leu	Lys	Ala	
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Asp	Asp	Leu	Arg	Ala	Leu	Lys	Gly	Lys	His	Phe	Leu	Leu	Asp	Pro	Leu	
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Pro	Leu	Tyr	Arg	Ala	Gly	His	Leu	Ile	Leu	Gln	Asp	Arg	Ala	Ser	Cys	
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Lys	Asn	Gln	Gly	Lys	Ile	Phe	Ala	Phe	Asp	Leu	Asp	Ala	Lys	Arg	Leu	
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Ala	Ser	Met	Ala	Thr	Leu	Leu	Ala	Arg	Ala	Gly	Val	Ser	Cys	Cys	Glu	
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Leu	Ala	Glu	Glu	Asp	Phe	Leu	Ala	Val	Ser	Pro	Ser	Asp	Pro	Arg	Tyr	
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His	Glu	Val	His	Tyr	Ile	Leu	Leu	Asp	Pro	Ser	Cys	Ser	Gly	Ser	Gly	
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 Arg Ser Leu Ser Leu Pro Cys Ser Gly Ser Ser Thr Pro Arg Ala Pro
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 Ser Ala Arg Arg Arg Met Lys Thr Trp Cys Glu Met Arg Cys Ser Arg
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 Gly Trp Ser Cys Leu Phe Ser Phe Ile Val Ser Gln Cys Cys Gln Glu
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Gln Thr His Val Pro Asn Arg Glu Pro Val Gln Ala Leu Pro Ser Ser			
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Ala Ser Arg Lys Arg Leu Asp Lys Lys Arg Ser Val Pro Val Ala Thr			
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Val Glu Leu Glu Glu Lys Arg Phe Arg Thr Leu Pro Leu Val Pro Pro			
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Phe Asp Gly Arg Glu Ser Leu Arg Pro Leu Trp Glu Gln Val Gln Gly	
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Phe Arg Glu Ala Val Val Pro Ile Met Ala Lys Ala Pro Gln Gly Val	

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Ser	Val	Met	Asp	Asp	His	Asn	Val	Asp	Ser	Phe	Ile	Ser	Leu	Ser	Ser	
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Pro	Gln	Met	Gly	Gln	Tyr	Gly	Asp	Thr	Asp	Tyr	Leu	Lys	Trp	Leu	Phe	
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Ser Pro Ile Asp Gln Cys Asn Pro Val His Ala Arg Glu Arg Leu Arg				
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Asn Ile Glu Arg Ile Cys Phe Leu Leu Arg Lys Leu Val Leu Pro Glu				
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Trp Leu Thr Leu Gly Leu Asn Val Pro Leu Leu Phe Tyr His Trp				
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Pro Val Val Met Asn Pro Asp Thr Leu Ser Tyr Cys Gln Lys Glu Ala				
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tgg tgt aag ctg gcc ttc tat ctc ctc tcc ttc ttc tac tac ctt tac				726
Trp Cys Lys Leu Ala Phe Tyr Leu Leu Ser Phe Phe Tyr Tyr Leu Tyr				
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Cys Met Ile Tyr Thr Leu Val Ser Ser				
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 Pro Arg Glu His Gln Phe Tyr Glu Thr Leu Pro Ser Glu Met Arg Lys
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 Phe Thr Pro Gln Tyr Lys Gly Val Val Ser Val Arg Phe Glu Glu Asp
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 Gly Ile Val Asp Ile Val Asp Asn Ser Asp Cys Glu Pro Lys Ser Lys
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 85 90 95
 aag acc cct aag gac tgg gtg cgt cag cac cgt aaa gag gag aaa atg 613
 Lys Thr Pro Lys Asp Trp Val Arg Gln His Arg Lys Glu Glu Lys Met
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 Lys Ser His Lys Leu Glu Glu Glu Phe Glu Trp Leu Lys Lys Ser Glu
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 130 135 140 145
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Lys Glu Ala Leu Phe Gln Phe Phe His Asn Gly Arg Tyr Leu Arg Arg
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gaa ctc ctg ggc cct gtg ctc aag aag ctg act gag ctc aag gca gtg      1141
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Leu Glu Arg Gln Glu Ser Tyr Arg Phe Tyr Ser Ser Ser Leu Leu Val
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Ile Tyr Asp Gly Lys Glu Arg Pro Glu Val Val Leu Asp Ser Asp Ala
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Ile Asp Phe Ala His Thr Thr Cys Arg Leu Tyr Gly Glu Asp Thr Val
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gggggttgaa	tatatgtaat	tc	aagacagt	tt	gaataaca	aa	aatgtttt	ac	tgtctatc							1582
accaccatct	ataaatctaa	tt	actaagg	at	aatctgtg	ta	aggtggct	gg	aaagaacc							1642
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tgagattctg	ttgttttgtt	tt	taagcgcc	ag	agacccaa	gt	tgaggaac	ag	cctataaa							1762
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 seq FLCALCSFCPISA/AS

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gcaatc	atg	gac	tac	agc	cgt	gtc	ttt	cag	ggt	gtg	ttc	ttc	acc	ttc			108
	Met	Asp	Tyr	Ser	Arg	Val	Phe	Gln	Gly	Val	Phe	Phe	Thr	Phe			
					-35					-30							
aag	cat	gct	ttt	gct	gat	ggt	gct	tgg	gat	ctt	tca	ttt	ctc	tgt	gct		156
Lys	His	Ala	Phe	Ala	Asp	Gly	Ala	Trp	Asp	Leu	Ser	Phe	Leu	Cys	Ala		
-25					-20				-15					-10			
ctt	tgc	agt	ttc	tgc	cca	atc	tca	gct	gcc	tct	ggc	aga	cct	tac	agg		204
Leu	Cys	Ser	Phe	Cys	Pro	Ile	Ser	Ala	Ala	Ser	Gly	Arg	Pro	Tyr	Arg		
				-5				1			5						
tac	ttg	gaa	ttc	tgg	aga	tta	tac	ctg	tct	cct	agt	tcc	atg	gaa	aat		252

Tyr	Leu	Glu	Phe	Trp	Arg	Leu	Tyr	Leu	Ser	Pro	Ser	Ser	Met	Glu	Asn	
	10						15				20					
gga	ggt	caa	aaa	ttc	cac	gaa	act	ttt	ttc	att	gtc	ttt	ttg	ctt	ttg	300
Gly	Val	Gln	Lys	Phe	His	Glu	Thr	Phe	Phe	Ile	Val	Phe	Leu	Leu	Leu	
	25						30				35					
ttt	gat	atc	gag	agg	aaa	gga	aaa	agt	tct	ggt	tgt	cca	ttt	tgt	tac	348
Phe	Asp	Ile	Glu	Arg	Lys	Gly	Lys	Ser	Ser	Val	Cys	Pro	Phe	Cys	Tyr	
40					45				50					55		
aga	taaggaaagt	ggtttcacaa	aggttaagca	acttggttcag	tgttaccag											401
Arg																
caaagagcag	aatgattttc	aacatttcagt	ttaaaagtcg	gcgggggggca	gtggttcaca											461
cctgtaatat	cagcaacttg	ggaggccaag	gtggtacggg	cgcttgaagc	caaggagttc											521
aagaccagcc	tggtcaacat	agcaaaacct	tgtctttaca	aaaagtaaaa	aaaaaaaaaa											581
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atgacctttc	tcctcgtgac	agtggcctgg	gcagcacaca	caaggttggt	ccaagttggt											180
gggaaaacag	acgacacact	tgccctgctc	aacctggccg	catcatggct	gtgatgccct											240
ccctccctcc	aggcctgc	atg	atg	acc	atc	acc	ttc	ctg	cct	tac	acg	ttt				291
		Met	Met	Thr	Ile	Thr	Phe	Leu	Pro	Tyr	Thr	Phe				
						-35					-30					
tcg	tta	atg	gtg	acc	ttc	cct	gat	gtg	cct	ctg	ggc	atc	ttc	ttg	ttc	339
Ser	Leu	Met	Val	Thr	Phe	Pro	Asp	Val	Pro	Leu	Gly	Ile	Phe	Leu	Phe	
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tgt	gtg	tgt	gtg	atc	gcc	atc	ggg	gtc	gtg	cag	gca	ctg	att	gtg	ggg	387
Cys	Val	Cys	Val	Ile	Ala	Ile	Gly	Val	Val	Gln	Ala	Leu	Ile	Val	Gly	
		-10				-5					1					
tac	gca	ttc	cac	ttc	ccg	cac	ctg	ctg	agc	ccg	cag	atc	cag	cgc	tct	435
Tyr	Ala	Phe	His	Phe	Pro	His	Leu	Ser	Pro	Gln	Ile	Gln	Arg	Ser		
5					10				15			20				
gcc	cac	agg	gct	ctg	tac	cga	cga	cac	gtc	ctg	ggc	atc	gtc	ctc	caa	483
Ala	His	Arg	Ala	Leu	Tyr	Arg	Arg	His	Val	Leu	Gly	Ile	Val	Leu	Gln	
			25						30					35		
ggc	ccg	gcc	ctg	tgc	ttt	gca	gcg	gcc	atc	ttc	tct	ctc	ttc	ttt	gtc	531
Gly	Pro	Ala	Leu	Cys	Phe	Ala	Ala	Ile	Phe	Ser	Leu	Phe	Phe	Val		
		40						45				50				
ccc	ttg	tct	tac	ctg	ctg	atg	gtg	act	gtc	atc	ctc	ctc	ccc	tat	gtc	579
Pro	Leu	Ser	Tyr	Leu	Leu	Met	Val	Thr	Val	Ile	Leu	Leu	Pro	Tyr	Val	
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agc	aag	gtc	acc	ggc	tgg	tgc	aga	gac	agg	ctc	ctg	ggc	cac	agg	gag	627

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Ser Lys Val Thr Gly Trp Cys Arg Asp Arg Leu Leu Gly His Arg Glu
 70      75      80
ccc tgc gct cac cca gtg gaa gtc ttc tgc ttt gac ctc cac gag cca      675
Pro Ser Ala His Pro Val Glu Val Phe Ser Phe Asp Leu His Glu Pro
85      90      95      100
ctc agc aag gag cgc gtg gaa gcc ttc agc gac gga gtc tac gcc atc      723
Leu Ser Lys Glu Arg Val Glu Ala Phe Ser Asp Gly Val Tyr Ala Ile
      105      110      115
gtg gcc acg ctt ctc atc ctg gac atc tgc ccc tcc tgc tcc ctt tgg      771
Val Ala Thr Leu Leu Ile Leu Asp Ile Cys Pro Ser Cys Ser Leu Trp
      120      125      130
ctg gct gtt gct tcc ttc cag cgt ctg ctc ctc cgc ggc ctc atc tgc      819
Leu Ala Val Ala Ser Phe Gln Arg Leu Leu Leu Arg Gly Leu Ile Cys
      135      140      145
ctc ttc gtc tgt tagagcgcgc gtctcgtctc agtcgtcacg tttttggttt      871
Leu Phe Val Cys
150
ttgtgggggt tttttttttt tttttttttg agacagtcct gctgtgtcgc ccaggctgga      931
gtatagtggc tcaagctcag ctcaactgcaa cctccgcctc ccagggttcaa gcaattctcc      991
tgcctcagcc tccaagtag ttgggattac aagcaccac caccatgccc agctaacttt      1051
ttgcattttt aatagagatg aggtttcacc aagttggcca ggctggtctt gaactcctga      1111
cctcagggtga tctgcccacc tcggcctccc aaagtgtctg gattacaggt gtaagccacc      1171
gtgcccggcc atcgtaatgt ttgaatttgc ttttttacat cttccatcct tttggagtgt      1231
cttgttccct cgtcatagtt cagcactgtg accaccttgg ggtagacac tatgggttta      1291
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<222> 111..377

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<221> sig_peptide
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                                     Met Pro
                                     ~40
ccc acc cgg gac cct ttc cag cag cct aca tta gat aac gat gat tcc      164
Pro Thr Arg Asp Pro Phe Gln Gln Pro Thr Leu Asp Asn Asp Asp Ser
      -35      -30      -25
tac tta gga gaa ctg cgg gct tcc aag gta ctg tgg ttt ctt gcg cag      212
Tyr Leu Gly Glu Leu Arg Ala Ser Lys Val Leu Trp Phe Leu Ala Gln
      -20      -15      -10
att ccc agt agg gtc gcc ggt agt ctt ctt tct gtc tgt gtg atg agc      260
Ile Pro Ser Arg Val Ala Gly Ser Leu Leu Ser Val Cys Val Met Ser
      -5      1      5
aga gat ggt aac ata aag gac tct ggt gaa gac act cag tgc ggt acc      308
Arg Asp Gly Asn Ile Lys Asp Ser Gly Glu Asp Thr Gln Ser Gly Thr

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10          15          20          25
agg gaa gtc tgt ttt ctg cct gcc tcc cta tct cca tat tca agt cgg      356
Arg Glu Val Cys Phe Leu Pro Ala Ser Leu Ser Pro Tyr Ser Ser Arg

          30          35          40
cta acg ttt cag agg cgt ttt tgagcagagg aaagtagagt tctagtctag      407
Leu Thr Phe Gln Arg Arg Phe

          45
aggaacaagg ggctctggca gctcaaatca attaaccaag atccaattcc ctggagaatt      467
tttaaccctt cccactccac ccatcacttg cctggctaac atcagacact ggatcaaccc      527
taaaaaggag tccatccaca gcatccaagg atccatagtg tcccctcaca ctgcagccac      587
caatggaggc tactcccgaa agaaagatgg tggtctcttc tccacctagt gttgacagat      647
ccctgaacta attatagtga aacatactgc ggcccacttc cattaaatag atttgtgcaa      707
aaaaaaaaaa aaa                                                    720

<210> 82
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<212> DNA
<213> Homo sapiens

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ccatatccac tctaggata caacaagagc aagcccaatt ctcttggtgg tgtgggcagt      180
cggcttgcac cagctaccta tctcagctct ttttgggaagc tt atg tcc tcc cca      234
                                     Met Ser Ser Pro
                                     -35
caa ctt cca gct ttc tta tgg gac aag ggt aca ctc acc act gcc ata      282
Gln Leu Pro Ala Phe Leu Trp Asp Lys Gly Thr Leu Thr Thr Ala Ile
          -30          -25          -20
tct aat cct gct tgc ctg gta aat gtt ctc ttc ttc ttt aca ccc ctg      330
Ser Asn Pro Ala Cys Leu Val Asn Val Leu Phe Phe Phe Thr Pro Leu
          -15          -10          -5
atg act ctg gtc act cta ctc atc ctg gtc tgg aaa gta acc aaa gac      378
Met Thr Leu Val Thr Leu Leu Ile Leu Val Trp Lys Val Thr Lys Asp
          1          5          10
aaa agc aac aag aac aga gag aca cac cca aga aag gag gca aca tgg      426
Lys Ser Asn Lys Asn Arg Glu Thr His Pro Arg Lys Glu Ala Thr Trp
          15          20          25          30
ctg cca taaagatctg gatctcttgg tggggactcc actgaggtga agacctgatt      482
Leu Pro
gtacaagaga ggcacggcca ctggagctgt ctcagagccc agagccaggg gagccagagc      542
tgcttttagcc accctgttcc tccattgccca gatgtccccc caggcctcat ttccttcctc      602
tgccaccatc cctcttataa tgcactcctc ctgcgggttct ttggcttgtc ccagcttctg      662
agtttgaatg tctttttttt tttttttttt tttttgkga tcttcaagac tgaaatagta      722
aatggctctt gatttctgca ctaacagagg aaagaaacaa gtacatggaa aagtaaaaat      782
tgattacaaa gcctaaatth tctctataaa attgggcatg tgctgactgt gggatattga      842
aattattggg agctcacagc atctcaagtt atataatgaa gctattctgg aagctcattt      902

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ccagaagatc cttaaaatga aatggctcac tctctgctga attaatttgg agcaagttaa 962
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aaaaaaa 1029

<210> 83
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<212> DNA
<213> Homo sapiens

<220>
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<222> 769..843
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score 5.65786415517206
seq AAHLLVVILPANA/AL

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tgggcgggtg tagccctggc tcctcttttaa atggatttgg tttcaaagac gatcatctcc 180
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gagccatgtc gcttgcccct tacgttctgt tacccttttt cttttttgtc atctctcgtg 540
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ttcttttctc ttctttcctt gttttcattc cagacttcag cactgggctg ggaaactttc 720
tggcttccat ctcgcttact catgtagcct tcgctttgca aggtggag atg agg ggt 777
Met Arg Gly

-25
ccc act gct ggt cct tca gtt ctt tct gct gca cac ttg ctg gtc gta 825
Pro Thr Ala Gly Pro Ser Val Leu Ser Ala Ala His Leu Leu Val Val
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ata ctg cct gca aac gcc gca ctc aag ctg ctg tct tgg gag aga ctg 873
Ile Leu Pro Ala Asn Ala Ala Leu Lys Leu Leu Ser Trp Glu Arg Leu
-5 1 5 10
gcg gcc ccc gcc atc gag gtg gaa gta cct tcc aag gag gtg ctt gca 921
Ala Ala Pro Ala Ile Glu Val Glu Val Pro Ser Lys Glu Val Leu Ala
15 20 25
gca ccc acc aag gcc aag cta ata ccc tct gag gat atg ttg gca gca 969
Ala Pro Thr Lys Ala Lys Leu Ile Pro Ser Glu Asp Met Leu Ala Ala
30 35 40
cct gcc atg gac ttg ctg gat tca ttt tct cct gga ttt ttg ata gct 1017
Pro Ala Met Asp Leu Leu Asp Ser Phe Ser Pro Gly Phe Leu Ile Ala
45 50 55
gct ccc gcc agc gct gtg atc act tgg cct ggg cct gca gat ttg gtt 1065
Ala Pro Ala Ser Ala Val Ile Thr Trp Pro Gly Pro Ala Asp Leu Val
60 65 70
gtt gct atg ctc ata gca cct gtt gca gga ctc att gct gcc cct gct 1113
Val Ala Met Leu Ile Ala Pro Val Ala Gly Leu Ile Ala Ala Pro Ala
75 80 85 90
att gcc aca tct gtt cta ggt cct gtt gct gtt cct gcc act gcc atg 1161

Ile	Ala	Thr	Ser	Val	Leu	Gly	Pro	Val	Ala	Val	Pro	Ala	Thr	Ala	Met	
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Pro	Pro	Ala	Val	Leu	Ala	Ala	Pro	Pro	Ser	Ala	Ala	Pro	Gly	Val	Leu	
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gtg	gat	gga	gaa	gcc	gca	cta	gcc	gtt	ccg	tgg	gag	gca	tgt	tgg	att	1257
Val	Asp	Gly	Glu	Ala	Ala	Leu	Ala	Val	Pro	Trp	Glu	Ala	Cys	Trp	Ile	
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Pro	Ser	Pro	Pro	Ala												
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caagaccagc	cttgccaaca	tagcaaaacc	ccgactctac	taaaaataca	aaaaattagc											1612
tggacaggat	ggcgcatgcc	tgtaatccca	gctactcagt	aggctgaggt	aggagtatcg											1672
cttgaactcg	gatggcggag	gctgcagtga	gccaagactg	cgccactcca	ctgcactcca											1732
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<211> 805

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<222> 30..74

<223> Von Heijne matrix

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Leu	Leu	Pro	Ala	Ile	Glu	Gly	Lys	Asn	Cys	Leu	Arg	Cys	Trp	Pro	Glu	
		-5					1				5					
ctg	tct	gcc	ttg	ata	gac	tat	gac	ctg	cag	atc	ctc	tgg	gtg	acc	cca	149
Leu	Ser	Ala	Leu	Ile	Asp	Tyr	Asp	Leu	Gln	Ile	Leu	Trp	Val	Thr	Pro	
				15						20					25	
ggg	cca	ccc	aca	gaa	ctt	tct	caa	aat	cgt	gac	cat	ttg	gaa	gaa	gaa	197
Gly	Pro	Pro	Thr	Glu	Leu	Ser	Gln	Asn	Arg	Asp	His	Leu	Glu	Glu	Glu	
			30						35					40		
aca	gcc	aaa	ttc	ttc	act	caa	gta	cac	caa	gcc	att	aaa	acg	tta	cga	245
Thr	Ala	Lys	Phe	Phe	Thr	Gln	Val	His	Gln	Ala	Ile	Lys	Thr	Leu	Arg	
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gat	gat	aaa	aca	gta	ctt	ctg	gaa	gag	atc	tac	acg	cac	aag	aat	ctc	293
Asp	Asp	Lys	Thr	Val	Leu	Leu	Glu	Glu	Ile	Tyr	Thr	His	Lys	Asn	Leu	
		60					65					70				
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Phe	Thr	Glu	Arg	Leu	Asn	Lys	Ile	Ser	Asp	Gly	Leu	Lys	Glu	Lys	Asp	
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ata cag tcc aca ctg aag gtc acc agc tgt gct gac tgc agg act cac      389
Ile Gln Ser Thr Leu Lys Val Thr Ser Cys Ala Asp Cys Arg Thr His
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ttc ctc tcc tgc aat gac ccc act ttc tgc cca gcc agg aac cgg cgg      437
Phe Leu Ser Cys Asn Asp Pro Thr Phe Cys Pro Ala Arg Asn Arg Arg
          110          115          120
acc tcc ctg tgg gct gtg agt ctc agc agt gct cta ctc ctg gcc ata      485
Thr Ser Leu Trp Ala Val Ser Leu Ser Ser Ala Leu Leu Leu Ala Ile
          125          130          135
gct gga gat gtt tct ttt act ggc aaa gga aga agg agg cag
Ala Gly Asp Val Ser Phe Thr Gly Lys Gly Arg Arg Arg Gln      527
          140          145          150
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ccgtcacaaa gttcactcat ctctgggtcc cgggtgacccc atccccccat accctccatc      647
ctgggtcctg gggcccaaaa gctctgaggc ctaggagact gcgctgtctc gtggtttgcc      707
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                        -15                      -10
acc ttc att atc tgt ggg ttg cta act cgg gtg acc aaa ggt agc ttt      104
Thr Phe Ile Ile Cys Gly Leu Leu Thr Arg Val Thr Lys Gly Ser Phe
          -5          1          5
gaa ccc caa aaa tgt tgg aag aat aat gta gga cat tgc aga aga cga      152
Glu Pro Gln Lys Cys Trp Lys Asn Asn Val Gly His Cys Arg Arg Arg
          10          15          20
tgt tta gat act gaa agg tac ata ctt ctt tgt agg aac aag cta tca      200
Cys Leu Asp Thr Glu Arg Tyr Ile Leu Leu Cys Arg Asn Lys Leu Ser
          25          30          35
tgc tgc att tct ata ata tca cat gaa tat act cga cga cca gca ttt      248
Cys Cys Ile Ser Ile Ile Ser His Glu Tyr Thr Arg Arg Pro Ala Phe
          40          45          50          55
cct gtg att cac cta gag gat ata aca ttg gat tat agt gat gtg gac      296
Pro Val Ile His Leu Glu Asp Ile Thr Leu Asp Tyr Ser Asp Val Asp
          60          65          70
tct ttt act ggt tcc cca gta tct atg ttg aat gat ctg ata aca ttt      344
Ser Phe Thr Gly Ser Pro Val Ser Met Leu Asn Asp Leu Ile Thr Phe
          75          80          85
gac aca act aaa ttt gga gaa acc atg aca cct gag acc aat act cct      392
Asp Thr Thr Lys Phe Gly Glu Thr Met Thr Pro Glu Thr Asn Thr Pro

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 gcagaaagga gagtctcgct ctgtcaccca ggctggagtg cagtggcagg atcttggctc 180
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 cagtcactcc acgcttgag agtccaatta acaagagcaa gttctggtag aaagaagggtg 300
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 Met Ser Asp Glu Asp Glu Ser
 -25
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 Ser Asp Tyr Leu Cys Leu Ser Ile Leu Gly Leu Phe Cys Cys Leu Pro
 -20 -15 -10 -5
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 Leu Ala Ile Pro Ala Val Ile Phe Ser Cys Leu Thr Lys Asn Tyr Asn
 1 5 10
 aaa tcc agt gac tat gag ctg gca gcc aag acc tcc aaa caa gcc tac 496
 Lys Ser Ser Asp Tyr Glu Leu Ala Ala Lys Thr Ser Lys Gln Ala Tyr
 15 20 25
 tac tgg gcc atc gcg agc atc act gtg gga atc tta ggt acc atc ttg 544
 Tyr Trp Ala Ile Ala Ser Ile Thr Val Gly Ile Leu Gly Thr Ile Leu
 30 35 40
 tac acc tac ctg ata tac tta ctt aga ttg taaactgctt cccagctctt 594
 Tyr Thr Tyr Leu Ile Tyr Leu Leu Arg Leu
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 Met Thr Asp Gln Asp Arg Ile Ile Asn Leu Val Val Gly
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 Ser Leu Thr Ser Leu Leu Ile Leu Val Thr Leu Ile Ser Ala Phe Val
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 Phe Pro Gln Leu Pro Pro Lys Pro Leu Asn Ile Phe Phe Ala Val Cys
 5 10 15
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 Ile Ser Leu Ser Ser Ile Thr Ala Cys Ile Ile Tyr Trp Tyr Arg Gln
 20 25 30
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 Gly Asp Leu Glu Pro Lys Phe Arg Lys Leu Ile Tyr Tyr Ile Ile Phe
 35 40 45 50
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 Ser Ile Ile Met Leu Cys Ile Cys Ala Asn Leu Tyr Phe His Asp Val
 55 60 65
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 Gly Arg
 aggacagtga gtaatttttg gataaggat gctgaagaat ctctgcaga agtctgatac 527
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 Met Ala
 -20
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Ala Ala Ala Val Pro Ser Leu Leu Leu Ser Leu Pro Pro His Gln Gly
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Leu Thr Phe Ser Asn Lys Ile Gln Pro Phe Gly Ala Gln Gly Val Leu
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cat ccg gaa cca gga ctg cga gac tgg ctg ctg cca acg tgc tcc aga 262
His Pro Glu Pro Gly Leu Arg Asp Trp Leu Leu Pro Thr Cys Ser Arg
15 20 25 30
caa ttg cga gtc gca ctg ccg gag aag ggg tcc gag ggc agt ctg tgt 310
Gln Leu Arg Val Ala Leu Pro Glu Lys Gly Ser Glu Gly Ser Leu Cys
35 40 45
caa acg cag ctg cca gct act cca tgc ttc ctg cct tgc aat acg gtg 358
Gln Thr Gln Leu Pro Ala Thr Pro Cys Phe Leu Pro Ser Asn Thr Val
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aga acg tgaagtcag agctgctgct aaggcatgtg gcaaccttga agagaaggtc 414
Arg Thr
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Val Pro Trp Leu Tyr Ala Val Phe Ala Val Leu Phe Val Phe Phe Leu
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Phe Ala Met Leu Ser Pro Phe Leu Leu Glu Ile Asp Gln His Ile Lys
1 5 10
aaa ttc ttg atc aga tgc agg tat tct ctg cat aac act gtg cat aag 194
Lys Phe Leu Ile Arg Cys Arg Tyr Ser Leu His Asn Thr Val His Lys
15 20 25 30
gac aaa aaa aac agt gag ata aag atg gac cat cta gaa agg cca ggc 242
Asp Lys Lys Asn Ser Glu Ile Lys Met Asp His Leu Glu Arg Pro Gly
35 40 45
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Cys Pro Leu Glu Ser Pro Arg Arg Gly Val Leu Gly Gly Lys Lys Asn
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Gly Met Gly Asn Asp Pro Leu Leu Phe Val Lys Val Thr Lys Glu Pro
65 70 75
agg gat tct gag gct gaa atc tat acc cct ggg cct tca gtt 380

Arg Asp Ser Glu Ala Glu Ile Tyr Thr Pro Gly Pro Ser Val
80 85 90
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gaccagaac agctaccagc agaatcagat tctc atg gac caa ctg gta ttc aaa 175
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Glu Thr Ile Trp Asn Asp Ala Phe Trp Gln Asn Pro Trp Asp Gln Gly
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Gly Leu Ala Val Ile Ile Leu Phe Ile Thr Ala Val Leu Leu Leu Ile
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Leu Phe Ala Ile Val Phe Gly Leu Leu Thr Ser Thr Glu Asn Thr Gln
-5 1 5
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Cys Glu Ala Gly Glu Glu
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 agctaattta gctattttta aatagctaaa ttttagctac ttttttttca attgacaaag 180
 aagg atg tct aat caa aga cta ccg ctg att ttt tct ctg ttg ttt atc 229
 Met Ser Asn Gln Arg Leu Pro Leu Ile Phe Ser Leu Leu Phe Ile
 -20 -15 -10
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 Cys Phe Phe Gly Glu Ser Phe Cys Ile Cys Asp Gly Thr Val Trp Thr
 -5 1 5
 aag gtt gga tgg gag att ctt cca gaa gaa gta cat tat tgg aaa ggt 325
 Lys Val Gly Trp Glu Ile Leu Pro Glu Glu Val His Tyr Trp Lys Gly
 10 15 20
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 Cys Leu Tyr Leu Ile Tyr Asn Leu Leu Gln Ala Val Phe Phe Val Leu
 25 30 35 40
 ttt gtt ttg tct gtg cat tac ctg tgg aag aaa tgg aag aaa cac caa 421
 Phe Val Leu Ser Val His Tyr Leu Trp Lys Lys Trp Lys Lys His Gln
 45 50 55
 aaa aag ctg aaa aag caa gcc tcc tta gaa aaa cct ggt aat gat cta 469
 Lys Lys Leu Lys Lys Gln Ala Ser Leu Glu Lys Pro Gly Asn Asp Leu
 60 65 70
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 Glu Ser Pro Leu Ile Asn Asn Ile Asp Gln Thr Leu His Arg Val Ala
 75 80 85
 acc aca gca tca gtg ata tac aag atc tgg gag cac agg tct cac cat 565
 Thr Thr Ala Ser Val Ile Tyr Lys Ile Trp Glu His Arg Ser His His
 90 95 100
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 Pro Ser Ser Lys Lys Ile Lys His Cys Lys Leu Lys Lys Lys Ser Lys
 105 110 115 120
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 score 4.95353272042967

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Gly Arg Pro Pro Trp Pro Val Ser Gly Val Leu Gly Ser Arg Val Cys
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Gly Pro Leu Tyr Ser Thr Ser Pro Ala Gly Pro Gly Arg Ala Ala Ser
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Leu Pro Arg Lys Gly Ala Gln Leu Glu Leu Glu Glu Met Val Pro Arg
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Lys Met Ser Val Ser Pro Leu Glu Ser Trp Leu Thr Ala Arg Cys Phe
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ctg ccc aga ctg gat acc ggg acc gca ggg act gtg gct cca ccg caa      346
Leu Pro Arg Leu Asp Thr Gly Thr Ala Gly Thr Val Ala Pro Pro Gln
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Ser Tyr Gln Cys Pro Pro Ser Gln Ile Gly Glu Gly Ala Glu Gln Gly
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Asp Glu Gly Val Ala Asp Ala Pro Gln Ile Gln Cys Lys Asn Val Leu
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Lys Ile Arg Arg Arg Lys Met Asn His His Lys Tyr Arg Lys Leu Val
                               120                              125           130
aag aag acg cgg ttc ctg cgg agg aag gtc cag gag gga cgc ctg aga      538
Lys Lys Thr Arg Phe Leu Arg Arg Lys Val Gln Glu Gly Arg Leu Arg
                               135                              140           145
cgc aag cag atc aag ttc gag aaa gac ctg agg cgc atc tgg ctg aag      586
Arg Lys Gln Ile Lys Phe Glu Lys Asp Leu Arg Arg Ile Trp Leu Lys
   150                              155                              160           165
gcg ggg cta aag gaa gcc ccc gaa ggc tgg cag acc ccc aag atc tac      634
Ala Gly Leu Lys Glu Ala Pro Glu Gly Trp Gln Thr Pro Lys Ile Tyr
                               170                              175           180
ctg cgg ggc aaa tgagtctggc gccgcccttc ccgccgttg ctgctgtgat      686
Leu Arg Gly Lys
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<213> Homo sapiens

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<222> 247..318

<223> Von Heijne matrix
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 Met Val Pro Leu Pro Lys Gln Ser Leu Lys Phe Phe Cys Ala
 -20 -15
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 10 15 20
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 25 30 35
 tca gat gca ttc cag aaa ctg ttg att gtt gtt cta ggt aag act gtc 480
 Ser Asp Ala Phe Gln Lys Leu Leu Ile Val Val Leu Gly Lys Thr Val
 40 45 50
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 cagagacggc aggttcatca ag atg gtg ctc atg tgg acc agt ggt gac gcc 172
 Met Val Leu Met Trp Thr Ser Gly Asp Ala
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 Phe Lys Thr Ala Tyr Phe Leu Leu Lys Gly Ala Pro Leu Gln Phe Ser
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 Val Cys Gly Leu Leu Gln Val Leu Val Asp Leu Ala Ile Leu Gly Gln
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Trp	Gly	Leu	His	Gln	Pro	Leu	Trp	Gly	Val	Ser	Gly	Trp	Ala	Val	Gly		
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<223> Von Heijne matrix

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Val Phe Leu Leu Met Val Asn Gly Gln Val Glu Ser Ala Gln Phe Pro
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Glu Tyr Asp Asp Phe Tyr Cys Lys Tyr Cys Phe Val Tyr Gly Gln Asp
5 10 15 20
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Trp Ala Pro Thr Ala Gly Leu Glu Glu Gly Ile Ser Gln Ile Thr Ser
25 30 35
aag agc caa gat gtg cgg caa gca ctg gtg tgg aac ttc ccc att gat 245
Lys Ser Gln Asp Val Arg Gln Ala Leu Val Trp Asn Phe Pro Ile Asp
40 45 50
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Val Thr Phe Lys Ser Thr Asn Pro Tyr Gly Trp Pro Gln Ile Val Leu
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agc gtg tat gga cca gat gtg ttc ggg aac gat gtg gtt cga ggc tat 341
Ser Val Tyr Gly Pro Asp Val Phe Gly Asn Asp Val Val Arg Gly Tyr
70 75 80
ggg gcc gtg cac gtg ccc ttc tca cct ggc cgg cac aaa agg acc atc 389
Gly Ala Val His Val Pro Phe Ser Pro Gly Arg His Lys Arg Thr Ile
85 90 95 100
ccc atg ttt gtc cca gaa tct acg tct aaa ctg cag aag ttt aca aga 437
Pro Met Phe Val Pro Glu Ser Thr Ser Lys Leu Gln Lys Phe Thr Arg
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tct gca agc tgc tcc acc cac tgaggacaaa tagaaacagg tcccctggga 488
Ser Ala Ser Cys Ser Thr His
120
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ccctgtgccc tgtgaaaaat ctttgtgtct gagggggcag aggaaaaact cttgtcagat 608
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aa 670

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Ala	Pro	Asn	Phe	Ser	Ser	His	Gly	Ser	Cys	Arg	Arg	Arg	Gln	Arg	Xaa	
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gac	atg	aca	agg	cgc	tgc	atg	ccc	gct	agg	cca	ggg	ttc	ccc	tca	tcc	192
Asp	Met	Thr	Arg	Arg	Cys	Met	Pro	Ala	Arg	Pro	Gly	Phe	Pro	Ser	Ser	
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cca	gcc	ccg	ggg	tcg	tcg	ccc	ccg	cgc	tgc	cat	ctg	aga	ccc	ggg	agt	240
Pro	Ala	Pro	Gly	Ser	Ser	Pro	Pro	Arg	Cys	His	Leu	Arg	Pro	Gly	Ser	
			40				45					50				
acc	gcc	cat	gct	gca	gcg	gga	aag	aga	aca	gag	agt	cct	ggg	gac	agg	288
Thr	Ala	His	Ala	Ala	Ala	Gly	Lys	Arg	Thr	Glu	Ser	Pro	Gly	Asp	Arg	
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tac	cgt	gca	gag	ggc	ttg	aga	agg	ggc	cgg	gtc	gcg	ggg	gca	agg	gta	336
Tyr	Arg	Ala	Glu	Gly	Leu	Arg	Arg	Gly	Arg	Val	Ala	Gly	Ala	Arg	Val	
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ctccaagagg	ctaatttttt	tgtaaagatt	ttgtgggagc	tatgtaatga	gatggggagt											876
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gcatactcac	ctcagaccat	cagttgggta	ggccaacagc	tcaccatcaa	ttc atg											176
					Met											
ccc tgc cta	gac caa	cag ctc	act gtt	cat gcc	cta ccc	tgc cct	gcc									224
Pro Cys Leu	Asp Gln	Gln Leu	Thr Val	His Ala	Leu Pro	Cys Pro	Ala									
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cag ccc tcc	tct ctg	gcc ttc	tgc caa	gtg ggg	ttc tta	aca gca	cag									272
Gln Pro Ser	Ser Leu	Ala Phe	Cys Gln	Val Gly	Phe Leu	Thr Ala	Gln									
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Pro Ser Pro	Pro Arg	Arg Arg	Asn Gly	Lys Asp	Arg Tyr	Thr Leu	Val									

	5		10		15											
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Leu	Gln	His	Gln	Glu	Cys	Gln	Asp	Asp	Leu	Ala	Thr	Ser	Ser	Leu	Val	
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tac	ctt	tcc	ctc	ccc	tgc	ttc	aaa	gac	ttg	ggt	cga	tcg	aag	cac	caa	416
Tyr	Leu	Ser	Leu	Pro	Cys	Phe	Lys	Asp	Leu	Gly	Arg	Ser	Lys	His	Gln	
	35		40		45											
agc	atc	act	gtt	gct	gac	act	aac	aag	tagtgccaag	ggattgcctt						463
Ser	Ile	Thr	Val	Ala	Asp	Thr	Asn	Lys								
50			55													
taaggaagat	caggagcggg	acatctggtg	gcaaagaaaa	tcttttcta	atagccccattc											523
tagtgaccac	cttcaacctc	ctcatagcag	gagagtttgg	gagtagggga	cttaggatgt											583
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cctttggcaa	ttccagcctt	ctgtggaaag	gccagtagaa	agcattgatt	tattcacctc											240
tacaggaatc	agactcagcc	tcttttggtt	ttcagtgaa	t atg cct ttt caa ttt												296
				Met Pro Phe Gln Phe												
				-35												
gga acc cag cca agg agg ttt cca gtg gaa gga gga gat tct tca att																344
Gly Thr Gln Pro Arg Arg Phe Pro Val Glu Gly Gly Asp Ser Ser Ile																
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gag ctg gaa cct ggg ctg agc tcc agt gct gcc tgt aat ggg aag gag																392
Glu Leu Glu Pro Gly Leu Ser Ser Ser Ala Ala Cys Asn Gly Lys Glu																
-10		-5		1												
atg tca cca acc agg caa ctc cgg agg tgc cct gga agt cat tgc ctg																440
Met Ser Pro Thr Arg Gln Leu Arg Arg Cys Pro Gly Ser His Cys Leu																
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aca ata act gat gtt ccc gtc act gtt tat gca aca acg aga aag cca																488
Thr Ile Thr Asp Val Pro Val Thr Val Tyr Ala Thr Thr Arg Lys Pro																
20		25		30												
cct gca caa agc agc aag gaa atg cat cct aaa tagcaccatt aagtcttttg																541
Pro Gln Gln Ser Ser Lys Glu Met His Pro Lys																
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atatgtcaaaa atg agt ctg ctg atg ttt aca caa cta ctg ctc tgt gga      289
          Met Ser Leu Leu Met Phe Thr Gln Leu Leu Cys Gly
          -15              -10              -5

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Phe Leu Tyr Val Arg Val Asp Gly Ser Arg Leu Arg Gln Glu Asp Phe
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ccc ccg cgg att gtg gag cat cct tcc gat gtc atc gtc tct aag ggc      385
Pro Pro Arg Ile Val Glu His Pro Ser Asp Val Ile Val Ser Lys Gly
15              20              25              30

gag ccc acg act ctg aac tgc aag gcg gag ggc cgg cca acg ccc acc      433
Glu Pro Thr Thr Leu Asn Cys Lys Ala Glu Gly Arg Pro Thr Pro Thr
          35              40              45

att gag tgg tac aaa gat ggg gag cga gtg gag act gac aag gac gat      481
Ile Glu Trp Tyr Lys Asp Gly Glu Arg Val Glu Thr Asp Lys Asp Asp
          50              55              60

ccc cgg tcc cac agg atg ctt ctg ccc agc gga tcc tta ttc ttc ttg      529
Pro Arg Ser His Arg Met Leu Leu Pro Ser Gly Ser Leu Phe Phe Leu
          65              70              75

cgc atc gtg cac ggg cgc agg agt aaa cct gat gaa gga agc tac gtt      577
Arg Ile Val His Gly Arg Arg Ser Lys Pro Asp Glu Gly Ser Tyr Val
          80              85              90

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Cys Val Ala Arg Asn Tyr Leu Gly Glu Ala Val Ser Arg Asn Ala Ser
95              100              105              110

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Leu Glu Val Ala Cys Lys
          115

cttttatttta tttcaagtaa gttttgatgt gttcccatag acgctgaaac ctaaagaatc      733
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caagccagggt tgttgtagta agttttgttta tatgaaatca agatgaccaa tatgttatta      853
taagaaaagca ggccggggcgc ggtgggtcac gcctgtaatc ccagcacttt gggaggcgga      913
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 gacttctgtc ttttcagctg cagtgaaggc tcggggctgc agaattgcaa ccttgcca 178
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 Met Asp Leu Ile Gly Phe Gly Tyr Ala Ala Leu Val Thr Phe Gly Ser
 -35 -30 -25
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 Ile Phe Gly Tyr Lys Arg Arg Gly Gly Val Pro Ser Leu Ile Ala Gly
 -20 -15 -10
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 Leu Phe Val Gly Cys Leu Ala Gly Tyr Gly Ala Tyr Arg Val Ser Asn
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 Thr Ile Met Gly Val Arg Phe Lys Arg Ser Lys Lys Ile Met Pro Ala
 30 35 40
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 Gly Leu Val Ala Gly Leu Ser Leu Met Met Ile Leu Arg Leu Val Leu
 45 50 55
 ttg ctg ctc tgagcatctg gaggaacaga aaactaagtt catgtcatcc 515
 Leu Leu Leu
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 ctaaagcaaa aattttaact gtttttcta tgtcaagcac tattttcatt aaaagtgtct 695
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 Glu Asn Arg Asp Ser Arg Arg Leu Gly Asp Ala Leu Leu Phe Leu Arg
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 Pro Ala Gly Ser Cys Ala Leu Gln Val Ser Trp Pro Ala Ala Leu Ala
 1 5 10
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 Gly Pro Arg Ser His Thr Gly Gln Leu Thr Gln His Phe Cys His Leu
 15 20 25
 aag aac gac acc tgc att cct cca tct ctg gga cca cca agg aac tca 294
 Lys Asn Asp Thr Cys Ile Pro Pro Ser Leu Gly Pro Pro Arg Asn Ser
 30 35 40
 ggg agc ttg gaa tct ctc aga tca aaa aga tac tgactcatcg gatagccatg 347
 Gly Ser Leu Glu Ser Leu Arg Ser Lys Arg Tyr
 45 50 55
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 Met Val Gly Ile Leu Pro Leu Cys Cys Ser Gly Cys Val Pro Ser
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Ser	Val	Arg	Val	Pro	His	Ser	Ala	Gly	His	Cys	Gly	Gln	Arg	Val	Leu	
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gcc	tgc	tcc	ctt	cct	caa	gta	ttc	tta	aag	cca	tgg	att	ttt	gtg	gag	491
Ala	Cys	Ser	Leu	Pro	Gln	Val	Phe	Leu	Lys	Pro	Trp	Ile	Phe	Val	Glu	
	30					35				40						
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His	Phe	Ser	Ser	Trp	Leu	Ser	Leu	Glu	Leu	Phe	Ser	Phe	Leu	Arg	Tyr	
	45				50					55					60	
ctt	ggg	act	ctt	ctt	tgt	gct	tgc	gga	cat	cgg	ttg	aga	gaa	gga	cga	587
Leu	Gly	Thr	Leu	Leu	Cys	Ala	Cys	Gly	His	Arg	Leu	Arg	Glu	Gly	Arg	
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Ser	Gln	Gly	Ser	His	Val	Ala	Ala	Phe	Leu	Pro	Glu	Ala	Ile	Gly	Pro	
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Gly	Val	Pro	Val	Pro	Val	Ser	Gly	Glu	Ser	Thr	Ser	Ala	Gln	Gln	Ser	
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Cys	Phe	Gly	Gly	Asp	Arg	Leu	Thr	Leu	His							
	190					195										
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score 8.42885652997473

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                                   -20                               -15

gtg gct gtg gtc ggg tgt ttg ctg gtg ccc cca gct gaa gcc aac aag      162
Val Ala Val Val Gly Cys Leu Leu Val Pro Pro Ala Glu Ala Asn Lys
                                   -10                               -5                               1

agt tct gaa gat atc cgg tgc aaa tgc atc tgt cca cct tat aga aac      210
Ser Ser Glu Asp Ile Arg Cys Lys Cys Ile Cys Pro Pro Tyr Arg Asn
                                   5                               10                               15

atc agt ggg cac att tac aac cag aat gta tcc cag aag gac tgc aac      258
Ile Ser Gly His Ile Tyr Asn Gln Asn Val Ser Gln Lys Asp Cys Asn
                                   20                               25                               30

tgc ctg cac gtg gtg gag ccc atg cca gtg cct ggc cat gac gtg gag      306
Cys Leu His Val Val Glu Pro Met Pro Val Pro Gly His Asp Val Glu
                                   35                               40                               45                               50

gcc tac tgc ctg ctg tgc gag tgc agg tac gag gag cgc agc acc acc      354
Ala Tyr Cys Leu Leu Cys Glu Cys Arg Tyr Glu Glu Arg Ser Thr Thr
                                   55                               60                               65

acc atc aag gtc atc att gtc atc tac ctg tcc gtg gtg ggt gcc ctg      402
Thr Ile Lys Val Ile Ile Val Ile Tyr Leu Ser Val Val Gly Ala Leu
                                   70                               75                               80

ttg ctc tac atg gcc ttc ctg atg ctg gtg gac cct ctg atc cga aag      450
Leu Leu Tyr Met Ala Phe Leu Met Leu Val Asp Pro Leu Ile Arg Lys
                                   85                               90                               95

ccg gat gca tac act gag caa ctg cac aat gag gag gag aat gag gat      498
Pro Asp Ala Tyr Thr Glu Gln Leu His Asn Glu Glu Glu Asn Glu Asp
                                   100                              105                              110

gct cgc tct atg gca gca gct gct gca tcc ctc ggg gga ccc cga gca      546
Ala Arg Ser Met Ala Ala Ala Ala Ala Ser Leu Gly Gly Pro Arg Ala
                                   115                              120                              125                              130

aac aca gtc ctg gag cgt gtg gaa ggt gcc cag cag cgg tgg aag ctg      594
Asn Thr Val Leu Glu Arg Val Glu Gly Ala Gln Gln Arg Trp Lys Leu
                                   135                              140                              145

cag gtg cag gag cag cgg aag aca gtc ttc gat cgg cac aag atg ctc      642
Gln Val Gln Glu Gln Arg Lys Thr Val Phe Asp Arg His Lys Met Leu
                                   150                              155                              160

agc tagatgggct ggtgtggttg ggtcaaggcc ccaacacccat ggctgccagc      695
Ser

ttccaggctg gacaaagcag ggggctactt ctcccttccc tcggttccag tcttcccttt      755
aaaagcctgt ggcatttttc ctcccttctc ctaactttag aaatgttgta cttggctatt      815
ttgattaggg aagaggggat tgggtctctga tctctgttgt cttcttgggg ctttggggtt      875
gaagggaggg ggaaggcagg ccasaaaggg aatggagaca ttcgaggcgg cctcaggagt      935
ggatgcgac ttgtctctcc tkggcctccc actcttngcc gccttccagc tctgagtctt      995
gggaatgttg ttacccttgg aagataaagy ctgggtcttc aggaactcag tgtctgggag     1055
gaaagcatgg ccagcattc agcatgtgtt cctttctgca gtggttctta tcaccacctc     1115
cctcccagcc ccagcgcctc agccccagcc ccagctccag ccctgaggac agctctgatg     1175
ggagagctgg gccccctgag cccactgggt cttcagggtg cactggaagc tgggtgttcgc     1235
tgccccctgt gcacttctcg cactggggca tggagtgcc atgcatactc tgctgccggg     1295
cccctcacct gcacttgagg ggtctgggca gtccctctc tccccagtgt ccacagtcac     1355
tgagccagac ggtcggtttg aacatgagac tcgaggctga gcgtggatct gaacaccaca     1415

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gccctgtac ttgggttgcc tcttgtccct gaacttcgtt gtaccagtgc atggagagaa 1475
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tatttctctc taaaaaaaaa aaaaaaaaaa 1563

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               Met Leu Val Leu Arg Ser Ala Leu Thr Arg Ala
               -10                               -5
ctg gcc tca cgg acg ctg gcg cct cag atg tgc tca tct ttt gct acg 160
Leu Ala Ser Arg Thr Leu Ala Pro Gln Met Cys Ser Ser Phe Ala Thr
               1           5           10
gga ccc aga caa tac gat gga ata ttc tat gaa ttt cgt tct tat tac 208
Gly Pro Arg Gln Tyr Asp Gly Ile Phe Tyr Glu Phe Arg Ser Tyr Tyr
15           20           25           30
ctt aag ccc tca aag atg aat gag ttc ctg gaa aat ttt gag aaa aac 256
Leu Lys Pro Ser Lys Met Asn Glu Phe Leu Glu Asn Phe Glu Lys Asn
               35           40           45
gct cat ctt cgg aca gct cac tct gaa ttg gtt gga tac tgg agt gta 304
Ala His Leu Arg Thr Ala His Ser Glu Leu Val Gly Tyr Trp Ser Val
               50           55           60
gaa ttt gga ggc aga atg aat aca gtg ttt cat att tgg aag tat gat 352
Glu Phe Gly Gly Arg Met Asn Thr Val Phe His Ile Trp Lys Tyr Asp
65           70           75
aat ttt gct cat cga act gaa gtt cag aaa gcc ttg gcc aaa gat aag 400
Asn Phe Ala His Arg Thr Glu Val Gln Lys Ala Leu Ala Lys Asp Lys
80           85           90
gaa tgg caa gaa caa ttc ctc att cca aat ttg gct ctc att gat aaa 448
Glu Trp Gln Glu Gln Phe Leu Ile Pro Asn Leu Ala Leu Ile Asp Lys
95           100           105           110
caa gag agt gag att act tat ctg gta cca tgg tgc aaa tta gaa aaa 496
Gln Glu Ser Glu Ile Thr Tyr Leu Val Pro Trp Cys Lys Leu Glu Lys
115           120           125
cct cca aaa gaa gga gtc tat gaa ctg gcc act ttt cag atg aaa cct 544
Pro Pro Lys Glu Gly Val Tyr Glu Leu Ala Thr Phe Gln Met Lys Pro
130           135           140
ggg ggg cca gct ctg tgg ggt gat gca ttt aaa agg gca gtt cat gct 592
Gly Gly Pro Ala Leu Trp Gly Asp Ala Phe Lys Arg Ala Val His Ala
145           150           155
cat gtc aat cta ggc tac aca aaa cta gtt gga gtg ttc cac aca gag 640
His Val Asn Leu Gly Tyr Thr Lys Leu Val Gly Val Phe His Thr Glu
160           165           170

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tac gga gca ctc aac aga gtt cat gtt ctt tgg tgg aat gag agt gca      688
Tyr Gly Ala Leu Asn Arg Val His Val Leu Trp Trp Asn Glu Ser Ala
175                      180                      185                      190
gat agt cgt gca gct ggg aga cat aag tcc cat gag gat ccc aga gtt      736
Asp Ser Arg Ala Ala Gly Arg His Lys Ser His Glu Asp Pro Arg Val
                      195                      200                      205
gtg gca gct gtt cgg gaa agt gtc aac tac cta gta tct cag cag aat      784
Val Ala Ala Val Arg Glu Ser Val Asn Tyr Leu Val Ser Gln Gln Asn
                      210                      215                      220
atg ctt ctg att cct aca tcg ttt tca cca ctg aaa tagtttttcta      830
Met Leu Leu Ile Pro Thr Ser Phe Ser Pro Leu Lys
                      225                      230
ctgaaataca aaacatttca ttaactgcta taggatctct ctgctaattgg tgcttaaatt      890
ctcccaagag gttctcactt ttatttgaag gaggtggtaa gttaatttgc tatgtttctt      950
gcattatgaa ggctacatct gtgctttgta agtaccactt caaaaaatag ttctgtttac    1010
tttctgcatg gtatttcagt gtctgtcata cattaaaaat acttgctact gttttaagat    1070
cttgactctt catttgtttc agaatagctc ttctactgta ttctgacaac tctttgcttt    1130
atagcattttt gttgtattca aatgataatg gtagcatttc catgcttgtg acagcatttll    1190
taagttatta atatatttta tcaacctttc catcatgtct gttttcctgg ttttttttgg    1250
ttgttttttg accagtaaaa tttattttgt aataccaaat aggatttaag aaaattaacg    1310
tatttccttta ctatggaaaa ccacattgtc atttgtgaca tcatctatat taaatatggg    1370
tttcacatta gttatttgtc acttacttgg aaaatgatgc tgtaggtcc tggattataa    1430
aatctagaaa agacttgttg gtttatgtgc tgaaatgtct ttatttataa ttaatttttaa    1490
ctactatttta ctttatttcg gatcctgttt aacaaagata cttgagacat ccatttgttt    1550
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aaaaaaaaaa a                                     1621

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      seq FLYLTLNQSCIFA/NY

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cctcccaaac caaaag atg ttc tct ccg cgc caa gct ttg acg ccc gac ccc      112
      Met Phe Ser Pro Arg Gln Ala Leu Thr Pro Asp Pro
                      -45                      -40
ctg cac tct ccc gcc tac tca ccg gtc cta ggg ggt tgg tcc cgc ttt      160
Leu His Ser Pro Ala Tyr Ser Pro Val Leu Gly Gly Trp Ser Arg Phe
-35                      -30                      -25                      -20
cgt agt gtg gat ttt cgt ttc ctc tac ttg act cta aat caa tcc tgt      208
Arg Ser Val Asp Phe Arg Phe Leu Tyr Leu Thr Leu Asn Gln Ser Cys
                      -15                      -10                      -5
ata ttc gca aac tac aaa gag gcg cat gca aat aga tac tgt act gag      256
Ile Phe Ala Asn Tyr Lys Glu Ala His Ala Asn Arg Tyr Cys Thr Glu
                      1                      5                      10
ggc aga tac acg cgc gag atc cag agg ctt aca tcc cca gcc gct tgg      304

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Gly	Arg	Tyr	Thr	Arg	Glu	Ile	Gln	Arg	Leu	Thr	Ser	Pro	Ala	Ala	Trp	
15						20					25					
ccc	acc	aga	gac	aag	aac	agg	atg	ata	agc	aat	gga	atg	gca	ttg	aac	352
Pro	Thr	Arg	Asp	Lys	Asn	Arg	Met	Ile	Ser	Asn	Gly	Met	Ala	Leu	Asn	
30					35					40				45		
tct	cct	gct	gaa	gga	ctt	gca	ttt	caa	tgt	aga	ttc	tgaggctggg				398
Ser	Pro	Ala	Glu	Gly	Leu	Ala	Phe	Gln	Cys	Arg	Phe					
					50				55							
tgaaaaacttc	tctgtcacct	ttactacagc	attctcaccc	atztatattt	ctttcccctt											458
ctacatctct	attactgttg	cactatgtta	tgcattacac	catggcaaaa	ttaatcaatt											518
aatacaataa	aagcttaatt	ttaaaaaaaa	aaaaaaaaaa													557

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ggaggcagag	cggtctgcc	atg gcc	aag tac	ctg gcc	cag atc	att gtg	atg									171
		Met	Ala	Lys	Tyr	Leu	Ala	Gln	Ile	Ile	Val	Met				
		-20						-15								
ggc gtg	cag gtg	gtg ggc	agg gcc	ttt gca	cgg gcc	ttg cgg	cag gag									219
Gly Val	Gln Val	Val Gly	Arg Ala	Phe Ala	Arg Ala	Leu Arg	Gln Glu									
-10		-5			1		5									
ttt gca	gcc agc	cgg gcc	gca gct	gat gcc	cga gga	cgc gct	gga cac									267
Phe Ala	Ala Ser	Arg Ala	Ala Ala	Asp Ala	Arg Gly	Arg Ala	Gly His									
		10			15		20									
cgg tct	gca gcc	gct tcc	aac ctc	tcc ggc	ctc agc	ctc cag	gag gca									315
Arg Ser	Ala Ala	Ala Ser	Asn Leu	Ser Gly	Leu Ser	Leu Gln	Glu Ala									
		25			30		35									
cag cag	att ctc	aac gtg	tcc aag	ctg agc	cct gag	gag gtc	cag aag									363
Gln Gln	Ile Leu	Asn Val	Ser Lys	Leu Ser	Pro Glu	Glu Val	Gln Lys									
		40			45		50									
aac tat	gaa cac	tta ttt	aag gtg	aat gat	aaa tcc	gtg ggt	ggc tcc									411
Asn Tyr	Glu His	Leu Phe	Lys Val	Asn Asp	Lys Ser	Val Gly	Gly Ser									
55		60			65		70									
ttc tac	ctg cag	tca aag	gtg gtc	cgc gca	aag gag	cgc ctg	gat gag									459
Phe Tyr	Leu Gln	Ser Lys	Val Val	Arg Ala	Lys Glu	Arg Leu	Asp Glu									
		75			80		85									
gaa ctc	aaa atc	cag gcc	cag gag	gac aga	gaa aaa	ggg cag	atg ccc									507
Glu Leu	Lys Ile	Gln Ala	Gln Glu	Asp Arg	Glu Lys	Gly Gln	Met Pro									
		90			95		100									
cat acg	tgactgctcg	gtcccccccg	cccaccccg	cgctctaat	ttatagcttg											563
His Thr																
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 Met Ala Pro Asn Ser Ile Thr Leu Leu Gly Leu
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 gcc gtc aac gtg gtc acc acg ctc gtg ctc atc tcc tac tgt ccc acg 161
 Ala Val Asn Val Val Thr Thr Leu Val Leu Ile Ser Tyr Cys Pro Thr
 -5 1 5
 gcc acc gaa gag gca cca tac tgg aca tac ctt tta tgt gca ctg gga 209
 Ala Thr Glu Glu Ala Pro Tyr Trp Thr Tyr Leu Leu Cys Ala Leu Gly
 10 15 20 25
 ctt ttt att tac cag tca ctg gat gct att gat ggg aaa caa gcc aga 257
 Leu Phe Ile Tyr Gln Ser Leu Asp Ala Ile Asp Gly Lys Gln Ala Arg
 30 35 40
 aga aca aac tct tgt tcc cct tta ggg gag ctc ttt gac cat ggc tgt 305
 Arg Thr Asn Ser Cys Ser Pro Leu Gly Glu Leu Phe Asp His Gly Cys
 45 50 55
 gac tct ctt tcc aca gta ttt atg gca gtg gga gct tca att gcc gct 353
 Asp Ser Leu Ser Thr Val Phe Met Ala Val Gly Ala Ser Ile Ala Ala
 60 65 70
 cgc tta gga act tat cct gac tgg ttt ttt ttc tgc tct ttt att ggg 401
 Arg Leu Gly Thr Tyr Pro Asp Trp Phe Phe Phe Cys Ser Phe Ile Gly
 75 80 85
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 Met Phe Val Phe Tyr Cys Ala His Trp Gln Thr Tyr Val Ser Gly Met
 90 95 100 105
 ttg aga ttt gga aaa gtg gat gta act gaa att cag ata gct tta gtg 497
 Leu Arg Phe Gly Lys Val Asp Val Thr Glu Ile Gln Ile Ala Leu Val
 110 115 120
 att gtc ttt gtg ttg tct gca ttt gga gga gca aca atg tgg gac tat 545
 Ile Val Phe Val Leu Ser Ala Phe Gly Gly Ala Thr Met Trp Asp Tyr
 125 130 135
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 Thr Gly Thr Ser Val Leu Ser Pro Gly Leu His Ile Gly Leu Ile Ile
 140 145 150
 ata ctg gca ata atg atc tat aaa aag tca gca act gat gtg ttt gaa 641
 Ile Leu Ala Ile Met Ile Tyr Lys Lys Ser Ala Thr Asp Val Phe Glu
 155 160 165
 aag cat cct tgt ctt tat atc cta atg ttt gga tgt gtc ttt gct aaa 689
 Lys His Pro Cys Leu Tyr Ile Leu Met Phe Gly Cys Val Phe Ala Lys
 170 175 180 185

gtc tca caa aaa tta gtg gta gct cac atg acc aaa agt gaa cta tat	737
Val Ser Gln Lys Leu Val Val Ala His Met Thr Lys Ser Glu Leu Tyr	
190 195 200	
ctt caa gac act gtc ttt ttg ggg cca ggt ctt ttg ttt tta gac cag	785
Leu Gln Asp Thr Val Phe Leu Gly Pro Gly Leu Leu Phe Leu Asp Gln	
205 210 215	
tac ttt aat aac ttt ata gac gaa tat gtt gtt cta tgg atg gca atg	833
Tyr Phe Asn Asn Phe Ile Asp Glu Tyr Val Val Leu Trp Met Ala Met	
220 225 230	
gtg att tct tca ttt gat atg gtg ata tac ttt agt gct ttg tgc ctg	881
Val Ile Ser Ser Phe Asp Met Val Ile Tyr Phe Ser Ala Leu Cys Leu	
235 240 245	
caa att tca aga cac ctt cat cta aat ata ttc aag act gca tgt cat	929
Gln Ile Ser Arg His Leu His Leu Asn Ile Phe Lys Thr Ala Cys His	
250 255 260 265	
caa gca cct gaa cag gtt caa gtt ctt tct tca aag agt cat cag aat	977
Gln Ala Pro Glu Gln Val Gln Val Leu Ser Ser Lys Ser His Gln Asn	
270 275 280	
aac atg gat tgaagagact tccgaacact tgctatctct tgctgctgct	1026
Asn Met Asp	
gtttcatgga aggagatatt aaacatttgt ttaattttta ttttaagtgtt atacctattt	1086
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taaattaatg cctcttttta aataactaact tgtactactt ttgtggctgt gaatggatc	180
ttttattgaa ctgaggcagc ttttaaaaga cttgcctgat catttagagc actccattg	240
aggttaaatt agacttgaat ctgta atg att ctc gta act gtt cct ggt gtg	292
Met Ile Leu Val Thr Val Pro Gly Val	
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Cys Pro Ala Gln Cys Cys Trp Ala Glu Gln Arg Gly Arg Gly Ser Gly	
-5 1 5 10	
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Met Tyr Phe Ile Asp Lys Trp Ala Arg Pro Ser Trp Val Pro His Trp	
15 20 25	
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Leu Asn Asp Leu Phe Ile Val Lys Ser Gly Tyr Leu Val Cys Ile Arg	
30 35 40	
act aca gta atc agg caa ggc att gtc aga att ggg agg aat aaa atc	484
Thr Thr Val Ile Arg Gln Gly Ile Val Arg Ile Gly Arg Asn Lys Ile	

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60              65              70              75
gtc atc ttt aag gta cct gat tgc atg cac tta aat gca gat tat ttt      580
Val Ile Phe Lys Val Pro Asp Cys Met His Leu Asn Ala Asp Tyr Phe
      80              85              90
gga gtt tgaaaaggga ctattaatga aatctttctt ttcctcctt tctctttttc      636
Gly Val
ccttccccgc cactgattca gtgagctgga gattggatca cagccgaagg agtaaagggtg      696
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Met Ser Phe Leu Gln Asp Pro Ser Phe Phe Thr Met Gly Met Trp Ser
      -30              -25              -20
att ggt gca gga gcc ctg ggg gct gct gcc ttg gca ttg ctg ctt gcc      154
Ile Gly Ala Gly Ala Leu Gly Ala Ala Leu Ala Leu Leu Leu Ala
      -15              -10              -5
aac aca gac gtg ttt ctg tcc aag ccc cag aaa gcg gcc ctg gag tac      202
Asn Thr Asp Val Phe Leu Ser Lys Pro Gln Lys Ala Ala Leu Glu Tyr
      1              5              10
ctg gag gat ata gac ctg aaa aca ctg gag aag gaa cca agg act ttc      250
Leu Glu Asp Ile Asp Leu Lys Thr Leu Glu Lys Glu Pro Arg Thr Phe
      15              20              25              30
aaa gca aag gag cta tgg gaa aaa aat gga gct gtg att atg gcc gtg      298
Lys Ala Lys Glu Leu Trp Glu Lys Asn Gly Ala Val Ile Met Ala Val
      35              40              45
cgg agg cca ggc tgt ttc ctc tgt cga gag gaa gct gcg gat ctg tcc      346
Arg Arg Pro Gly Cys Phe Leu Cys Arg Glu Glu Ala Ala Asp Leu Ser
      50              55              60
tcc ctg aaa agc atg ttg gac cag ctg ggc gtc ccc ctc tat gca gtg      394
Ser Leu Lys Ser Met Leu Asp Gln Leu Gly Val Pro Leu Tyr Ala Val
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gta aag gag cac atc agg act gaa gtg aag gat ttc cag cct tat ttc      442
Val Lys Glu His Ile Arg Thr Glu Val Lys Asp Phe Gln Pro Tyr Phe
      80              85              90
aaa gga gaa atc ttc ctg gat gaa aag aaa aag ttc tat ggt cca caa      490
Lys Gly Glu Ile Phe Leu Asp Glu Lys Lys Lys Phe Tyr Gly Pro Gln
      95              100              105              110

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agg cgg aag atg atg ttt atg gga ttt atc cgt ctg gga gtg tgg tac      538
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aac ttc ttc cga gcc tgg aac gga ggc ttc tct gga aac ctg gaa gga      586
Asn Phe Phe Arg Ala Trp Asn Gly Gly Phe Ser Gly Asn Leu Glu Gly
                               130                               135                               140
gaa ggc ttc atc ctt ggg gga gtt ttc gtg gtg gga tca gga aag cag      634
Glu Gly Phe Ile Leu Gly Gly Val Phe Val Val Gly Ser Gly Lys Gln
                               145                               150                               155
ggc att ctt ctt gag cac cga gaa aaa gaa ttt gga gac aaa gta aac      682
Gly Ile Leu Leu Glu His Arg Glu Lys Glu Phe Gly Asp Lys Val Asn
                               160                               165                               170
cta ctt tct gtt ctg gaa gct gct aag atg atc aaa cca cag act ttg      730
Leu Leu Ser Val Leu Glu Ala Ala Lys Met Ile Lys Pro Gln Thr Leu
                               175                               180                               185                               190
gcc tca gag aaa aaa tgattgtgtg aaactgccca gctcagggat aaccagggac      785
Ala Ser Glu Lys Lys
                               195
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aagctaaaac ctgggaaata ggagggtttta aattgactgc caggctgggt gcagtggtc      1025
acacctgtaa tcccagcact ttgggaggcc aagggtgagca agtcacttga ggtcgggagt      1085
tcgagaccag cctgagcaac atggcgaaac ccgctctcta ctaaaaatac aaaaatcacc      1145
cgggtgtggt ggcaggcacc tgtagtccca gctaccggg aggctgaggc aggagaatca      1205
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ggtgactgag actctaacta aaaaaaaaaa aaaaaa      1301

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<220>
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<222> 59..676

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<222> 59..160
<223> Von Heijne matrix
      score 5.94384548075359
      seq LGAAALALLLANT/DV

<400> 111
attcaaaacc aggctgaaga ttggaaggaa gttggccagc ctcggtgca ggacagaa      58
atg tct ttc ctc cag gac cca agt ttc ttc acc atg ggg atg tgg tcc      106
Met Ser Phe Leu Gln Asp Pro Ser Phe Phe Thr Met Gly Met Trp Ser
                               -30                               -25                               -20
att ggt gca gga gcc ctg ggg gct gct gcc ttg gca ttg ctg ctt gcc      154
Ile Gly Ala Gly Ala Leu Gly Ala Ala Leu Ala Leu Leu Ala
                               -15                               -10                               -5
aac aca gac gtg ttt ctg tcc aag ccc cag aaa gcg gcc ctg gag tac      202
Asn Thr Asp Val Phe Leu Ser Lys Pro Gln Lys Ala Ala Leu Glu Tyr
                               1                               5                               10
ctg gag gat ata gac ctg aaa aca ctg gag aag gaa cca agg act ttc      250
Leu Glu Asp Ile Asp Leu Lys Thr Leu Glu Lys Glu Pro Arg Thr Phe
                               15                               20                               25                               30

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aaa gca aag gag cta tgg gaa aaa aat gga gct gtg att atg gcc gtg      298
Lys Ala Lys Glu Leu Trp Glu Lys Asn Gly Ala Val Ile Met Ala Val
                               35                               40                               45
cgg agg cca ggc tgt ttc ctc tgt cga gag gaa gct gcg gat ctg tcc      346
Arg Arg Pro Gly Cys Phe Leu Cys Arg Glu Glu Ala Ala Asp Leu Ser
                               50                               55                               60
tcc ctg aaa agc atg ttg gac cag ctg ggc gtc ccc ctc tat gca gtg      394
Ser Leu Lys Ser Met Leu Asp Gln Leu Gly Val Pro Leu Tyr Ala Val
                               65                               70                               75
gta aag gag cac atc agg act gaa gtg aag gat ttc cag cct tat ttc      442
Val Lys Glu His Ile Arg Thr Glu Val Lys Asp Phe Gln Pro Tyr Phe
                               80                               85                               90
aaa gga gaa atc ttc ctg gat gaa aag aaa aag ttc tat ggt cca caa      490
Lys Gly Glu Ile Phe Leu Asp Glu Lys Lys Lys Phe Tyr Gly Pro Gln
                               95                               100                               105                               110
agg cgg aag atg atg ttt atg gga ttt atc cgt ctg gga gtg tgg tac      538
Arg Arg Lys Met Met Phe Met Gly Phe Ile Arg Leu Gly Val Trp Tyr
                               115                               120                               125
aac ttc ttc cga gcc tgg aac gga ggc ttc tct gga aac ctg gaa gga      586
Asn Phe Phe Arg Ala Trp Asn Gly Gly Phe Ser Gly Asn Leu Glu Gly
                               130                               135                               140
gaa ggc ttc atc ctt ggg gga gtt ttc gtg gtg gga tca gga agc agg      634
Glu Gly Phe Ile Leu Gly Gly Val Phe Val Val Gly Ser Gly Ser Arg
                               145                               150                               155
gca ttc ttc ttg agc acc gag aaa aag aat ttg gag aca aag      676
Ala Phe Phe Leu Ser Thr Glu Lys Lys Asn Leu Glu Thr Lys
                               160                               165                               170
taaacctact ttctgttctg gaagctgcta agatgatcaa accacagact ttggcctcag      736
agaaaaaatg attgtgtgaa actgcccagc tcagggataa ccagggacat tcacctgtgt      796
tcatgggatg tattgtttcc actcgtgtcc ctaaggagtg agaaaacccat ttatactcta      856
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gccccaaaac aagactgaca aaaatctgaa aaactaatga ggattattaa gctaaaacct      976
gggaaatagg aggttttaaaa ttgactgcca ggctgggtgc agtggctcac acctgtaatc     1036
ccagcacttt gggaggccaa ggtgagcaag tcacttgagg tcgggagttc gagaccagcc     1096
tgagcaacat ggcgaaaacc cgtctctact aaaaatacaa aaatcacccg ggtgtggtgg     1156
caggcacctg tagtcccagc taccggggag gctgaggcag gagaatcact tgaacctggg     1216
aggtggaggt tgcggtgagc tgagatcaca ccactgtatt ccagcctggg tgactgagac     1276
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<210> 112

<211> 1617

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> 15..278

<220>

<221> sig_peptide

<222> 15..146

<223> Von Heijne matrix

score 12.2610572403264

seq PLFLLLLLGSVTA/DI

<400> 112

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gagaggagag gaga atg gcg gcg gaa ggc tgg att tgg cgt tgg ggc tgg      50
Met Ala Ala Glu Gly Trp Ile Trp Arg Trp Gly Trp

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ggc cgg cgg tgc ctg gga agg cct ggg ctt ctc ggc ccc ggc cct ggc				98
Gly Arg Arg Cys Leu Gly Arg Pro Gly Leu Leu Gly Pro Gly Pro Gly				
	-30	-25	-20	
ccc act aca cct ctc ttt ctt ttg ttg ttg ggg tct gtg act gcg				146
Pro Thr Thr Pro Leu Phe Leu Leu Leu Leu Ser Val Thr Ala				
	-15	-10	-5	
gat ata act gac ggc aac att gaa cat ctc aag cgg gag cat tcg ctc				194
Asp Ile Thr Asp Gly Asn Ile Glu His Leu Lys Arg Glu His Ser Leu				
1	5	10	15	
att aag ccc tac caa ggg gtc ggt tcc agc tcc ccc tct ggg act tcc				242
Ile Lys Pro Tyr Gln Gly Val Gly Ser Ser Ser Pro Ser Gly Thr Ser				
	20	25	30	
agg gca gca cta tgc tca cga gcc agt acg tac gtc tgaccacctga				288
Arg Ala Ala Leu Cys Ser Arg Ala Ser Thr Tyr Val				
	35	40		
cgagcgcagc aaagagggct ctatctggaa ccaccagccg tgcttcctca aagactggga				348
aatgcacgtc cacttcaaag tccacggcac agggagaagaag aacctccatg gagacygcat				408
cgccttgtagg tacacccggg accgcctcgt gccagggcct gtgtttggaa gcaaagataa				468
cttccacggc ttagccatct tcctggacac ctaccccaat gatgagacca ctgagcgcgt				528
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aaaaaaaaaa				1617
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	seq LLSSCGLPPSTAS/AV			
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cctggggaat agtctggccc gctccttgga accacactca gactca atg gac tct 175
Met Asp Ser
-30
gcc tca aat ccc acc aac ctt gtc agc acc tcc caa agg cac cgg ccc 223
Ala Ser Asn Pro Thr Asn Leu Val Ser Thr Ser Gln Arg His Arg Pro
-25 -20 -15
ttg ctt tca tcc tgt ggc ctc cca cca agc act gcc tca gct gtg cgc 271
Leu Leu Ser Ser Cys Gly Leu Pro Pro Ser Thr Ala Ser Ala Val Arg
-10 -5 1
agg cta tgc tcc agg gga gtg tta aaa gga tca aat gaa aga agg gat 319
Arg Leu Cys Ser Arg Gly Val Leu Lys Gly Ser Asn Glu Arg Arg Asp
5 10 15
atg gaa tca ttt tgg aaa cta aat cgt tcc cca ggg tcg gac cga tac 367
Met Glu Ser Phe Trp Lys Leu Asn Arg Ser Pro Gly Ser Asp Arg Tyr
20 25 30 35
ctg gag agc cgc gat gcc tct cga ctg agt ggc cgg gac ccc tcc tca 415
Leu Glu Ser Arg Asp Ala Ser Arg Leu Ser Gly Arg Asp Pro Ser Ser
40 45 50
tgg aca gtc gag gat gtg atg cag ttt gtc cgg gaa gct gat cct cag 463
Trp Thr Val Glu Asp Val Met Gln Phe Val Arg Glu Ala Asp Pro Gln
55 60 65
ctt gga ccc cac gct gac ctg ttt cgc aaa cac gag atc gat ggc aag 511
Leu Gly Pro His Ala Asp Leu Phe Arg Lys His Glu Ile Asp Gly Lys
70 75 80
gcc ctg ctg ctg ctg cgc agt gac atg atg atg aag tac atg ggc ctg 559
Ala Leu Leu Leu Leu Arg Ser Asp Met Met Met Lys Tyr Met Gly Leu
85 90 95
aag ctg ggg cct gca ctc aag ctc tcc tac cac att gac cgg ctg aag 607
Lys Leu Gly Pro Ala Leu Lys Leu Ser Tyr His Ile Asp Arg Leu Lys
100 105 110 115
cag ggc aag ttc tgaaccagga gaggcagcct agacaaccaa gtggcagcag 659
Gln Gly Lys Phe
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aaaaaaaaaaaa aaaaa 1634

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<212> DNA
<213> Homo sapiens

<220>
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<222> 223..417

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<221> sig_peptide

<222> 223..270

<223> Von Heijne matrix

score 4.19788230215007

seq LACVRESTSVAWA/CK

<400> 114

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gccagcgggc mgtgtcgggg tccgccccga ccccatccac gaccccgact cctatccgat 120
cctatccccg gccccgctcg ggcctttccc cttgcgcctt ggctcggctg gctcgacgag 180
cagtaagttc gtagecgccc tccgaagccg ggcgtgcatg gg atg gca gag ttg 234
                                     Met Ala Glu Leu
                                     -15
gcg tgc gtg cgt gag tcc acc agt gtg gca tgg gca tgt aag gtg cgc 282
Ala Cys Val Arg Glu Ser Thr Ser Val Ala Trp Ala Cys Lys Val Arg
      -10                -5                1
gga ggg act gca cct tct cca tca ggt gca gaa ggc cac gtc atg ctg 330
Gly Gly Thr Ala Pro Ser Pro Ser Gly Ala Glu Gly His Val Met Leu
5          10          15          20
aac aag agc cga gaa gta gaa tcg cca gtg tca agc cgt cca cgt tgt 378
Asn Lys Ser Arg Glu Val Glu Ser Pro Val Ser Ser Arg Pro Arg Cys
      25          30          35
ggg atg ccc act gtt ccc cca gga tca ctc aag acc ctg tgacttggtg 427
Gly Met Pro Thr Val Pro Pro Gly Ser Leu Lys Thr Leu
      40          45
tcaactgatga gtggaccaag tgaagtccac aagatggctg ctgtggctcc aggcattcacg 487
tccacatgca aatccatcca gaggcaggaa ctgggaatag gcttggaggt ggccaggaca 547
gcaagtgggc tgtctgtata aacctcccct ccacttgga aggaaaatca cccccaagt 607
cgattttctg tccatcttat tgatcagaga gcgttataaa ttcaccatt aaataatctg 667
gacaagggga aaaaaaaaaa aaaaaa 693
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<210> 115

<211> 784

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> 166..732

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<222> 166..237

<223> Von Heijne matrix

score 6.60662787180923

seq KMVHLLVLSGAWG/MQ

<400> 115

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gggcgtggga gtgaggtacc agattcagcc catttgccc cgacgcctct gttctcggaa 120
tccgggtgct gcggattgag gtcccggttc ctaacggact gcaag atg gag gaa ggc 177
                                     Met Glu Glu Gly
ggg aac cta gga ggc ctg att aag atg gtc cat cta ctg gtc ttg tca 225
Gly Asn Leu Gly Gly Leu Ile Lys Met Val His Leu Leu Val Leu Ser
-20          -15          -10          -5
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ggg gcc tgg ggc atg caa atg tgg gtg acc ttc gtc tca ggc ttc ctg      273
Gly Ala Trp Gly Met Gln Met Trp Val Thr Phe Val Ser Gly Phe Leu
      1      5      10
ctt ttc cga agc ctt ccc cga cat acc ttc gga cta gtg cag agc aaa      321
Leu Phe Arg Ser Leu Pro Arg His Thr Phe Gly Leu Val Gln Ser Lys
      15      20      25
ctc ttc ccc ttc tac ttc cac atc tcc atg ggc tgt gsc ttc atc aac      369
Leu Phe Pro Phe Tyr Phe His Ile Ser Met Gly Cys Xaa Phe Ile Asn
      30      35      40
ctc tgc atc ttg gct tca cag cat gct tgg gct cag ctc aca ttc tgg      417
Leu Cys Ile Leu Ala Ser Gln His Ala Trp Ala Gln Leu Thr Phe Trp
      45      50      55      60
gag gcc agc cag ctt tac ctg ctg ttc ctg agc ctt acg ctg gcc act      465
Glu Ala Ser Gln Leu Tyr Leu Leu Phe Leu Ser Leu Thr Leu Ala Thr
      65      70      75
gtc aac gcc cgc tgg ctg gaa ccc cgc acc aca gct gcc atg tgg gcc      513
Val Asn Ala Arg Trp Leu Glu Pro Arg Thr Thr Ala Ala Met Trp Ala
      80      85      90
ctg caa acc gtg gag aag gag cga ggc ctg ggt ggg gag gta cca ggc      561
Leu Gln Thr Val Glu Lys Glu Arg Gly Leu Gly Gly Glu Val Pro Gly
      95      100      105
agc cac cag ggt ccc gat ccc tac cgc cag ctg cga gag aag gac ccc      609
Ser His Gln Gly Pro Asp Pro Tyr Arg Gln Leu Arg Glu Lys Asp Pro
      110      115      120
aag tac agt gct ctc cgc cag aat ttc ttc cgc tac cat ggg ctg tcc      657
Lys Tyr Ser Ala Leu Arg Gln Asn Phe Phe Arg Tyr His Gly Leu Ser
      125      130      135      140
tct ctt tgc aat ctg ggc tgc gtc ctg agc aat ggg ctc tgt ctc gct      705
Ser Leu Cys Asn Leu Gly Cys Val Leu Ser Asn Gly Leu Cys Leu Ala
      145      150      155
ggc ctt gcc ctg gaa ata agg agc ctc tagcatgggc cctgcatgct      752
Gly Leu Ala Leu Glu Ile Arg Ser Leu
      160      165
aataaatgct tctccaaaaa aaaaaaaaaa aa      784

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<210> 116

<211> 804

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> 75..623

<220>

<221> sig_peptide

<222> 75..215

<223> Von Heijne matrix

score 8.34104221735598

seq RLLLPCLVRMALC/AP

<400> 116

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aacaaacagt aata atg act gaa tgt aca agt ctt cag ttt gtc agc cct 110

Met Thr Glu Cys Thr Ser Leu Gln Phe Val Ser Pro

-45 -40

ttt gct ttt gag gca atg cag aag gtg gat gtt gtt tgc ctg gca tct 158

Phe Ala Phe Glu Ala Met Gln Lys Val Asp Val Val Cys Leu Ala Ser


```

cgg ttc gtg tcg ttg cgc gcc aag cag aac atg atc cgc cgc ctg gag      149
Arg Phe Val Ser Leu Arg Ala Lys Gln Asn Met Ile Arg Arg Leu Glu
      15      20      25
atc gag gcg gag aac cat tac tgg ctg agc atg ccc tac atg acc cgg      197
Ile Glu Ala Glu Asn His Tyr Trp Leu Ser Met Pro Tyr Met Thr Arg
      30      35      40
gag cag gag cgc ggc cac gcc gcg gtg cgc agg agg gag gcc ttc gag      245
Glu Gln Glu Arg Gly His Ala Ala Val Arg Arg Arg Glu Ala Phe Glu
      45      50      55
gcc ata aag gcg gcc gcc act tcc aag ttc ccc ccg cat aga ttc att      293
Ala Ile Lys Ala Ala Ala Thr Ser Lys Phe Pro Pro His Arg Phe Ile
      60      65      70
gcg gac cag ctc gac cat ctc aat gtc acc aag aaa tgg tcc      335
Ala Asp Gln Leu Asp His Leu Asn Val Thr Lys Lys Trp Ser
      75      80      85
taatcctgag tcgtcaccct tggattttat ggatcacgga gctgaccatc tttacctggt      395
cctggaactg aaaaactgta gcttgtgtga aaatgagcct ttggaccagt ctttattaaa      455
acaaacaaac acaaaaaaaaaa aaaaaaaaaa      484

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<210> 118
<211> 985
<212> DNA
<213> Homo sapiens

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<221> CDS
<222> 21..752

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<220>
<221> sig_peptide
<222> 21..107
<223> Von Heijne matrix
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      seq FPLYLLNFLGLWS/WI

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      -25      -20
att tac atc ctg aca ttt ccc ttg tac ctg ctg aac ttt ctg ggc ttg      101
Ile Tyr Ile Leu Thr Phe Pro Leu Tyr Leu Leu Asn Phe Leu Gly Leu
      -15      -10      -5
tgg agc tgg ata tgc aaa aaa tgg ttc ccc tac ttc ttg gtg agg ttc      149
Trp Ser Trp Ile Cys Lys Lys Trp Phe Pro Tyr Phe Leu Val Arg Phe
      1      5      10
act gtg ata tac aac gaa cag atg gca agc aag aag cgg gag ctc ttc      197
Thr Val Ile Tyr Asn Glu Gln Met Ala Ser Lys Lys Arg Glu Leu Phe
      15      20      25      30
agt aac ctg cag gag ttt gcg ggc ccc tcc ggg aaa ctc tcc ctg ctg      245
Ser Asn Leu Gln Glu Phe Ala Gly Pro Ser Gly Lys Leu Ser Leu Leu
      35      40      45
gaa gtg ggc tgt ggc acg ggg gcc aac ttc aag ttc tac cca cct ggg      293
Glu Val Gly Cys Gly Thr Gly Ala Asn Phe Lys Phe Tyr Pro Pro Gly
      50      55      60
tgc agg gtg acc tgt att gac ccc aac ccc aac ttt gag aag ttt ttg      341
Cys Arg Val Thr Cys Ile Asp Pro Asn Pro Asn Phe Glu Lys Phe Leu
      65      70      75
atc aag agc att gca gag aac cga cac ctg cag ttt gag cgc ttt gtg      389

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Ile	Lys	Ser	Ile	Ala	Glu	Asn	Arg	His	Leu	Gln	Phe	Glu	Arg	Phe	Val		
80						85					90						
gta	gct	gcc	ggg	gag	aac	atg	cac	cag	gtg	gct	gat	ggc	tct	gtg	gat	437	
Val	Ala	Ala	Gly	Glu	Asn	Met	His	Gln	Val	Ala	Asp	Gly	Ser	Val	Asp		
95					100					105					110		
gtg	gtg	gtc	tgc	acc	ctg	gtg	ctg	tgc	tct	gtg	aag	aac	cag	gag	cgg	485	
Val	Val	Val	Cys	Thr	Leu	Val	Leu	Cys	Ser	Val	Lys	Asn	Gln	Glu	Arg		
				115					120					125			
att	ctc	cgc	gag	gtg	tgc	aga	gtg	ctg	aga	ccg	gga	ggg	gct	ttc	tat	533	
Ile	Leu	Arg	Glu	Val	Cys	Arg	Val	Leu	Arg	Pro	Gly	Gly	Ala	Phe	Tyr		
				130				135					140				
ttc	atg	gag	cat	gtg	gca	gct	gag	tgt	tcg	act	tgg	aat	tac	ttc	tgg	581	
Phe	Met	Glu	His	Val	Ala	Ala	Glu	Cys	Ser	Thr	Trp	Asn	Tyr	Phe	Trp		
				145			150					155					
caa	caa	gtc	ctg	gat	cct	gcc	tgg	cac	ctt	ctg	ttt	gat	ggg	tgc	aac	629	
Gln	Gln	Val	Leu	Asp	Pro	Ala	Trp	His	Leu	Leu	Phe	Asp	Gly	Cys	Asn		
				160		165				170							
ctg	acc	aga	gaq	agc	tgg	aag	gcc	ctg	gag	cgg	gcc	agc	ttc	tct	aag	677	
Leu	Thr	Arg	Glu	Ser	Trp	Lys	Ala	Leu	Glu	Arg	Ala	Ser	Phe	Ser	Lys		
					180				185						190		
ctg	aag	ctg	cag	cac	atc	cag	gcc	cca	ctg	tcc	tgg	gag	ttg	gtg	cgc	725	
Leu	Lys	Leu	Gln	His	Ile	Gln	Ala	Pro	Leu	Ser	Trp	Glu	Leu	Val	Arg		
				195				200						205			
cct	cat	atc	tat	gga	tat	gct	gtg	aaa	tagtgtgagc	tggcagttaa						772	
Pro	His	Ile	Tyr	Gly	Tyr	Ala	Val	Lys									
				210			215										
gagctgaatg	gctcaaagaa	tttaaagctt	cagttttaca	tttaaaatgc	taggtgggtg											832	
cctgtaatcc	caggtacttg	gaaggctgag	gcaggagaat	ctcttgaacc	cagaaggcga											892	
aggttgacgt	gaaccgagat	catgccattg	tactctagcc	tggttgacaa	gagcaagact											952	
ccgtctcaaa	aaaaaataaa	aaaaaaaaaa	aaa													985	

<210> 119

<211> 839

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> 185..715

<220>

<221> sig_peptide

<222> 185..253

<223> Von Heijne matrix

score 9.49395175807817

seq SLLFICFFGESFC/IC

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cagctcctgg tattttctgc ttcccttcgt agggaattta gttattttat tttattatatt 120

agctaattta gctattttta aatagctaaa ttttagctac ttttttttca attgacaaag 180

aagg atg tct aat caa aga cta ccg ctg att ttt tct ctg ttg ttt atc 229

Met Ser Asn Gln Arg Leu Pro Leu Ile Phe Ser Leu Leu Phe Ile

-20

-15

-10

tgc ttc ttc ggg gag agt ttc tgc att tgt gat gga act gtc tgg aca 277

Cys Phe Phe Gly Glu Ser Phe Cys Ile Cys Asp Gly Thr Val Trp Thr

-5

1

5

aag gtt gga tgg gag att ctt cca gaa gaa gta cat tat tgg aaa gtt 325

Lys	Val	Gly	Trp	Glu	Ile	Leu	Pro	Glu	Glu	Val	His	Tyr	Trp	Lys	Val		
10						15					20						
aag	ggt	tct	cca	tct	cac	tgc	ctg	cct	tat	ctt	ctg	gat	aaa	cta	tgc	373	
Lys	Gly	Ser	Pro	Ser	His	Cys	Leu	Pro	Tyr	Leu	Leu	Asp	Lys	Leu	Cys		
25					30					35				40			
tgc	gac	ttt	gct	aac	atg	gat	ata	ttt	cag	ggt	tgt	tta	tat	ctc	att	421	
Cys	Asp	Phe	Ala	Asn	Met	Asp	Ile	Phe	Gln	Gly	Cys	Leu	Tyr	Leu	Ile		
				45				50						55			
tat	aat	tta	tta	caa	gct	gtc	ttc	ttc	gtc	tta	ttt	ggt	ttg	tct	gtg	469	
Tyr	Asn	Leu	Leu	Gln	Ala	Val	Phe	Phe	Val	Leu	Phe	Val	Leu	Ser	Val		
				60				65					70				
cat	tac	ctg	tgg	aag	aaa	tgg	aag	aaa	cac	caa	aaa	aag	ctg	aaa	aag	517	
His	Tyr	Leu	Trp	Lys	Lys	Trp	Lys	Lys	His	Gln	Lys	Lys	Leu	Lys	Lys		
				75			80					85					
caa	gcc	tcc	tta	gaa	aaa	cct	ggt	aat	gat	cta	gaa	agc	cca	ttg	atc	565	
Gln	Ala	Ser	Leu	Glu	Lys	Pro	Gly	Asn	Asp	Leu	Glu	Ser	Pro	Leu	Ile		
				90			95						100				
aac	aac	att	gac	caa	aca	ctc	cac	aga	gtg	gca	acc	aca	gca	tca	gtg	613	
Asn	Asn	Ile	Asp	Gln	Thr	Leu	His	Arg	Val	Ala	Thr	Thr	Ala	Ser	Val		
					110					115					120		
ata	tac	aag	atc	tgg	gag	cac	agg	tct	cac	cat	cct	tcc	tct	aag	aaa	661	
Ile	Tyr	Lys	Ile	Trp	Glu	His	Arg	Ser	His	His	Pro	Ser	Ser	Lys	Lys		
				125				130						135			
att	aag	cac	tgc	aaa	tta	aag	aag	aag	agt	aaa	gaa	gaa	gga	gcc	aga	709	
Ile	Lys	His	Cys	Lys	Leu	Lys	Lys	Lys	Ser	Lys	Glu	Glu	Gly	Ala	Arg		
				140				145					150				
aga	tac	taaataaatg	catatgcaaa	tgtagcttac	tcaattatag	atatcacaaa										765	
Arg	Tyr																
agaaatctat	catctaagga	ttaaaaattg	ttctttggaa	acctttataa	aaaaaaaaaga											825	
aaaaaaaaaa	aaaaa															839	

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 <211> 583
 <212> DNA
 <213> Homo sapiens

<220>
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 <222> 54..527

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 <222> 54..116
 <223> Von Heijne matrix
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 seq ALXSLNLAPPTVA/AP

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						Met											
gcc	ctg	tgc	gca	ctg	acc	cgc	gct	ctg	ccs	tct	ctg	aac	ctg	gcg	ccc	104	
Ala	Leu	Cys	Ala	Leu	Thr	Arg	Ala	Leu	Pro	Ser	Leu	Asn	Leu	Ala	Pro		
-20					-15					-10					-5		
ccg	acc	gtc	gcc	gcc	cct	gcc	ccg	agt	ctg	ttc	ccc	gcc	gcc	cag	atg	152	
Pro	Thr	Val	Ala	Ala	Pro	Ala	Pro	Ser	Leu	Phe	Pro	Ala	Ala	Gln	Met		
				1			5						10				
atg	aac	aat	ggc	ctc	ctc	caa	cag	ccc	tct	gcc	ttg	atg	ttg	ctc	ccc	200	
Met	Asn	Asn	Gly	Leu	Leu	Gln	Gln	Pro	Ser	Ala	Leu	Met	Leu	Leu	Pro		

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      15      20      25
tgc cgc cca gtt ctt act tct gtg gcc ctt aat gcc aac ttt gtg tcc      248
Cys Arg Pro Val Leu Thr Ser Val Ala Leu Asn Ala Asn Phe Val Ser
      30      35      40
tgg aag agt cgt acc aag tac acc att aca cca gtg aag atg agg aag      296
Trp Lys Ser Arg Thr Lys Tyr Thr Ile Thr Pro Val Lys Met Arg Lys
      45      50      55      60
tct ggg ggc cga gac cac aca ggt gct gga aac gtg cgt aga aca gta      344
Ser Gly Gly Arg Asp His Thr Gly Ala Gly Asn Val Arg Arg Thr Val
      65      70      75
ggc cga gta tcc aac gtt gat cat aac aaa cgg gtc att ggc aag gca      392
Gly Arg Val Ser Asn Val Asp His Asn Lys Arg Val Ile Gly Lys Ala
      80      85      90
ggg cgc aac cgc tgg ctg ggc aag agg cct aac agt ggg cgg tgg cac      440
Gly Arg Asn Arg Trp Leu Gly Lys Arg Pro Asn Ser Gly Arg Trp His
      95      100      105
cgc aag ggg ggc tgg gct ggc cga aag att cgg cca cta ccc ccc atg      488
Arg Lys Gly Gly Trp Ala Gly Arg Lys Ile Arg Pro Leu Pro Pro Met
      110      115      120
aag agt tac gtg aag ctg cct tct gct tct gcc caa agc tgatattcct      537
Lys Ser Tyr Val Lys Leu Pro Ser Ala Ser Ala Gln Ser
      125      130      135
gtactctaat aaaatgcccc cccccctca aaaaaaaaaa aaaaaa      583

<210> 121
<211> 1024
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> 129..686

<220>
<221> sig_peptide
<222> 129..185
<223> Von Heijne matrix
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      seq SVFLLMVNGQVES/AQ

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gcaacgccgg cgtctcttag caaccgcgcg cggcctaggt gggcccccc ggcaccccc      120
gacctgcc atg gcg acc gcg agt cct agc gtc ttt cta ctc atg gtc aac      170
      Met Ala Thr Ala Ser Pro Ser Val Phe Leu Leu Met Val Asn
      -15      -10
ggg cag gtg gag agc gcc cag ttt cca gag tat gat gac ctc tac tgc      218
Gly Gln Val Glu Ser Ala Gln Phe Pro Glu Tyr Asp Asp Leu Tyr Cys
      -5      1      5      10
aag tac tgc ttt gtg tac ggc cag gac tgg gcc ccc aca gcg ggt ctg      266
Lys Tyr Cys Phe Val Tyr Gly Gln Asp Trp Ala Pro Thr Ala Gly Leu
      15      20      25
gag gag ggg atc tca cag atc aca tcc aag agc caa gat gtg cgg caa      314
Glu Glu Gly Ile Ser Gln Ile Thr Ser Lys Ser Gln Asp Val Arg Gln
      30      35      40
gca ctg gtg tgg aac ttc ccc att gat gtc acc ttt aaa agc acc aac      362
Ala Leu Val Trp Asn Phe Pro Ile Asp Val Thr Phe Lys Ser Thr Asn
      45      50      55

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ccc tac ggc tgg cca cag atc gtg ctc agc gtg tat gga cca gat gtg      410
Pro Tyr Gly Trp Pro Gln Ile Val Leu Ser Val Tyr Gly Pro Asp Val
60          65          70          75
ttc ggg aac gat gtg gtt cga ggc tat ggg gcc gtg cac gtg ccc ttc      458
Phe Gly Asn Asp Val Val Arg Gly Tyr Gly Ala Val His Val Pro Phe
80          85          90
tca cct ggc cgg cac aaa agg acc atc ccc atg ttt gtc cca gaa tct      506
Ser Pro Gly Arg His Lys Arg Thr Ile Pro Met Phe Val Pro Glu Ser
95          100          105
acg tct aaa ctg cag aag ttt aca agc tgg ttc atg ggg cgg cgg ccc      554
Thr Ser Lys Leu Gln Lys Phe Thr Ser Trp Phe Met Gly Arg Arg Pro
110          115          120
gag tac aca gac ccc aag gtg gtg gct cag ggt gaa ggc cgg gaa gct      602
Glu Tyr Thr Asp Pro Lys Val Val Ala Gln Gly Glu Gly Arg Glu Ala
125          130          135
atc aca gct ccc cgg aaa gct gtc ttc tct gtc cat ggc ctc acc tca      650
Ile Thr Ala Pro Arg Lys Ala Val Phe Ser Val His Gly Leu Thr Ser
140          145          150          155
ccc agg gca ctg gcc ttg gtc cac atc aag ggg acc tgaagcttcc      696
Pro Arg Ala Leu Ala Leu Val His Ile Lys Gly Thr
160          165
ctgaagcctc tagcctgtgg tgtgcacgta caagcctcag gccccatttg tccagcctgt      756
cagcagctgg gaaataactaa gtcaccctct tctgggtatg ttttaattttc caatttttct      816
caacattact gaaatgtcta aatgtggaaa agttgacatc attttacagt gaacaccaca      876
taccaccac ctagatttta ccattaccaa tttcctgttc cgtacttgta tattcacata      936
tatccaacta ttcattccctg cttcaatcca tcctattttt attgcatttc aaaataaact      996
gtgaaatcag gaaaaaaaaa aaaaaaaaaa      1024

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<212> DNA
<213> Homo sapiens

<220>
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<222> 165..614

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<221> sig_peptide
<222> 165..305
<223> Von Heijne matrix
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      seq ALGLALCSTKALS/VG

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gcctctccag gcctcgaagg cttctcctgg gctgatgcga gctggggaac gggagggacg      120
gacgtgggag cgagaacgtc acactggagg cagctgggtg cacg atg ggg gac aga      176
                               Met Gly Asp Arg
                               -45
gtg aaa ggt agc aag tca aga gcc ttc gtg tca cca tgg cca cac acc      224
Val Lys Gly Ser Lys Ser Arg Ala Phe Val Ser Pro Trp Pro His Thr
-40          -35          -30
ccg atg gct tcc ggc ttg agg gac ccc tgg ctg cag ccc aca gcc ctg      272
Pro Met Ala Ser Gly Leu Arg Asp Pro Trp Leu Gln Pro Thr Ala Leu
-25          -20          -15
ggc ctt gca ctg tgc tct acg aag gcc ctg tcc gtg ggc tct gcc cct      320
Gly Leu Ala Leu Cys Ser Thr Lys Ala Leu Ser Val Gly Ser Ala Pro

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-10	-5	1	5	
ttg ccc ccg cga aat tcc aac acc atg gcg gcg gct gcc ctg gct gcc	368			
Leu Pro Pro Arg Asn Ser Asn Thr Met Ala Ala Ala Leu Ala Ala				
10 15 20				
ccc agc ctg ggc ttc gat ggg gtg att ggg gtg ctc gtg gct gat acc	416			
Pro Ser Leu Gly Phe Asp Gly Val Ile Gly Val Leu Val Ala Asp Thr				
25 30 35				
agc ctc acg gac atg cac gtg gtg gat gta gag ctg agc gga ccc cgg	464			
Ser Leu Thr Asp Met His Val Val Asp Val Glu Leu Ser Gly Pro Arg				
40 45 50				
ggc ccc acg ggc cga agc ttt gct gtg cac acc cgc aga gag aac cct	512			
Gly Pro Thr Gly Arg Ser Phe Ala Val His Thr Arg Arg Glu Asn Pro				
55 60 65				
gcc gag cca ggc gcg gtc acc ggc tcc gcc acc gtc acg gcc ttc tgg	560			
Ala Glu Pro Gly Ala Val Thr Gly Ser Ala Thr Val Thr Ala Phe Trp				
70 75 80 85				
cgg agc ctc ctg gcc tgc tgc cag ctc ccc tcc agg ccg ggg atc cat	608			
Arg Ser Leu Leu Ala Cys Cys Gln Leu Pro Ser Arg Pro Gly Ile His				
90 95 100				
ctc tgc tgagaagcct cctccctccc gagacaagat catctgcctg gcctctcacc	664			
Leu Cys				
accaccatcc caccctgcc ctgccccact tccccagggt ctcccttctg actcagtaaa	724			
gatcaccgct gcctccctca aaaaaaaaaa aaaaaa	760			

<210> 123
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 <212> DNA
 <213> Homo sapiens

<220>
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 <222> 192..476

<220>
 <221> sig_peptide
 <222> 192..326
 <223> Von Heijne matrix
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 seq FILLLLLSGPAEM/SA

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ggagaaggca ggtcctcttt atgttttcgc agctggttca aggggttttg ggttttctat	120
ctaggttaaa gattgcgtaa tacacagctg gagccataga cattaatgca tgtttatcac	180
acgcaacaac g atg ctg cat cat gtg att aca gct ggg cct gtg ctg ctt	230
Met Leu His His Val Ile Thr Ala Gly Pro Val Leu Leu	
-45 -40 -35	
cta cac ctc cct cgc cct gac act tcc acc agg ttg ctc ctc acc tcc	278
Leu His Leu Pro Arg Pro Asp Thr Ser Thr Arg Leu Leu Leu Thr Ser	
-30 -25 -20	
gtc tct gct ttt atc ctc tta ctg ctc ctt tca gga cca gca gaa atg	326
Val Ser Ala Phe Ile Leu Leu Leu Leu Ser Gly Pro Ala Glu Met	
-15 -10 -5	
tca gct tcc cag gaa tcc ttc cct gga tct ctg cag caa gaa ata gct	374
Ser Ala Ser Gln Glu Ser Phe Pro Gly Ser Leu Gln Gln Glu Ile Ala	
1 5 10 15	
tct ctg atc act gta gca ctt ggt tct tta ata tct tta tct tgc tct	422
Ser Leu Ile Thr Val Ala Leu Gly Ser Leu Ile Ser Leu Ser Cys Ser	

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                20                25                30
acc ttg tta tat ttt tct tgt gaa ctt aaa att ccc tgt gag gac gta      470
Thr Leu Leu Tyr Phe Ser Cys Glu Leu Lys Ile Pro Cys Glu Asp Val
                35                40                45
aac ctt tgaaggtatg tctcatatct ctgaacctct ttaaaatgcc tagcatccct      526
Asn Leu
                50
gtgtgggtgc caattgcttg tgtattgaat taaattgtga ttgttaactt gaaaaaaaaa      586
aaaaaaaaa      594

<210> 124
<211> 559
<212> DNA
<213> Homo sapiens

<220>
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<222> 16..297

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<221> sig_peptide
<222> 16..93
<223> Von Heijne matrix
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      seq FCGSACLLAVIRA/FF

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      Met Ala Ala Ile Glu Ile Glu Val Lys Pro Asn Gln
                -25                -20                -15
ggc ttt tgc ggg agc gca tgc ctt ttg gct gta att cgt gca ttt ttt      99
Gly Phe Cys Gly Ser Ala Cys Leu Leu Ala Val Ile Arg Ala Phe Phe
                -10                -5                1
ttt aag aaa aac gcc tgc ctt ctg cgt gag att ctc cag agc aaa ctg      147
Phe Lys Lys Asn Ala Cys Leu Leu Arg Glu Ile Leu Gln Ser Lys Leu
                5                10                15
ggc ggc atg ggc cct gtg gtc ttt tcg tac aga ggg ctt cct ctt tgg      195
Gly Gly Met Gly Pro Val Val Phe Ser Tyr Arg Gly Leu Pro Leu Trp
                20                25                30
ctc ttt gcc tgg ttg ttt cca aga tgt act gtg cct ctt act ttc ggt      243
Leu Phe Ala Trp Leu Phe Pro Arg Cys Thr Val Pro Leu Thr Phe Gly
                35                40                45                50
ttt gaa aac atg agg ggg ttg ggc gtg gta gct tac gcc tgt aat ccc      291
Phe Glu Asn Met Arg Gly Leu Gly Val Val Ala Tyr Ala Cys Asn Pro
                55                60                65
agc act tagggaggcc gaggcgggag gatggcttga ggtccgtagt tgagaccagc      347
Ser Thr
ctggccaaca tgggtgaagcc tgggtctctac aaaaaaataa taacaaaaat tagccgggtg      407
tgggtggctcg tgccctgtggt cccagctgct cccgtggctg aggcgggagg atctcttgag      467
cttaggcttt tgagctatca tggcgccagt gcactccagc gtgggcaaca gagcgagacc      527
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<210> 125
<211> 744
<212> DNA
<213> Homo sapiens

<220>

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<221> CDS
 <222> 216..635

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 <221> sig_peptide
 <222> 216..335
 <223> Von Heijne matrix
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 seq ITLVSAAPGKVIC/EM

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 cctttgtgtc ctccctcttt cactaacttc tggactttcc agctcttccg aagttcgttc 180
 ttgcgcaaaag cccaaaggct ggaaaaccgt ccacg atg acc agc atg act cag 233
 Met Thr Ser Met Thr Gln
 -40 -35
 tct ctg cgg gag gtg ata aag gcc atg acc aag gct cgc aat ttt gag 281
 Ser Leu Arg Glu Val Ile Lys Ala Met Thr Lys Ala Arg Asn Phe Glu
 -30 -25 -20
 aga gtt ttg gga aag att act ctt gtc tct gct gct cct ggg aaa gtg 329
 Arg Val Leu Gly Lys Ile Thr Leu Val Ser Ala Ala Pro Gly Lys Val
 -15 -10 -5
 att tgt gaa atg aaa gta gaa gaa gag cat acc aat gca ata ggc act 377
 Ile Cys Glu Met Lys Val Glu Glu Glu His Thr Asn Ala Ile Gly Thr
 1 5 10
 ctc cac ggc ggt ttg aca gcc acg tta gta gat aac ata tca aca atg 425
 Leu His Gly Gly Leu Thr Ala Thr Leu Val Asp Asn Ile Ser Thr Met
 15 20 25 30
 gct ctg cta tgc acg gaa agg gga gca ccc gga gtc agt gtc gat atg 473
 Ala Leu Leu Cys Thr Glu Arg Gly Ala Pro Gly Val Ser Val Asp Met
 35 40 45
 aac ata acg tac atg tca cct gca aaa tta gga gaa gat ata gtg att 521
 Asn Ile Thr Tyr Met Ser Pro Ala Lys Leu Gly Glu Asp Ile Val Ile
 50 55 60
 aca gca cat gtt ctg aag caa gga aaa aca ctt gca ttt acc tct gtg 569
 Thr Ala His Val Leu Lys Gln Gly Lys Thr Leu Ala Phe Thr Ser Val
 65 70 75
 gat ctg acc aac aag gcc aca gga aaa tta ata gca caa gga aga cac 617
 Asp Leu Thr Asn Lys Ala Thr Gly Lys Leu Ile Ala Gln Gly Arg His
 80 85 90
 aca aaa cac ctg gga aac tgagagaaca gcagaatgac ctaaagaaac 665
 Thr Lys His Leu Gly Asn
 95 100
 ccaacaatga atatcaagta tagatttgac tcaaacaatt gtaatttttg aaataaacta 725
 gcaaaaaaaaa aaaaaaaaaa 744

<210> 126
 <211> 824
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> 164..280

<220>
 <221> sig_peptide

<222> 164..268
 <223> Von Heijne matrix
 score 5.73290676305402
 seq TLPLCPVTSPVWG/WS

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 ccaggagacc tacacagtgg cccacgagga gaatgtccgc tttgtgtccg aaggtagcga 120
 gcggggccag aggggtgcggc ataggctgct gggtcgcaaa acc atg gac ccg gga 175
 Met Asp Pro Gly
 -35
 tgg ccc cac ttc aag ctg acc cac agc cgc tgc atg gct gtg ctt ttc 223
 Trp Pro His Phe Lys Leu Thr His Ser Arg Cys Met Ala Val Leu Phe
 -30 -25 -20
 ctt ggc act ctg ccc ttg tgt cct gtg acc agc cct gtg tgg ggc tgg 271
 Leu Gly Thr Leu Pro Leu Cys Pro Val Thr Ser Pro Val Trp Gly Trp
 -15 -10 -5 1
 agt cca ggg tgaccatcag gccctgggtg ggcgatgggg tgccctgggac 320
 Ser Pro Gly
 ctggctcagc ccgactgccc tcctcccaca gcctggcagc aggtgcaaca gcagctggat 380
 ggtggcccgag ccggtgaggg cgggccaaag cctgtgcagt acgtggagag gacccccaat 440
 ccccggtgc agaactttgt gcccatctac ctagacgagt ggtgggcgca gcagttcctg 500
 gcgagaatca ccagctgttc ctagtggctg ctgggagggg gcgctgctac acggccgacc 560
 tgtcgccagg agagaagcat ggcgcctgc ccaccactg cgccctggctg ggtgccggcc 620
 acacctgaag tgccagcatt tggacttttg cacctttttt tcccttggcc cggctgtccc 680
 aaccaagctg ccatggccaa gggccgaacc cgtctgacct cagccctgct cactgtgccc 740
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 aaactgtcaa aaaaaaaaaa aaaa 824

<210> 127
 <211> 526
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> 68..301

<220>
 <221> sig_peptide
 <222> 68..190
 <223> Von Heijne matrix
 score 4.68908216483476
 seq AYLLYILLTGALQ/FG

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 acatccggtg tggtcgacgg gtcctccaag agtttggggc gcggaccgga gtaccttgcg 60
 tgcagtt atg tcg gcg tcg gta gtg tct gtc att tcg cgg ttc tta gaa 109
 Met Ser Ala Ser Val Val Ser Val Ile Ser Arg Phe Leu Glu
 -40 -35 -30
 gag tac ttg agc tcc act ccg cag cgt ctg aag ttg ctg gac gcg tac 157
 Glu Tyr Leu Ser Ser Thr Pro Gln Arg Leu Lys Leu Leu Asp Ala Tyr
 -25 -20 -15
 ctg ctg tat ata ctg ctg acc ggg gcg ctg cag ttc ggt tac tgt ctc 205
 Leu Leu Tyr Ile Leu Leu Thr Gly Ala Leu Gln Phe Gly Tyr Cys Leu
 -10 -5 1 5
 ctc gtg ggg acc ttc ccc ttc aac tct ttt ctc tcg ggc ttc atc tct 253
 Leu Val Gly Thr Phe Pro Phe Asn Ser Phe Leu Ser Gly Phe Ile Ser

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          10          15          20
tgt gtg ggg agt ttc atc cta gcg ggt tca ctc ttt gaa ttt cct gga    301
Cys Val Gly Ser Phe Ile Leu Ala Gly Ser Leu Phe Glu Phe Pro Gly
          25          30          35
taagagttct ggagatggca gcttattgga cacatggatt ttcttcagat ttgcacttac    361
tgctagctct gctttttatg caggagaaaa gccagagatt cactgtgtgt cagaacaact    421
ttctaacaaa catattattaa tccagcctct gcctttcatt aaatgtaacc ttttgccttc    481
caaattaaag aactccatgc cactcctcaa aaaaaaaaaa aaaaa                    526

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<210> 128
 <211> 618
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> 179..427

<220>
 <221> sig_peptide
 <222> 179..298
 <223> Von Heijne matrix
 score 7.72883276007822
 seq CLVVVTMATLSLA/RP

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<400> 128
aagcgaagag atgggtctgc actttggagg agcgggacac tgttgacttt cctgatgtga    60
aatctaccca ggaacaaaaac accagtgact gcagcagcag cggcagcgcc tcggttcctg    120
agcccaccgc aggetgaagg cattgcgcgt agtccatgcc cgtagaggaa gtgtgcag    178
atg gga tta acg tcc aca tgg aga tat gga aga gga ccg ggg att ggt    226
Met Gly Leu Thr Ser Thr Trp Arg Tyr Gly Arg Gly Pro Gly Ile Gly
-40          -35          -30          -25
acc gta acc atg gtc agc tgg ggt cgt ttc atc tgc ctg gtc gtg gtc    274
Thr Val Thr Met Val Ser Trp Gly Arg Phe Ile Cys Leu Val Val Val
          -20          -15          -10
acc atg gca acc ttg tcc ctg gcc cgg ccc tcc ttc agt tta gtt gag    322
Thr Met Ala Thr Leu Ser Leu Ala Arg Pro Ser Phe Ser Leu Val Glu
          -5          1          5
gat acc aca tta gag cca gaa gat gcc atc tca tcc gga gat gat gag    370
Asp Thr Thr Leu Glu Pro Glu Asp Ala Ile Ser Ser Gly Asp Asp Glu
          10          15          20
gat gac acc gat ggt gcg gaa gat ttt gtc agt gag aac agt aac aac    418
Asp Asp Thr Asp Gly Ala Glu Asp Phe Val Ser Glu Asn Ser Asn Asn
          25          30          35          40
aag agt aag taactgccc gctccgatgg tccccgagag aggagcatgg    467
Lys Ser Lys
agggaagttc tgctgtcac ctgtcttctt gtgcactctt ctgcgccatg ctgtgtcccg    527
cggcccttgc ctttccccgc tgtgtctact ttcttgactt tcaaacctga gaataaacca    587
gtgttgcctg acataaaaaa aaaaaaaaaa a                    618

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<210> 129
 <211> 776
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> 22..297


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<220>
<221> sig_peptide
<222> 22..66
<223> Von Heijne matrix
      score 4.68058603039206
      seq VLAGSLLGPTSRS/AA

<400> 129
actgcgggac ccaactgcgga t atg gct gtc ttg gct gga tcc ctg ttg ggc      51
                      Met Ala Val Leu Ala Gly Ser Leu Leu Gly
                      -15                      -10

ccc acg agt agg tcg gca gcg ttg ctg ggt ggc agg tgg ctc cag ccc      99
Pro Thr Ser Arg Ser Ala Ala Leu Leu Gly Gly Arg Trp Leu Gln Pro
-5                      1                      5                      10

cgg gcc tgg ctg ggg ttc cca gac gcc tgg ggc ctc ccc acc ccg cag      147
Arg Ala Trp Leu Gly Phe Pro Asp Ala Trp Gly Leu Pro Thr Pro Gln
                      15                      20                      25

cag gcc cgg ggc aag gct cgc ggg aat gag tat cag ccg agc aat atc      195
Gln Ala Arg Gly Lys Ala Arg Gly Asn Glu Tyr Gln Pro Ser Asn Ile
                      30                      35                      40

aaa cgc aag aac aag cac ggc tgg gtc cgg cgc ctg agc acg ccg gcc      243
Lys Arg Lys Asn Lys His Gly Trp Val Arg Arg Leu Ser Thr Pro Ala
                      45                      50                      55

ggc gtg cag gtc atc ctt cgc cga atg ctc aag ggc cgc aag tcg ctg      291
Gly Val Gln Val Ile Leu Arg Arg Met Leu Lys Gly Arg Lys Ser Leu
60                      65                      70                      75

agc cat tgaggatcgc gacgcagtcg gcgggggaccc tcatggaagc atcgccctcg      347
Ser His

cctcggacct tgcctggcgc tatttttgca gggagctggg gagcaggaac gcctcggacc      407
tgagtgtctt ccatattgtg ggtttgaagt ctggatggga gccttgccaa gtcccttttt      467
aggcttttta attaggaagc atttcgaacc tgcgcaacag accaaagaac agtacaaaga      527
acatccgtgt acccagtacc ctgactaccg actacctaca acccgccctt gccccatcct      587
gagttctttt gaagctgacg tcaggcatcg gattatttct tctgtaaata ttccagaatg      647
tatctctcca agatgagagc tcattaaaaa ataattacaa agcttatcac atccaaaaga      707
attatcaata attttgaaat attattaaac gtgtaataaa tgttcaaagt tcaaaaaaaaa      767
aaaaaaaaaa

<210> 130
<211> 998
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> 9..845

<220>
<221> sig_peptide
<222> 9..134
<223> Von Heijne matrix
      score 6.13963522287438
      seq RSLALAAPSSNG/SP

<400> 130
aacgaaag atg gcg gcg ccc gta agg cgg acg ctg tta ggg gtg gcg ggg      50
      Met Ala Ala Pro Val Arg Arg Thr Leu Leu Gly Val Ala Gly
      -40                      -35                      -30

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<213> Homo sapiens

<220>

<221> CDS

<222> 27..578

<220>

<221> sig_peptide

<222> 27..119

<223> Von Heijne matrix

score 4.50637135496675

seq TALMVGAASLLEG/RP

<400> 131

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atcttttctgg actggccctg cagagg atg gca tgc acc act act gcc ccc gcc      53
                               Met Ala Cys Thr Thr Thr Ala Pro Ala
                               -30                               -25
cag gaa cac atg ctt ctc acc cct ctc act gct ctg atg gtg ggg gct      101
Gln Glu His Met Leu Leu Thr Pro Leu Thr Ala Leu Met Val Gly Ala
      -20                               -15                               -10
gct tct ctg ctt gag ggc cgg cca cag atc tca gct cca tac tcc cga      149
Ala Ser Leu Leu Glu Gly Arg Pro Gln Ile Ser Ala Pro Tyr Ser Arg
      -5                               1                               5                               10
gct gca tgt tgc agc cct ggg gca ctg gga tgt cct gca gct cgg gtt      197
Ala Ala Cys Cys Ser Pro Gly Ala Leu Gly Cys Pro Ala Ala Arg Val
                               15                               20                               25
ggg att ctg gat ctg atg tat tcc tgg gtt gcc agg aaa gtg ctc agg      245
Gly Ile Leu Asp Leu Met Tyr Ser Trp Val Ala Arg Lys Val Leu Arg
                               30                               35                               40
tgc agc aat act ggg ctg cag ggg ctg cac tgt gca cca gct tat gca      293
Cys Ser Asn Thr Gly Leu Gln Gly Leu His Cys Ala Pro Ala Tyr Ala
      45                               50                               55
gca cag ctt ggt atg gac cct ggg agg ggc caa cga gca gga ggg cct      341
Ala Gln Leu Gly Met Asp Pro Gly Arg Gly Gln Arg Ala Gly Gly Pro
      60                               65                               70
gta gag cag aca tac ttc agt ccc atg ggg aag ctg ccc act ctt tgc      389
Val Glu Gln Thr Tyr Phe Ser Pro Met Gly Lys Leu Pro Thr Leu Ser
      75                               80                               85                               90
tgg ctg gaa ggc tgt aca gca gtc atg acg ctg gca tct gct tgg ctt      437
Trp Leu Glu Gly Cys Thr Ala Val Met Thr Leu Ala Ser Ala Trp Leu
      95                               100                               105
ctg ggg agc cct cgg gaa act tac aat cat gag aag gtg aag gag aag      485
Leu Gly Ser Pro Arg Glu Thr Tyr Asn His Glu Lys Val Lys Glu Lys
      110                               115                               120
cag tgt cca ttc tcc agt atg gtt ttg ggg gag tat ggc ttc cta cct      533
Gln Cys Pro Phe Ser Ser Met Val Leu Gly Glu Tyr Gly Phe Leu Pro
      125                               130                               135
act gtg gac cac ctg tca act ctg ggc tgt aac atg aga gaa ttg      578
Thr Val Asp His Leu Ser Thr Leu Gly Cys Asn Met Arg Glu Leu
      140                               145                               150
tgaacttctg tcttggttga gccatggttt cattctcttt ttcagccatg tagcctgtgc      638
tgtaactcag taccacatta gcaactagtg aaagtcaatg tgggtaaatt tgtcattctt      698
caggtagaaa catttcttcc ttttattctt gtgttttttg ctaaataaac tgggaaatta      758
tagtaaaaaa aaaaaaaaaa a                                     779
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<210> 132

<211> 1025

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> 408..710

<220>

<221> sig_peptide

<222> 408..533

<223> Von Heijne matrix

score 5.66440183652506

seq QLCFHLSWLYSWA/SQ

<400> 132

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atggttttgtt gtgagttcca tgtcctcttg gatcagtcac tgtggccatg catgtttggc      60
cacatgatta atccagtctg ggtcatgacc ttttcttcat ccaaaacaag gtgatgggaa      120
gacaaaaaca atagctacta caaacaatag gagtttataa ttatgtgctg atgtattcga      180
agatgtgttg acagtcgtga gtgtgtatcc taggaaaggc gagctggact ctgtctccat      240
ggttggtctc accccagggg cctaggaaca gcctgtcacc acacaattac ttttataacc      300
ctggagatga aaatctcctt gtcctcaaaa tacttccaga agaacaacca gatgggaagg      360
accttggttg ggactctttc cagttcactt ggggcagagg gaattta atg gct cac      416
                                     Met Ala His
                                     -40
gta gct gaa aag gat ggg cta gat tgg gct tca ggc tgc atc cca gga      464
Val Ala Glu Lys Asp Gly Leu Asp Trp Ala Ser Gly Cys Ile Pro Gly
                                     -35          -30          -25
ctc caa aca ggg atc tgt ctc ttt ggc tct cag ctc tgc ttt cat ttg      512
Leu Gln Thr Gly Ile Cys Leu Phe Gly Ser Gln Leu Cys Phe His Leu
                                     -20          -15          -10
agt tgg ctt tat tct tgg gct tca cag tgt ggc ccc aca gca cca gtt      560
Ser Trp Leu Tyr Ser Trp Ala Ser Gln Cys Gly Pro Thr Ala Pro Val
                                     -5          1          5
att gat aaa aag agc tcc cct ttg ctg aca gaa ctg ctg gat ttg gtt      608
Ile Asp Lys Lys Ser Ser Pro Leu Leu Thr Glu Leu Leu Asp Leu Val
10          15          20          25
ctc att ggt cca gac gag gaa ggt atc cag cct caa gtc atc att gtg      656
Leu Ile Gly Pro Asp Glu Glu Gly Ile Gln Pro Gln Val Ile Ile Val
30          35          40
gcc agg aag atg gaa tac acc aaa tgg aca ggc ctg gca tgt acc cac      704
Ala Arg Lys Met Glu Tyr Thr Lys Trp Thr Gly Leu Ala Cys Thr His
45          50          55
aga gac tgagagttgg tgctgggtgg tgtgggtggca gatgatatta cctgaagaag      760
Arg Asp
ggacgaatgg gtgctgggca ggacaaagca tcagctgtcc agttcaggcc tctcctcttt      820
ccctgggtgc ttcattttcc tccgtctccc tgctgtccct taccctctgc ccaatctcat      880
tactcctggg cttgggagtt gccttctgag gatactccac tgggggtacc tgagcctgga      940
ttagagggca gggggaggat attgcctagc caaagtgggt gttcaataaa gaaccatttg     1000
gagatggcaa aaaaaaaaaa aaaaaa                                1025
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<210> 133

<211> 607

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> 247..501

<220>
 <221> sig_peptide
 <222> 247..306
 <223> Von Heijne matrix
 score 6.43040298500966
 seq LLLVTLVASTVPG/NS

<400> 133
 tgttacaaat attccctatg atctctcctt taaatattct tatcaggata ttggaaattc 60
 ttgattttca caactctgct tcagtggcat atgttttagct ttttgtcttc tgaattaatt 120
 gggctttctga tgggtccctag aggtatcagc tactcagtca gaaaacatac atggggaaga 180
 aactgaagtt catgccacaa actgtagcag ctttgggaaca gaagggacca gacaacctca 240
 aggaga atg ggc cca aat acc aaa aat tta ctc ttg gtg acc ctt gtt 288
 Met Gly Pro Asn Thr Lys Asn Leu Leu Leu Val Thr Leu Val
 -20 -15 -10
 gct tct act gta cca ggc aac tct ctt ggg cag gat ttt act ttt gca 336
 Ala Ser Thr Val Pro Gly Asn Ser Leu Gly Gln Asp Phe Thr Phe Ala
 -5 1 5 10
 cac tta gaa aga tcc tgc acc agg gaa aat cgg tct cct ggg gag gta 384
 His Leu Glu Arg Ser Cys Thr Arg Glu Asn Arg Ser Pro Gly Glu Val
 15 20 25
 ttc cag caa cca tgc aag tct gga ggc ggg ggg gtt gga gaa cca aat 432
 Phe Gln Gln Pro Cys Lys Ser Gly Gly Gly Gly Val Gly Glu Pro Asn
 30 35 40
 gcc caa ggg cag cta ctt agc cag cac cca cta cct gcc ttc att aat 480
 Ala Gln Gly Gln Leu Leu Ser Gln His Pro Leu Pro Ala Phe Ile Asn
 45 50 55
 tgt tct cac ggg cag gcc ttt tgaaccaccc tggtacagaa caccaaccct 531
 Cys Ser His Gly Gln Ala Phe
 60 65
 ggtgcttttag gctgtctgtg ccatttctag gcaatgaacg agtagttact gtaccaaccc 591
 aaaaaaaaaa aaaaaa 607

<210> 134
 <211> 774
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> 333..602

<220>
 <221> sig_peptide
 <222> 333..416
 <223> Von Heijne matrix
 score 4.79986448293481
 seq VPALPLLSSLCMA/MV

<400> 134
 ctcttcagtc cggggccttg ttgaacggac tcaccaggaa acgtgacttt cgtgtccgac 60
 ctctgtctga tcaggattcg attcttgggtg ttaaacaaga caacgctgaa ggctcggtgc 120
 agcagccctg caaaggtttt tccagcgtc ttgggaggtg ggctgtgccc tgccctggccc 180
 acctggccca cctggcccac cattacctga agggaagcat gaacagcctt tgacgtggga 240
 gtggcgactg ctgagaggga actgtctgta cacaagcaat gtagccttat gggacctgag 300
 tggagcccca acccacgcag ggcgtgktct tc atg gct ttt cct ggc caa tct 353
 Met Ala Phe Pro Gly Gln Ser
 -25

```

gat acc aag atg cag tgg cca gaa gta cct gca ctt cca ctc ctg tca      401
Asp Thr Lys Met Gln Trp Pro Glu Val Pro Ala Leu Pro Leu Leu Ser
-20 -15 -10
agt ctc tgc atg gct atg gtg agg aag agc tct gca ctg ggc aag gaa      449
Ser Leu Cys Met Ala Met Val Arg Lys Ser Ser Ala Leu Gly Lys Glu
-5 1 5 10
gtt ggc cgt cga gtg aag gaa atg gtg atg ctg gtg gcc cct ttc cgg      497
Val Gly Arg Arg Val Lys Glu Met Val Met Leu Val Ala Pro Phe Arg
15 20 25
cag tca agt tcc cta tca agg aca ttc agt tct cgg aaa gtg gtg aag      545
Gln Ser Ser Ser Leu Ser Arg Thr Phe Ser Ser Arg Lys Val Val Lys
30 35 40
gca cat gct tcc ctg cat ggt gcc cgc ctc tct cca ctc tct aga aat      593
Ala His Ala Ser Leu His Gly Ala Arg Leu Ser Pro Leu Ser Arg Asn
45 50 55
att aga ggc taggctgctg ctgtatgtca gggctagtcc ctcttctatg      642
Ile Arg Gly
60
aatccagaat aactctgaag aagccgagta acagggcatga agtgaagaga aatcgctgta      702
acaggaagac agcaaagcag atgctaataga ccacactatt taacgaactg gaaccaacaa      762
aaaaaaaaaa aa      774

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<210> 135
<211> 611
<212> DNA
<213> Homo sapiens

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<220>
<221> CDS
<222> 110..376

<220>
<221> sig_peptide
<222> 110..208
<223> Von Heijne matrix
      score 3.64796206065748
      seq LVPHSPLPGALSS/AP

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<220>
<221> misc_feature
<222> 347
<223> n=a, g, c or t

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<400> 135
tcttgtcaac actgccact cagcgaggaa gcagccgcga cgccacact tcctgttgga      60
gcctgcgag agccagaggc ctcagaagcc acaggaacat ggcctaggc atg gct cag      118
                                     Met Ala Gln
cca gca gcc ccc tcc ctg acg cgg ccc ttc ctg gca gag gcc ccg aca      166
Pro Ala Ala Pro Ser Leu Thr Arg Pro Phe Leu Ala Glu Ala Pro Thr
-30 -25 -20 -15
gca ctg gtc cca cac agc ccc ctg cct ggg gcc ctg tca agc gcc cct      214
Ala Leu Val Pro His Ser Pro Leu Pro Gly Ala Leu Ser Ser Ala Pro
-10 -5 1
ggc ccg aag cag ccc ccg acg gca agc aca ggc ccg gag ctg ctg ctg      262
Gly Pro Lys Gln Pro Pro Thr Ala Ser Thr Gly Pro Glu Leu Leu Leu
5 10 15
ctg cct ctt tcc tcc ttc atg ccc tgc ggg gcg gct gca cca gcc agg      310
Leu Pro Leu Ser Ser Phe Met Pro Cys Gly Ala Ala Ala Pro Ala Arg

```

```

      20              25              30
gtg tca tca cag cgg gct act cct agg gat aag ccc ncc ggt ccc ctc      358
Val Ser Ser Gln Arg Ala Thr Pro Arg Asp Lys Pro Xaa Gly Pro Leu
35              40              45              50
atc cct ggc cag tgt ccc tgacccccat ctactccttc ctggggactt      406
Ile Pro Gly Gln Cys Pro
      55
ctcagcgcca gccattggc gcctgcgttg cccgcattcca ggccctgcgg caggccctgt      466
gctagcgtgt tcgcaccagg aacgcaggtg ctgggctgtc ggggaggcct caggccacct      526
ccaggaacag aacacagttt taagtttgat tttttttatt tcaaaatgct ttgcaattaa      586
atgaattact gttcaaaaaa aaaaaa      611

<210> 136
<211> 925
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> 22..417

<220>
<221> sig_peptide
<222> 22..66
<223> Von Heijne matrix
      score 5.47092708754574
      seq RVLCPAAGAVRA/LR

<400> 136
agtcgaggag tcaaggcagc a atg aat cgt gtc ttg tgt gcc ccg gcg gcc      51
                        Met Asn Arg Val Leu Cys Ala Pro Ala Ala
                        -15                        -10
ggg gcc gtc cgg gcg ctg agg ctc ata ggc tgg gct tcc cga agc ctt      99
Gly Ala Val Arg Ala Leu Arg Leu Ile Gly Trp Ala Ser Arg Ser Leu
-5              1              5              10
cat ccg ttg ccc ggt tcc cgg gat cgg gcc cac cct gcc gcc gag gaa      147
His Pro Leu Pro Gly Ser Arg Asp Arg Ala His Pro Ala Ala Glu Glu
      15              20              25
gag gac gac cct gac cgc ccc att gag ttt tcc tcc agc aaa gcc aac      195
Glu Asp Asp Pro Asp Arg Pro Ile Glu Phe Ser Ser Ser Lys Ala Asn
      30              35              40
cct cac cgc tgg tgc gtg ggc cat acc atg gga aag gga cat cag cgg      243
Pro His Arg Trp Ser Val Gly His Thr Met Gly Lys Gly His Gln Arg
      45              50              55
ccc tgg tgg aag gtg ctg ccc ctc agc tgc ttc ctc gtg gcg ctg atc      291
Pro Trp Trp Lys Val Leu Pro Leu Ser Cys Phe Leu Val Ala Leu Ile
      60              65              70              75
atc tgg tgc tac ctg agg gag gag agc gag gcg gac cag tgg ttg aga      339
Ile Trp Cys Tyr Leu Arg Glu Glu Ser Glu Ala Asp Gln Trp Leu Arg
      80              85              90
cag gtg tgg gga gag gtg cca gag ccc agt gat cgt tct gag gag cct      387
Gln Val Trp Gly Glu Val Pro Glu Pro Ser Asp Arg Ser Glu Glu Pro
      95              100              105
gag act cca gct gcc tac aga gcg aga act tgacgggggtg cccgtgagg      437
Glu Thr Pro Ala Ala Tyr Arg Ala Arg Thr
      110              115
ctggcaggaa gggagccgac agccgccctt cggatttgat gtcacgtttg cccgtgactg      497
tcctggctat gcgtgcgtcc tcagcactga aggacttggc tggtggatgg ggcacttggc      557

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[illegible]

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<220>  
<221> CDS  
<222> 62..367
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<400> 137		
acgccacggc gtctgctggc ggccgeggag acgcagagtc ttgagcagcg cggcaggcac		60
c atg ttc ctg act gcg ctc ctc tgg cgc ggc cgc att ccc ggc cgt cag		109
Met Phe Leu Thr Ala Leu Leu Trp Arg Gly Arg Ile Pro Gly Arg Gln		
-10 -5 1		
tgg atc ggg aag cac cgg cgg cgg ttc gtg tgc ttg cgc gcc aag		157
Trp Ile Gly Lys His Arg Arg Pro Arg Phe Val Ser Leu Arg Ala Lys		
5 10 15		
cag aac atg atc cgc cgc ctg gag atc gat gcg gag aac cat tac tgg		205
Gln Asn Met Ile Arg Arg Leu Glu Ile Asp Ala Glu Asn His Tyr Trp		
20 25 30		
ctg agc atg ccc tac atg acc cgg gag cag gag cgc ggc cac gcc gsg		253
Leu Ser Met Pro Tyr Met Thr Arg Glu Gln Glu Arg Gly His Ala Xaa		
35 40 45 50		
dtg cgc agg agg gag gcc ttc gag gcc ata aag gcg gcc gcc act tcc		301
Xaa Arg Arg Arg Glu Ala Phe Glu Ala Ile Lys Ala Ala Ala Thr Ser		
55 60 65		
aag ttc ccc ccg cat aga ttc att gcg gac cag ctc gac cat ctc aat		349
Lys Phe Pro Pro His Arg Phe Ile Ala Asp Gln Leu Asp His Leu Asn		
70 75 80		
gtc acc aag aaa tgg tcc taatcctgag tagtcaccct tggattttat		397
Val Thr Lys Lys Trp Ser		
85		
ggatcacgga gctgaccatc tttacctggt cctggaactg aaaaactgta gcttgtgtga		457
aaatgagcct ttggaccagt ctttattaaa acaaacaaac atgagtagtc tgcatatcga		517
atatctgagct ctctaaaccc cccaataact aaaagctctaa ttgctgtcct gtggtttcat		577
tagtctgata ggaagatagg gatttctcca gtcacagatg atattttgaa ggaaagctgc		637
aataaagcca caatgattcg aaaaaaaaaa aaaaaaa		674

156

<220>
 <221> CDS
 <222> 107..1618

<220>
 <221> sig_peptide
 <222> 107..178
 <223> Von Heijne matrix
 score 6.19650168602189
 seq LGLYSLVLSGALA/YA

<400> 138
 agagctcagc cggtcgcacg gacggacagt tggaagccgg accccagagc ctgaggtggg 60
 cagtgtgccca ggggtcccttg cggcctcctc aagccctgtc caggct atg ggc atc 115
 Met Gly Ile
 aag aca gca ttg ccg gcg gct gag ctg ggc ctc tac tct ctg gtg ctg 163
 Lys Thr Ala Leu Pro Ala Glu Leu Gly Leu Tyr Ser Leu Val Leu
 -20 -15 -10
 agt ggg gcc ctg gcc tat gct ggc cgg ggc ctc ctt gag gct tca caa 211
 Ser Gly Ala Leu Ala Tyr Ala Gly Arg Gly Leu Leu Glu Ala Ser Gln
 -5 1 5 10
 gat ggg gcc cac agg aag gcc ttc cgg gag tct gtg cga cct ggc tgg 259
 Asp Gly Ala His Arg Lys Ala Phe Arg Glu Ser Val Arg Pro Gly Trp
 15 20 25
 gag tac att ggc cgg aag atg gat gtg gct gac ttc gag tgg gtg atg 307
 Glu Tyr Ile Gly Arg Lys Met Asp Val Ala Asp Phe Glu Trp Val Met
 30 35 40
 tgg ttc acc tcc ttt cgc aac gtc atc atc ttt gcc ctc tcc gga cat 355
 Trp Phe Thr Ser Phe Arg Asn Val Ile Ile Phe Ala Leu Ser Gly His
 45 50 55
 gtg ctg ttt gct aaa ctc tgc acg atg gtt gcc cca aag ctc cgc tcc 403
 Val Leu Phe Ala Lys Leu Cys Thr Met Val Ala Pro Lys Leu Arg Ser
 60 65 70 75
 tgg atg tat gct gtg tac ggg gcc ttg gct gtg atg ggc aca atg ggc 451
 Trp Met Tyr Ala Val Tyr Gly Ala Leu Ala Val Met Gly Thr Met Gly
 80 85 90
 cct tgg tac ctg ctg ctg ctg ctt ggt cac tgt gtg ggc ctc tat gtg 499
 Pro Trp Tyr Leu Leu Leu Leu Leu His Cys Val Gly Leu Tyr Val
 95 100 105
 gcc tcg ctt ttg ggc cag ccc tgg ctc tgt ctt ggc ctt ggc ttg gcc 547
 Ala Ser Leu Leu Gly Gln Pro Trp Leu Cys Leu Gly Leu Gly Leu Ala
 110 115 120
 agc ctg gcc tcc ttc aag atg gac ccc cta atc tct tgg cag agc ggg 595
 Ser Leu Ala Ser Phe Lys Met Asp Pro Leu Ile Ser Trp Gln Ser Gly
 125 130 135
 ttt gta aca ggc act ttt gat ctt caa gag gtg ctg ttt cat ggg ggc 643
 Phe Val Thr Gly Thr Phe Asp Leu Gln Glu Val Leu Phe His Gly Gly
 140 145 150 155
 agc agc ttc aca gtg ctg cgt tgc acc agc ttt gca ctg gag agc tgt 691
 Ser Ser Phe Thr Val Leu Arg Cys Thr Ser Phe Ala Leu Glu Ser Cys
 160 165 170
 gcc cac cct gac cgc cac tac tcc tta gct gac ctg ctc aag tac agc 739
 Ala His Pro Asp Arg His Tyr Ser Leu Ala Asp Leu Leu Lys Tyr Ser
 175 180 185
 ttc tac ctg ccc ttc ttc ttc ttc ggg ccc atc atg acc ttt gat cgc 787
 Phe Tyr Leu Pro Phe Phe Phe Phe Gly Pro Ile Met Thr Phe Asp Arg
 190 195 200
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<212> DNA
<213> Homo sapiens

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<222> 16..471

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<222> 16..93
<223> Von Heijne matrix
score 5.809301698725
seq FCVVCVIAIGVVQA/LI

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tacacgtttt cgtta atg gtg acc ttc cct gat gtg cct ctg ggc atc ttc 51
Met Val Thr Phe Pro Asp Val Pro Leu Gly Ile Phe
-25 -20 -15
ttg ttc tgt gtg tgt gtg atc gcc atc ggg gtc gtg cag gca ctg att 99
Leu Phe Cys Val Cys Val Ile Ala Ile Gly Val Val Gln Ala Leu Ile
-10 -5 1
gta ggg tac gca ttc cac ttc ccg cac ctg ctg agc ccg cag atc cag 147
Val Gly Tyr Ala Phe His Phe Pro His Leu Leu Ser Pro Gln Ile Gln
5 10 15
cgc tct gcc cac agg gct ctg tac cga cga cac gtc ctg ggc atc gtc 195
Arg Ser Ala His Arg Ala Leu Tyr Arg Arg His Val Leu Gly Ile Val
20 25 30
ctc caa ggc ccg gcc ctg tgc ttt gca gcg gcc atc ttc tct ctc ttc 243
Leu Gln Gly Pro Ala Leu Cys Phe Ala Ala Ala Ile Phe Ser Leu Phe
35 40 45 50
ttt gtc ccc ttg tct tac ctg ctg atg gtg act gtc atc ctc ctc ccc 291
Phe Val Pro Leu Ser Tyr Leu Leu Met Val Thr Val Ile Leu Leu Pro
55 60 65
tat gtc agc aag gtc acc ggc tgg tgc aga gac agg ctc ctg ggc cac 339
Tyr Val Ser Lys Val Thr Gly Trp Cys Arg Asp Arg Leu Leu Gly His
70 75 80
agg gag ccc tcg gct cac cca gtg gaa gtc ttc tcg ttt gac ctc cac 387
Arg Glu Pro Ser Ala His Pro Val Glu Val Phe Ser Phe Asp Leu His
85 90 95
gag cca ctc agc aag gag cgc gtg gaa gcc ttc agc gac gga gtc tac 435
Glu Pro Leu Ser Lys Glu Arg Val Glu Ala Phe Ser Asp Gly Val Tyr
100 105 110
gcc atc gtg gcc acg ctt ctc atc ctg gac atc tgg tgaggacccc 481
Ala Ile Val Ala Thr Leu Leu Ile Leu Asp Ile Trp
115 120 125
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gtgatctgcc	cacctcggcc	tcccaaagtg	ctgggattac	aggtgtaagc	caccgtgccc	1321
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 <212> DNA
 <213> Homo sapiens

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 <222> 222..374

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 <222> 222..299
 <223> Von Heijne matrix
 score 4.28353322771141
 seq ILFKFSLCPYAAA/LS

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gattgtcagt	ttgttcaagc	tcttttttagt tgttgctcct ccagtgccta gctttgagct 120
ttgtacacgg	tagttattga	gttgagtaac atagtttggt ctgagtcatt tgttccacat 180
gcttgaagac	ttggcttaac	ctagtagata ataggaaaga a atg gaa atg ctc ttt 236
		Met Glu Met Leu Phe
		-25
gat gaa aga gcc cct ctc tta ttc atc ctt ttt aaa ttt tct ttg tgc 284		
Asp Glu Arg Ala Pro Leu Leu Phe Ile Leu Phe Lys Phe Ser Leu Cys		
-20 -15 -10		
cca tat gca gca gct ctc agc aaa cct ata ttt ggc agt gtg gcc tgt 332		
Pro Tyr Ala Ala Ala Leu Ser Lys Pro Ile Phe Gly Ser Val Ala Cys		
-5 1 5 10		
atg act aaa gaa atc ctg gcc agg cac ggt ggc tca cgc ctg 374		
Met Thr Lys Glu Ile Leu Ala Arg His Gly Gly Ser Arg Leu		
15 20 25		
taatcccagc actttgggag gccgaggcgg gtggattacg aggtcaggag attgagacca 434		
tcctggctaa catggcgaaa ccccatctct acgaaaaata caaaaaaaaaa aattagccgg 494		
gcatcatggc gggcgccctgt agtcttagct actcaggagg ctgaggcagg agaatggcgt 554		
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caacagagca agactccgtc tcaaaaaaaaaa aaaaaaaaaa 653		

<210> 141
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 <212> DNA
 <213> Homo sapiens

<220>
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 <222> 59..274

<220>
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 <222> 59..127
 <223> Von Heijne matrix
 score 7.37647149292058
 seq LGLCSLLVGAEAA/PS

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atg ctg cgt cca gcg tta ccg tgg ctg tac ctt ggc ctc tgc agc ctc      106
Met Leu Arg Pro Ala Leu Pro Trp Leu Tyr Leu Gly Leu Cys Ser Leu
      -20      -15      -10
ctg gtg ggg gag gca gag gcc ccg agc ccc gtg gat ccg ctg gag cgg      154
Leu Val Gly Glu Ala Glu Ala Pro Ser Pro Val Asp Pro Leu Glu Arg
      -5      1      5
agc cgg ccg tac gcg gtg ctg cga ggg cag aac ctg gtg ttg atg gga      202
Ser Arg Pro Tyr Ala Val Leu Arg Gly Gln Asn Leu Val Leu Met Gly
10      15      20      25
acc att ttc agc atc ctg ctg gtg act gtc atc ctt atg gca ttt tgt      250
Thr Ile Phe Ser Ile Leu Leu Val Thr Val Ile Leu Met Ala Phe Cys
      30      35      40
gtc tac aag ccc att cgg cgt cgg tgacagccag acaagttctt caatgagtat      304
Val Tyr Lys Pro Ile Arg Arg Arg
      45
ttgggaatag gataagttgt gttgcacaca ggccagtgga gaagttggaa ccaaaaacttt      364
cctacttgga aatgaccttt ggtctggaca gttggtaaat gctaaatgaa ttagaagaaa      424
acatgtacta gacattatth tttcctaaca ctgtagcgca aataattggc ccctgagtcc      484
gcttctcagt gtttctgact gtacttgtaa aaagtaagac ctgaaagctc caaaggctcag      544
tgtaaagatg gagtgttcat gagaaagaaa acatggtaac cttgtgagtg cctgtaagaa      604
ccacactgta aagaactcat cattaatgct tgaaaatgtt attaagaagg agacttacca      664
tgcagacatt ccctatttaa gaaccatttg gttacagtgg gttaagaatc acagattttt      724
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aacgtcaatt aaaactaaag taaaatctta aaaaaaaaaa aaaaaa      1490

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<210> 142
<211> 661
<212> DNA
<213> Homo sapiens

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<220>
<221> CDS
<222> 158..442

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<220>
<221> sig_peptide
<222> 158..301
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ccaaaaagat tcaaaagagc aagtgggaatc tctaaga atg gct tcc agc cac tgg 175
Met Ala Ser Ser His Trp

-45

aat gaa acc act acc tct gtt tat cag tac ctt ggt ttt caa gtt caa 223
Asn Glu Thr Thr Thr Ser Val Tyr Gln Tyr Leu Gly Phe Gln Val Gln

-40 -35 -30

aaa att tac cct ttc cat gac aac tgg aac act gcc tgc ttt gtc atc 271
Lys Ile Tyr Pro Phe His Asp Asn Trp Asn Thr Ala Cys Phe Val Ile

-25 -20 -15

ctg ctt tta ttt ata ttt aca gtg gta tct tta gtg gtg ctg gct ttc 319
Leu Leu Leu Phe Ile Phe Thr Val Val Ser Leu Val Val Leu Ala Phe

-10 -5 1 5

ctt tat gaa gtg ctt gac tgc tgc tgc tgt gta aaa aac aaa acc gtg 367
Leu Tyr Glu Val Leu Asp Cys Cys Cys Cys Val Lys Asn Lys Thr Val

10 15 20

aaa gac ttg aaa agt gaa ccc aac cct ctt aga agt atg atg gac aac 415
Lys Asp Leu Lys Ser Glu Pro Asn Pro Leu Arg Ser Met Met Asp Asn

25 30 35

atc aga aaa cgt gaa act gaa gtg gtc taacactcta tagaagatga 462
Ile Arg Lys Arg Glu Thr Glu Val Val

40 45

acaaaatctc tgaaagcagc tcaacctctt ctgagaaaaa aaatatattc tgaggccaac 522

tggtgctaca aaacaaattc tgactgaatg tttaaaacat ttctagtaga aggggaaaaa 582

aaagttaaac atgcactgtt tgtgtgtata gccatttcat taaatatata gtaaaacttc 642

ataaaaaaaa aaaaaaaaaa 661

<210> 143

<211> 1789

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> 5..454

<220>

<221> sig_peptide

<222> 5..64

<223> Von Heijne matrix

score 6.64507667657896

seq LLPLLSLLVGAWL/KL

<400> 143

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Met Ala Arg His Gly Leu Pro Leu Leu Pro Leu Leu Ser Leu Leu

-20 -15 -10

gtc ggc gcg tgg ctc aag cta gga aat gga cag gct act agc atg gtc 97
Val Gly Ala Trp Leu Lys Leu Gly Asn Gly Gln Ala Thr Ser Met Val

-5 1 5 10

caa ctg cag ggt ggg aga ttc ctg atg gga aca aat tct cca gac agc 145
Gln Leu Gln Gly Gly Arg Phe Leu Met Gly Thr Asn Ser Pro Asp Ser

15 20 25

aga gat ggt gaa ggg cct gtg cgg gag gcg aca gtg aaa ccc ttt gcc 193
Arg Asp Gly Glu Gly Pro Val Arg Glu Ala Thr Val Lys Pro Phe Ala

30 35 40

atc gac ata ttt cct gtc acc aac aaa gat ttc agg gat ttt gtc agg 241
Ile Asp Ile Phe Pro Val Thr Asn Lys Asp Phe Arg Asp Phe Val Arg

45 50 55

gag aaa aag tat cgg aca gaa gct gag atg ttt gga tgg agc ttt gtc	289
Glu Lys Lys Tyr Arg Thr Glu Ala Glu Met Phe Gly Trp Ser Phe Val	
60 65 70 75	
ttt gag gac ttt gtc tct gat gag ctg aga aac aaa gcc acc cag cca	337
Phe Glu Asp Phe Val Ser Asp Glu Leu Arg Asn Lys Ala Thr Gln Pro	
80 85 90	
atg aag gtc aag ttt acc cat ggg gga act ggt tcc agc caa acc gca	385
Met Lys Val Lys Phe Thr His Gly Gly Thr Gly Ser Ser Gln Thr Ala	
95 100 105	
cca acc tgt ggc agg gaa agt tcc cca agg gag aca aag ctg agg atg	433
Pro Thr Cys Gly Arg Glu Ser Ser Pro Arg Glu Thr Lys Leu Arg Met	
110 115 120	
gct tcc atg gag tct ccc cag tgaatgcttt ccccgcccag aacaactacg	484
Ala Ser Met Glu Ser Pro Gln	
125 130	
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 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> 241..1302

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ctccccagtg aggcctacag tctgagcaga cagcatggcc tgccactggc agtgaacacc	240
atg tct gca gga ggt ggc cgg gcc ttt gct tgg caa gtg ttc ccc ccc	288
Met Ser Ala Gly Gly Gly Arg Ala Phe Ala Trp Gln Val Phe Pro Pro	
1 5 10 15	
atg ccc act tgc cgg gtc tat ggc aca gtg gca cac caa gat ggg cac	336
Met Pro Thr Cys Arg Val Tyr Gly Thr Val Ala His Gln Asp Gly His	
20 25 30	

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Ala	Glu	Thr	Leu	Asp	Met	Ala	Ser	His	Thr	Trp	Leu	Ala	Leu	Ala	Pro	
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Leu	Pro	Thr	Ala	Arg	Ala	Gly	Ala	Ala	Ala	Val	Val	Leu	Gly	Lys	Gln	
	65				70					75					80	
gtg	cta	gtg	gtg	tgt	ggt	gtg	gat	gag	gtc	cag	agc	ccg	gta	gct	gct	528
Val	Leu	Val	Val	Cys	Gly	Val	Asp	Glu	Val	Gln	Ser	Pro	Val	Ala	Ala	
				85					90					95		
gta	gag	gcc	ttc	ctg	atg	gat	gag	ggc	cgc	tgg	gag	cgt	cgg	gcc	acc	576
Val	Glu	Ala	Phe	Leu	Met	Asp	Glu	Gly	Arg	Trp	Glu	Arg	Arg	Ala	Thr	
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Leu	Pro	Gln	Ala	Ala	Met	Gly	Val	Ala	Thr	Val	Glu	Arg	Asp	Gly	Met	
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Val	Tyr	Ala	Leu	Gly	Gly	Met	Gly	Pro	Asp	Thr	Ala	Pro	Gln	Ala	Gln	
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Val	Arg	Val	Tyr	Asp	Pro	Arg	Arg	Asp	Cys	Trp	Leu	Ser	Leu	Pro	Ser	
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Met	Pro	Thr	Pro	Cys	Tyr	Gly	Ala	Ser	Thr	Phe	Leu	His	Gly	Asn	Lys	
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atc	tat	gtc	ctg	ggg	ggc	cgc	cag	ggc	aag	ctc	ccg	gtg	act	gct	ttt	816
Ile	Tyr	Val	Leu	Gly	Gly	Arg	Gln	Gly	Lys	Leu	Pro	Val	Thr	Ala	Phe	
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gaa	gcc	ttt	gat	ctg	gag	gcc	cgt	aca	tgg	acc	cgg	cat	cca	agc	cta	864
Glu	Ala	Phe	Asp	Leu	Glu	Ala	Arg	Thr	Trp	Thr	Arg	His	Pro	Ser	Leu	
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Pro	Ser	Arg	Arg	Ala	Phe	Ala	Gly	Cys	Ala	Met	Ala	Glu	Gly	Ser	Val	
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Arg	Pro	His	Phe	Val	Asn	Thr	Val	Glu	Met	Phe	Asp	Leu	Glu	His	Gly	
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Ser	Trp	Thr	Lys	Leu	Pro	Arg	Ser	Leu	Arg	Met	Arg	Asp	Lys	Arg	Ala	
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Asp	Phe	Val	Val	Gly	Ser	Leu	Gly	Gly	His	Ile	Val	Glu	Ile	Gly	Gly	
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Ser	Cys	Ser	Ser	Leu	Gln	Ala	Gly	Pro	Arg	Leu	Phe	Val	Ile	Gly	Gly	
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Gly	Val															
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Gly	Val	Ser	Phe	Lys	Leu	Glu	Lys	Thr	Ala	His	Ser	Ser	Leu	Ala		
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Leu	Phe	Arg	Asp	Asp	Thr	Gly	Val	Lys	Tyr	Gly	Leu	Val	Gly	Leu	Glu	
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Pro	Thr	Lys	Val	Ala	Leu	Asn	Val	Glu	Arg	Phe	Arg	Glu	Trp	Ala	Val	
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Thr	Val	Lys	Arg	Ser	Gln	Gln	Phe	Arg	Ile	Gly	Val	Ala	Asp	Val	Asp	
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Thr	Tyr	Ala	Gln	Arg	Lys	Trp	Tyr	Thr	Met	Leu	Ala	Asn	Glu	Lys	Ala	
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Ala Leu Trp Asp Gly Glu Leu Leu Thr His Ser Gly Leu Glu Val Pro
190      195      200
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Glu Gly Leu
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Ser Val Glu Gln Arg Glu Gly Thr Ile Gln Val Gln Gly Gln Ala Leu
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Phe Phe Arg Glu Ala Leu Pro Gly Ser Gly Gln Ala Arg Phe Ser Val
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ctg ctg ctg cat ggt att cgc ttc tcc tcc gag acc tgg cag aac ctg 261
Leu Leu Leu His Gly Ile Arg Phe Ser Ser Glu Thr Trp Gln Asn Leu
40 45 50
ggc aca ctg cac agg ctg gcc cag gct ggc tac cgg gct gtg gcc att 309
Gly Thr Leu His Arg Leu Ala Gln Ala Gly Tyr Arg Ala Val Ala Ile
55 60 65
gac ctg cca ggt ctg ggg cac tcc aag gaa gca gca gcc cct gcc cct 357
Asp Leu Pro Gly Leu Gly His Ser Lys Glu Ala Ala Ala Pro Ala Pro
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att ggg gag ctg gcc cct ggc agc ttc ctg gcg gct gtg gtg gat gcc 405
Ile Gly Glu Leu Ala Pro Gly Ser Phe Leu Ala Ala Val Val Asp Ala
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Leu Glu Leu Gly Pro Pro Val Val Ile Ser Pro Ser Leu Ser Gly Met
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Tyr Ser Leu Pro Phe Leu Thr Ala Pro Gly Ser Gln Leu Pro Gly Phe
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Cys	Pro	Leu	Leu	Leu	Pro	Gln	Asn	Arg	Ser	Lys	Thr	Val	Tyr	Glu	Gly	
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Met Ala Ala Ile Gly Val His Leu Gly Cys Thr Ser Ala Cys
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Gly Asp Arg Val Thr Pro Ala Val Val Ala Tyr Ser Glu Asn Glu Glu
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Ile Val Gly Leu Ala Ala Lys Gln Ser Arg Ile Arg Asn Ile Ser Asn
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aca gta atg aaa gta aag cag atc ctg ggc aga agc tcc agt gat cca 303
Thr Val Met Lys Val Lys Gln Ile Leu Gly Arg Ser Ser Ser Asp Pro
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caa gct cag aaa tac atc gcg gaa agt aaa tgt tta gtc att gaa aaa 351
Gln Ala Gln Lys Tyr Ile Ala Glu Ser Lys Cys Leu Val Ile Glu Lys
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aat ggg aaa tta cga tat gaa ata gat act gga gaa gaa aca aaa ttt 399
Asn Gly Lys Leu Arg Tyr Glu Ile Asp Thr Gly Glu Glu Thr Lys Phe
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Val Asn Pro Glu Asp Val Ala Arg Leu Ile Phe Ser Lys Met Lys Glu
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Thr Ala His Ser Val Leu Gly Ser Asp Ala Asn Asp Val Val Ile Thr
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Ala Arg Ala Ala Gly Phe Asn Val Leu Arg Leu Ile His Glu Pro Ser
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gca gct ctt ctt gct tat gga att gga caa gac tcc cct act gga aaa 639
Ala Ala Leu Leu Ala Tyr Gly Ile Gly Gln Asp Ser Pro Thr Gly Lys
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Ser Asn Ile Leu Val Phe Lys Leu Gly Gly Thr Ser Leu Ser Leu Ser
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Glu	Gly	Gln	Asp	Phe	Asp	Cys	Asn	Val	Ser	Arg	Ala	Arg	Phe	Glu	Leu	
			290					295					300			
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Leu	Cys	Ser	Pro	Leu	Phe	Asn	Lys	Cys	Ile	Glu	Ala	Ile	Arg	Gly	Leu	
		305					310					315				
tta	gat	caa	aat	gga	ttt	aca	aca	gat	gat	atc	aac	aag	gtt	gtc	ctt	1071
Leu	Asp	Gln	Asn	Gly	Phe	Thr	Thr	Asp	Asp	Ile	Asn	Lys	Val	Val	Leu	
	320					325					330					
tgt	gga	ggg	tct	tct	cga	atc	cca	aag	cta	cag	caa	ctg	att	aaa	gat	1119
Cys	Gly	Gly	Ser	Ser	Arg	Ile	Pro	Lys	Leu	Gln	Gln	Leu	Ile	Lys	Asp	
335					340					345					350	
ctt	ttc	cca	gct	gtt	gag	ctt	ctc	aat	tct	atc	cct	cct	gat	gaa	gtg	1167
Leu	Phe	Pro	Ala	Val	Glu	Leu	Leu	Asn	Ser	Ile	Pro	Pro	Asp	Glu	Val	
				355					360						365	
atc	cct	att	ggg	gca	gct	ata	gaa	gca	gga	att	ctt	att	ggg	aaa	gaa	1215
Ile	Pro	Ile	Gly	Ala	Ala	Ile	Glu	Ala	Gly	Ile	Leu	Ile	Gly	Lys	Glu	
			370					375					380			
aac	ctg	ttg	gtg	gaa	gac	tct	ctt	atg	ata	gag	tgt	tca	gcc	aga	gat	1263
Asn	Leu	Leu	Val	Glu	Asp	Ser	Leu	Met	Ile	Glu	Cys	Ser	Ala	Arg	Asp	
		385					390					395				
att	tta	gtt	aag	ggg	gtg	gac	gaa	tca	gga	gcc	agt	aga	ttc	aca	gtg	1311
Ile	Leu	Val	Lys	Gly	Val	Asp	Glu	Ser	Gly	Ala	Ser	Arg	Phe	Thr	Val	
	400					405					410					
ctg	ttt	cca	tca	ggg	act	cct	ttg	cca	gct	cga	aga	caa	cac	aca	ttg	1359
Leu	Phe	Pro	Ser	Gly	Thr	Pro	Leu	Pro	Ala	Arg	Arg	Gln	His	Thr	Leu	
415					420					425					430	
caa	gcc	cct	gga	agc	ata	tct	tca	gtg	tgc	ctt	gaa	ctc	tat	gag	tct	1407
Gln	Ala	Pro	Gly	Ser	Ile	Ser	Ser	Val	Cys	Leu	Glu	Leu	Tyr	Glu	Ser	
				435					440						445	
gat	ggg	aag	aac	tct	gcc	aaa	gag	gaa	acc	aag	ttt	gca	cag	gtt	gta	1455
Asp	Gly	Lys	Asn	Ser	Ala	Lys	Glu	Glu	Thr	Lys	Phe	Ala	Gln	Val	Val	
		450						455					460			
ctc	cag	gat	tta	gat	aaa	aaa	gaa	aat	gga	tta	cgt	gat	ata	tta	gct	1503
Leu	Gln	Asp	Leu	Asp	Lys	Lys	Glu	Asn	Gly	Leu	Arg	Asp	Ile	Leu	Ala	
		465					470					475				
gtt	ctt	act	atg	aaa	agg	gat	gga	tct	tta	cat	gtg	aca	tgc	aca	gat	1551
Val	Leu	Thr	Met	Lys	Arg	Asp	Gly	Ser	Leu	His	Val	Thr	Cys	Thr	Asp	
	480					485					490					
caa	gaa	act	gga	aaa	tgt	gaa	gca	atc	tct	att	gag	ata	gca	tct		1596
Gln	Glu	Thr	Gly	Lys	Cys	Glu	Ala	Ile	Ser	Ile	Glu	Ile	Ala	Ser		
495					500					505						
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ataagtggg	tttgtattaa	aatacttttt	caatgaactg	tataaactat	gtttttattaa											1716

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1747

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<211> 658

<212> DNA

<213> Homo sapiens

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<221> CDS

<222> 129..362

<400> 149

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agcagtcattg ttagcagttt gaaggggctg gagcaagatg gaatcaggaa taaggagtca 120

gtggggacc atg tac aac act gga aga cac gta tcc ctt cgc ctg gac aag 170

Met Tyr Asn Thr Gly Arg His Val Ser Leu Arg Leu Asp Lys

1 5 10

gag cac ttg gtc aac ata tct gga ggg ccc atg aca tac agc cac cgg 218

Glu His Leu Val Asn Ile Ser Gly Gly Pro Met Thr Tyr Ser His Arg

15 20 25 30

ctg gag gag atc cga cta cac ttt ggg agt gag gac agc caa ggg tcg 266

Leu Glu Glu Ile Arg Leu His Phe Gly Ser Glu Asp Ser Gln Gly Ser

35 40 45

gag cac ctc ctc aat gga cag gcc ttc tct ggg gag ctt caa gag agg 314

Glu His Leu Leu Asn Gly Gln Ala Phe Ser Gly Glu Leu Gln Glu Arg

50 55 60

gat ttg ttc atc ttg ttg act tct gta tca gga cat ctg ccc gat aca 362

Asp Leu Phe Ile Leu Leu Thr Ser Val Ser Gly His Leu Pro Asp Thr

65 70 75

tagaaaaagt ctgctgaccc ctgaattaca gtatgagcca ttcggaatgc atttctcttt 422

aaaagttctc gcctcattca gtgtctggaa cacagtgggt gctccccaat aggtgacacc 482

ttcctcaagt ttccttggga gaacagactc aatgtcggat ccacaaagga gacctgcaca 542

tacctaacc cttatttctgc agaagctgaa ggctgtatta tctattgctt gcataataaa 602

tattgcataa cgacaacaat agtaaaaaaa aaaaaaaaaa gaaaaaaaaa aaaaaa 658

<210> 150

<211> 2045

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> 109..594

<400> 150

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aagtagcagt tccggagtcc agctggctaa aactcatccc agaggata atg gca acc 117

Met Ala Thr

1

cat gcc tta gaa atc gct ggg ctg ttt ctt ggt ggt gtt gga atg gtg 165

His Ala Leu Glu Ile Ala Gly Leu Phe Leu Gly Gly Val Gly Met Val

5 10 15

ggc aca gtg gct gtc act gtc atg cct cag tgg ata gtg tcg gcc ttc 213

Gly Thr Val Ala Val Thr Val Met Pro Gln Trp Ile Val Ser Ala Phe

20 25 30 35

att gaa aac aac atc gtg gtt ttt gaa aac ttc tgg gaa gga ctg tgg 261

Ile Glu Asn Asn Ile Val Val Phe Glu Asn Phe Trp Glu Gly Leu Trp

40 45 50

atg aat tgc gtg agg cag gct aac atc agg atg cag tgc aaa atc tat	309
Met Asn Cys Val Arg Gln Ala Asn Ile Arg Met Gln Cys Lys Ile Tyr	
55 60 65	
gat tcc ctg ctg gct ctt tct ccg gac cta cag gca gcc aga gga ctg	357
Asp Ser Leu Leu Ala Leu Ser Pro Asp Leu Gln Ala Ala Arg Gly Leu	
70 75 80	
atg tgt gct gct tcc gtg atg tcc ttc ttg gct ttc atg atg gcc atc	405
Met Cys Ala Ala Ser Val Met Ser Phe Leu Ala Phe Met Met Ala Ile	
85 90 95	
ctt ggc atg aaa tgc acc agg tgc acg ggg gac aat gag aag gtg aag	453
Leu Gly Met Lys Cys Thr Arg Cys Thr Gly Asp Asn Glu Lys Val Lys	
100 105 110 115	
gct cac att ctg ctg acg gct gga atc atc ttc atc atc acg ggc atg	501
Ala His Ile Leu Leu Thr Ala Gly Ile Ile Phe Ile Ile Thr Gly Met	
120 125 130	
gtg gtg ctc atc cct gtg agc tgg gtt gcc aat gcc atc atc aga gat	549
Val Val Leu Ile Pro Val Ser Trp Val Ala Asn Ala Ile Ile Arg Asp	
135 140 145	
ttc tat aac cca ata gtg aat gtt gcc caa aaa cgt gag ctt gga	594
Phe Tyr Asn Pro Ile Val Asn Val Ala Gln Lys Arg Glu Leu Gly	
150 155 160	
taagctctct acttaggatg gaccacggca ctgggtgctga ttggtggagg agctctgttc	654
tgctgcgttt tttgttgcaa cgaaaagagc agtagctaca gatactcgat accttcccat	714
cgcacaaccc aaaaaagtta tcacaccgga aagaagtcac cgagcgtcta ctccagaagt	774
cagtatgtgt agttgtgtat gtttttttaa ctttactata aagccatgca aatgacaaaa	834
atctatatta ctttctcaaa atggacccca aagaaacttt gatttactgt tcttaactgc	894
ctaactcttaa ttacaggaac tgtgcatcag ctatttatga ttctataagc tatttcagca	954
gaatgagata ttaaatacaa tgctttgatt gttctagaaa gtatagtaat ttgttttcta	1014
aggtggttca agcatctact ctttttatca tttacttcaa aatgacattg ctaaagactg	1074
cattatttta ctactgtaat ttctccacga catagcatta tgtacataga tgagtgaac	1134
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ttacactgaa taaatagaac tcaactattg cttttcaggg aaatcatgga taggggtgaa	1254
gaaggttact attaattgtt taaaaacagc ttagggtatta atgtcctcca tttataatga	1314
agattaaaat gaaggcttta atcagcattg taaaggaaat tgaatggctt tctgatatgc	1374
tgtttttttag cctaggagtt agaaatccta acttctttat cctcttctcc cagaggcttt	1434
ttttttcctg tgtattaaat taacattttt aaaaagcaga tattttgtca aggggctttg	1494
cattcaaat gcttttcag ggctatactc agaagaaaga taaaagtgtg atctaagaaa	1554
aagtgatggg tttaggaaag tgaaaatatt tttgtttttg tatttgaaga agaattgatgc	1614
attttgacaa gaaatcatat atgtatggat atatttttaat aagtatttga gtacagactt	1674
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ccaaaaaac aacaacaaaa aaagttgtcc tttgagaact tcacctgctc ctatgtgggt	1794
acctgagtc aattgtcat tttgttctg tgaaaaataa atttccttct tgtaccattt	1854
ctgttttagtt ttactaaaaat ctgtaaatac tgtatttttc tgtttattcc aaatttgatg	1914
aaactgacaa tccaatttga aagtttgtgt cgacgtctgt ctagcttaaa tgaatgtgtt	1974
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aaaaaaaaa a	2045

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<211> 788

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> 150..587

<400> 151

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gttgttcgat ttcacggttt ggaatctctt gtcaagggac tgggactctt caattaatct	120
gacatttcac aaatccaaaa ttgccgtgg atg aac tct tta ctt cac ttc ggg	173
Met Asn Ser Leu Leu His Phe Gly	
1 5	
ata ttg ctg gag ctg agt ctc ctg aaa cag ttt aag tct gta tat gtt	221
Ile Leu Leu Glu Leu Ser Leu Leu Lys Gln Phe Lys Ser Val Tyr Val	
10 15 20	
cct gga aat cat acc cac cag gca tct tat aag cca ttg ttg aag caa	269
Pro Gly Asn His Thr His Gln Ala Ser Tyr Lys Pro Leu Leu Lys Gln	
25 30 35 40	
gtt gtg gag gaa ata ttt cat ccc gag agg cca gat tcc gtt gat att	317
Val Val Glu Glu Ile Phe His Pro Glu Arg Pro Asp Ser Val Asp Ile	
45 50 55	
gaa cac atg tct tca ggc ctc act gat ctc ctt aaa act gga ttt agc	365
Glu His Met Ser Ser Gly Leu Thr Asp Leu Leu Lys Thr Gly Phe Ser	
60 65 70	
atg ttc atg aag gtg agc cgg cct cat cct agt gac tac ccc ctc ctg	413
Met Phe Met Lys Val Ser Arg Pro His Pro Ser Asp Tyr Pro Leu Leu	
75 80 85	
atc ctc ttt gtg gta ggt ggg gtc aca gtc tct gaa gtg aaa atg gtc	461
Ile Leu Phe Val Val Gly Gly Val Thr Val Ser Glu Val Lys Met Val	
90 95 100	
aaa gat ctt gtg gca tcg ttg aag cca gga acc cag gta atc gtg ctg	509
Lys Asp Leu Val Ala Ser Leu Lys Pro Gly Thr Gln Val Ile Val Leu	
105 110 115 120	
tcc aca cga ctc ctg aag cca ctt aac att cct gag ctg tta ttt gca	557
Ser Thr Arg Leu Leu Lys Pro Leu Asn Ile Pro Glu Leu Leu Phe Ala	
125 130 135	
act gac cga ctg cat cca gac ctt ggc ttc tgagcatccg ctaagaagat	607
Thr Asp Arg Leu His Pro Asp Leu Gly Phe	
140 145	
aagacctact caagctggaa atgccgatgc aattttctgc caccactcca aatactcctc	667
cacaaccagc gtccctgtca ctaattgcga gaatgatgga attctgcctg aagggtcttg	727
atacctactc agtgaggtag stttgcttgg attgctgtga ttccaaaaaa aaaaaaaaaa	787
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<210> 152

<211> 1931

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> 173..847

<400> 152

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cgagttcatt actacaggaa aaactgttct cttctgtggc acagagaacc ctgcttcaaa	120
gcagaagtag cagttccgga gtccagctgg ctaaaactca tcccagagga ta atg gca	178
Met Ala	
1	
acc cat gcc tta gaa atc gct ggg ctg ttt ctt ggt ggt gtt gga atg	226
Thr His Ala Leu Glu Ile Ala Gly Leu Phe Leu Gly Gly Val Gly Met	
5 10 15	
gtg ggc aca gtg gct gtc act gtc atg cct cag tgg aga gtg tcg gcc	274
Val Gly Thr Val Ala Val Thr Val Met Pro Gln Trp Arg Val Ser Ala	
20 25 30	
ttc att gaa aac aac atc gtg gtt ttt gaa aac ttc tgg gaa gga ctg	322

<213> Homo sapiens

<220>

<221> CDS

<222> 100..441

<400> 153

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cagctctcaa gtctgacttg catctacact gcgggcaag atg cgg ctg caa gac      114
                               Met Arg Leu Gln Asp
                               1           5

cgc atc gcc acg ttc ttc ttc cca aaa ggc atg atg ctc acc acg gct      162
Arg Ile Ala Thr Phe Phe Phe Pro Lys Gly Met Met Leu Thr Thr Ala
                10           15           20

gcg ctg atg ctc ttc ttc tta cac ctg ggc atc ttc atc aga gac gtg      210
Ala Leu Met Leu Phe Phe Leu His Leu Gly Ile Phe Ile Arg Asp Val
                25           30           35

cac aac ttc tgc atc acc tac cac tat gac cac atg agc ttt cac tac      258
His Asn Phe Cys Ile Thr Tyr His Tyr Asp His Met Ser Phe His Tyr
                40           45           50

acg gtc gtc ctg atg ttc tcc cag gtg atc agc atc tgc tgg gct gcc      306
Thr Val Val Leu Met Phe Ser Gln Val Ile Ser Ile Cys Trp Ala Ala
                55           60           65

atg ggg tca ctc tat gct gag atg aca gaa aac aat gct caa cgg agc      354
Met Gly Ser Leu Tyr Ala Glu Met Thr Glu Asn Asn Ala Gln Arg Ser
                70           75           80           85

cat gtt ctt caa ccg cct gtc ctt gga gtt tct ggc cat cga gta ccg      402
His Val Leu Gln Pro Pro Val Leu Gly Val Ser Gly His Arg Val Pro
                90           95           100

gga gga gca cca ctg agg cct ggg gag tcg gaa cag ggc taaggagggg      451
Gly Gly Ala Pro Leu Arg Pro Gly Glu Ser Glu Gln Gly
                105           110

gaagcaaaag gctgcctcgg gtgttttaaat aaagttgttg tttattccaa aaaaaaaaaa      511
aaa                                                                514
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<210> 154

<211> 1183

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> 32..1132

<400> 154

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                               Met Ala Thr Pro Asn Asn Leu
                               1           5

acc ccc acc aac tgc agc tgg tgg ccc atc tcc gcg ctg gag agc gat      100
Thr Pro Thr Asn Cys Ser Trp Trp Pro Ile Ser Ala Leu Glu Ser Asp
                10           15           20

gcg gcc aag cca gcg gag gcc ccc gac gct ccc gag gcg gcc agc ccc      148
Ala Ala Lys Pro Ala Glu Ala Pro Asp Ala Pro Glu Ala Ala Ser Pro
                25           30           35

gcc cat tgg ccc agg gag agc ctg gtt ctg tac cac tgg acc cag tcc      196
Ala His Trp Pro Arg Glu Ser Leu Val Leu Tyr His Trp Thr Gln Ser
                40           45           50           55

ttc agc tcg cag aag gtg cgg ctg gtg atc gcc gag aag ggc ctg gtg      244
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Phe	Ser	Ser	Gln	Lys	Val	Arg	Leu	Val	Ile	Ala	Glu	Lys	Gly	Leu	Val		
				60					65					70			
tgc	gag	gag	cgg	gac	gtg	agc	ctg	cca	cag	agc	gag	cac	aag	gag	ccc		292
Cys	Glu	Glu	Arg	Asp	Val	Ser	Leu	Pro	Gln	Ser	Glu	His	Lys	Glu	Pro		
			75					80					85				
tgg	ttc	atg	cgg	ctc	aac	ctg	ggc	gag	gag	gtg	ccc	gtc	atc	atc	cac		340
Trp	Phe	Met	Arg	Leu	Asn	Leu	Gly	Glu	Glu	Val	Pro	Val	Ile	Ile	His		
		90					95					100					
cgc	gac	aac	atc	atc	agt	gac	tat	gac	cag	atc	att	gac	tat	gtg	gag		388
Arg	Asp	Asn	Ile	Ile	Ser	Asp	Tyr	Asp	Gln	Ile	Ile	Asp	Tyr	Val	Glu		
	105					110					115						
cgc	acc	ttc	aca	gga	gag	cac	gtg	gtg	gcc	ctg	atg	ccc	gag	gtg	ggc		436
Arg	Thr	Phe	Thr	Gly	Glu	His	Val	Val	Ala	Leu	Met	Pro	Glu	Val	Gly		
	120					125					130				135		
agc	ctg	cag	cac	gca	cgg	gtg	ctg	cag	tac	cgg	gag	ctg	ctg	gac	gca		484
Ser	Leu	Gln	His	Ala	Arg	Val	Leu	Gln	Tyr	Arg	Glu	Leu	Leu	Asp	Ala		
				140					145					150			
ctg	ccc	atg	gat	gcc	tac	acg	cat	ggc	tgc	atc	ctg	cat	ccc	gag	ctc		532
Leu	Pro	Met	Asp	Ala	Tyr	Thr	His	Gly	Cys	Ile	Leu	His	Pro	Glu	Leu		
			155					160					165				
acc	acc	gac	tcc	atg	atc	ccc	aag	tac	gcc	acg	gcc	gag	atc	cgc	aga		580
Thr	Thr	Asp	Ser	Met	Ile	Pro	Lys	Tyr	Ala	Thr	Ala	Glu	Ile	Arg	Arg		
		170					175					180					
cat	tta	gcc	aat	gcc	acc	acg	gac	ctc	atg	aaa	ctg	gac	cat	gaa	gag		628
His	Leu	Ala	Asn	Ala	Thr	Thr	Asp	Leu	Met	Lys	Leu	Asp	His	Glu	Glu		
	185					190					195						
gag	ccc	cag	ctc	tcc	gag	ccc	tac	ctt	tct	aaa	caa	aag	aag	ctc	atg		676
Glu	Pro	Gln	Leu	Ser	Glu	Pro	Tyr	Leu	Ser	Lys	Gln	Lys	Lys	Leu	Met		
	200				205					210					215		
gtc	aag	atc	ttg	gag	cat	gat	gat	gtg	agc	tac	ctg	aag	aag	atc	ctc		724
Val	Lys	Ile	Leu	Glu	His	Asp	Asp	Val	Ser	Tyr	Leu	Lys	Lys	Ile	Leu		
				220					225					230			
ggg	gaa	ctg	gcc	atg	gtg	ctg	gac	cag	att	gag	gag	gag	ctg	gag	aag		772
Gly	Glu	Leu	Ala	Met	Val	Leu	Asp	Gln	Ile	Glu	Ala	Glu	Leu	Glu	Lys		
			235				240						245				
agg	aag	ctg	gag	aac	gag	ggg	cag	aaa	tgc	gag	ctg	tgg	ctc	tgt	ggc		820
Arg	Lys	Leu	Glu	Asn	Glu	Gly	Gln	Lys	Cys	Glu	Leu	Trp	Leu	Cys	Gly		
		250				255						260					
tgt	gcc	ttc	acc	ctc	gct	gat	gtc	ctc	ctg	gga	gcc	acc	ctg	cac	cgc		868
Cys	Ala	Phe	Thr	Leu	Ala	Asp	Val	Leu	Leu	Gly	Ala	Thr	Leu	His	Arg		
	265					270					275						
ctc	aag	ttc	ctg	gga	ctg	tcc	aag	aaa	tac	tgg	gaa	gat	ggc	agc	cgg		916
Leu	Lys	Phe	Leu	Gly	Leu	Ser	Lys	Lys	Tyr	Trp	Glu	Asp	Gly	Ser	Arg		
	280				285					290					295		
ccc	aac	ctg	cag	tcc	ttc	ttt	gag	agg	gtc	cag	aga	cgc	ttt	gcc	ttc		964
Pro	Asn	Leu	Gln	Ser	Phe	Phe	Glu	Arg	Val	Gln	Arg	Arg	Phe	Ala	Phe		
				300					305					310			
cgg	aaa	gtc	ctg	ggt	gac	atc	cac	acc	ctg	ctg	tcg	gcc	gtc	atc			1012
Arg	Lys	Val	Leu	Gly	Asp	Ile	His	Thr	Leu	Leu	Ser	Ala	Val	Ile			
			315					320					325				
ccc	aat	gct	ttc	cgg	ctg	gtc	aag	agg	aaa	ccc	cca	tcc	ttc	ttc	ggg		1060
Pro	Asn	Ala	Phe	Arg	Leu	Val	Lys	Arg	Lys	Pro	Pro	Ser	Phe	Phe	Gly		
		330					335					340					
gcg	tcc	ttc	ctc	atg	ggc	tcc	ctg	ggt	ggg	atg	ggc	tac	ttt	gcc	tac		1108
Ala	Ser	Phe	Leu	Met	Gly	Ser	Leu	Gly	Gly	Met	Gly	Tyr	Phe	Ala	Tyr		
	345					350					355						
tgg	tac	ctc	aag	aaa	aaa	tac	atc	tagggccagg	cctggggcctt	ggtgtctgac							1162
Trp	Tyr	Leu	Lys	Lys	Lys	Tyr	Ile										

360 365
tgtcaaaaaa aaaaaaaaaa a

1183

<210> 155
<211> 1545
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<220>
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<222> 160..996

<400> 155
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tatgcaccg tgctgtggcg tgcccgtcgt ctgtgtggc atg cct gtc tgt gca 174
Met Pro Val Cys Ala
1 5
ccc gtg ctg tgg cgt gcc cgt cgt ctg tgt ggc atg cct gtc tgt gca 222
Pro Val Leu Trp Arg Ala Arg Arg Leu Cys Gly Met Pro Val Cys Ala
10 20
ccc gtg ccg tgg cgt gcc cgt cgt ctg tgc acc cgt gct gtg gtg tgc 270
Pro Val Pro Trp Arg Ala Arg Arg Leu Cys Thr Arg Ala Val Val Cys
25 30 35
cct tcg tct gtt cct ttt att gcc ggg cag ggt tgc acc cac atg tgc 318
Pro Ser Ser Val Pro Phe Ile Ala Gly Gln Gly Cys Thr His Met Cys
40 45 50
aag cca gcg acg gac ccc agg ttc acc cgt tca ccg ctg gct gga ggc 366
Lys Pro Ala Thr Asp Pro Arg Phe Thr Arg Ser Pro Leu Ala Gly Gly
55 60 65
gtg atc ctg ggt gtg gcc ctg tgg ctc cgc cat gac ccg cag acc acc 414
Val Ile Leu Gly Val Ala Leu Trp Leu Arg His Asp Pro Gln Thr Thr
70 75 80 85
aac ctc ctg tat ctg gag ctg gga gac aag ccc gcg ccc aac acc ttc 462
Asn Leu Leu Tyr Leu Glu Leu Gly Asp Lys Pro Ala Pro Asn Thr Phe
90 95 100
tat gta ggc atc tac atc ctc atc gct gtg ggc gct gtc atg atg ttc 510
Tyr Val Gly Ile Tyr Ile Leu Ile Ala Val Gly Ala Val Met Met Phe
105 110 115
gtt ggc ttc ctg ggc tgc tac ggg gcc atc cag gaa tcc cag tgc ctg 558
Val Gly Phe Leu Gly Cys Tyr Gly Ala Ile Gln Glu Ser Gln Cys Leu
120 125 130
ctg ggg acg ttc ttc act tgc ctg gtc atc ctg ttt gcc tgt gag gtg 606
Leu Gly Thr Phe Phe Thr Cys Leu Val Ile Leu Phe Ala Cys Glu Val
135 140 145
gcc gcc ggc atc tgg ggc ttt gtc aac aag gac cag atc gcc aag gat 654
Ala Ala Gly Ile Trp Gly Phe Val Asn Lys Asp Gln Ile Ala Lys Asp
150 155 160 165
gtg aag cag ttc tat gac cag gcc cta cag cag gcc gtg gtg gat gat 702
Val Lys Gln Phe Tyr Asp Gln Ala Leu Gln Gln Ala Val Val Asp Asp
170 175 180
gac gcc aac aac gcc aag gct gtg gtg aag acc ttc cac gag acg ctt 750
Asp Ala Asn Asn Ala Lys Ala Val Val Lys Thr Phe His Glu Thr Leu
185 190 195
gac tgc tgt ggc tcc agc aca ctg act gct ttg acc acc tca gtg ctc 798
Asp Cys Cys Gly Ser Ser Thr Leu Thr Ala Leu Thr Thr Ser Val Leu
200 205 210
aag aac aat ttg tgt ccc tcg ggc agc aac atc atc agc aac ctc ttc 846

Lys Asn Asn Leu Cys Pro Ser Gly Ser Asn Ile Ile Ser Asn Leu Phe
 215 220 225
 aag gag gac tgc cac cag aag atc gat gac ctc ttc tcc ggg aag ctg 894
 Lys Glu Asp Cys His Gln Lys Ile Asp Asp Leu Phe Ser Gly Lys Leu
 230 235 240 245
 tac ctc atc ggc att gct gcc atc gtg gtc gct gtg atc atg atc ttc 942
 Tyr Leu Ile Gly Ile Ala Ala Ile Val Val Ala Val Ile Met Ile Phe
 250 255 260
 gag atg atc ctg agc atg gtg ctg tgc tgt ggc atc cgg aac agc tcc 990
 Glu Met Ile Leu Ser Met Val Leu Cys Cys Gly Ile Arg Asn Ser Ser
 265 270 275
 gtg tac tgaggccccg cagctctggc cacagggacc tctgcagtgc cccctaagtg 1046
 Val Tyr
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 ttttcagggc tgacgtcaca tgtaggtggc gtgtatgagt ggagacgggc ctgggtcttg 1226
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 Leu Leu Val Lys Arg Leu Gln Glu Val Ser Ser Arg Asp Gly Lys Gly
 15 20 25
 gac ctg ggg gag ccg ccc ccg aca cgg ccc acg gtg ggc acc aat ctt 145
 Asp Leu Gly Glu Pro Pro Pro Thr Arg Pro Thr Val Gly Thr Asn Leu
 30 35 40 45
 act gac atc gtg gca cag aga aag atc acc atc cgg gag ctt ggg ggg 193
 Thr Asp Ile Val Ala Gln Arg Lys Ile Thr Ile Arg Glu Leu Gly Gly
 50 55 60
 tgc atg ggc ccc atc tgg tcc agt tac tat gga aac tgc cgt tct ctc 241
 Cys Met Gly Pro Ile Trp Ser Ser Tyr Gly Asn Cys Arg Ser Leu
 65 70 75
 ctg ttt gtg atg gac gcc tct gac ccc acc cag ctc tct gca tcc tgt 289
 Leu Phe Val Met Asp Ala Ser Asp Pro Thr Gln Leu Ser Ala Ser Cys
 80 85 90
 gtg cag ctc tta ggt ctc ctt tct gca gaa caa ctt gca gaa gca tcg 337
 Val Gln Leu Leu Gly Leu Leu Ser Ala Glu Gln Leu Ala Glu Ala Ser
 95 100 105
 gtg ctg ata ctc ttc aat aaa atc gac cta ccc tgt tac atg tcc acg 385
 Val Leu Ile Leu Phe Asn Lys Ile Asp Leu Pro Cys Tyr Met Ser Thr
 110 115 120 125
 gag gag atg aag tca tta atc agg ctt cca gac atc att gct tgt gcc 433

Glu	Glu	Met	Lys	Ser	Leu	Ile	Arg	Leu	Pro	Asp	Ile	Ile	Ala	Cys	Ala		
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Lys	Gln	Asn	Ile	Thr	Thr	Ala	Glu	Ile	Ser	Ala	Arg	Glu	Gly	Thr	Gly		
				145					150					155			
tta	gca	ggg	gtg	ctg	gcc	tgg	ctc	cag	gcc	acc	cac	aga	gcc	aac	gat		529
Leu	Ala	Gly	Val	Leu	Ala	Trp	Leu	Gln	Ala	Thr	His	Arg	Ala	Asn	Asp		
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gctttgctgc	caatagtttc	ttctcacagg	ggcagaataa	cccaaagtaa	ccctacatga												649
tggggctctg	tgctgggatg	caatgatgtg	taaaactgagg	catgtggaga	tggaagtga												709
catctggcct	ctgaaaaaag	tgtccccagg	ggctaggcat	ggtggctcac	acctgtaatc												769
ccagcacttt	gagaggccga	ggcgggtgta	tcacctgagg	tcgggagttc	gagactagcc												829
tgaccaacat	ggagaaaccc	tgtctctact	aaaaatacaa	aattagctgg	gtgtgctggt												889
gcatgcctgt	aatctcagct	acttgggagg	ctgagacagg	agaatccctt	gaacctggga												949
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gcaccttccg	gaaa	atg	gcg	gct	gcc	agg	ccc	agc	ctg	ggc	mga	gtc	ctc				170
		Met	Ala	Ala	Ala	Arg	Pro	Ser	Leu	Gly	Arg	Val	Leu				
		1				5					10						
cca	gga	tcc	tct	gtc	ctg	ttc	ctg	tgt	gac	atg	cag	gag	aag	ttc	cgc		218
Pro	Gly	Ser	Ser	Val	Leu	Phe	Leu	Cys	Asp	Met	Gln	Glu	Lys	Phe	Arg		
		15				20					25						
cac	aac	atc	gcc	tac	ttc	cca	cag	atc	gtc	tca	gtg	gct	gcc	cgc	atg		266
His	Asn	Ile	Ala	Tyr	Phe	Pro	Gln	Ile	Val	Ser	Val	Ala	Ala	Arg	Met		
		30				35					40						
ctc	aag	gtg	gcc	cgg	ctg	ctt	gag	gtg	cca	gtc	atg	ctg	acg	gag	cag		314
Leu	Lys	Val	Ala	Arg	Leu	Leu	Glu	Val	Pro	Val	Met	Leu	Thr	Glu	Gln		
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tac	cca	caa	ggc	ctg	ggc	ccc	acg	gtg	ccc	gag	ctg	ggg	act	gag	ggc		362
Tyr	Pro	Gln	Gly	Leu	Gly	Pro	Thr	Val	Pro	Glu	Leu	Gly	Thr	Glu	Gly		
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ctt	cgg	ccg	ctg	gcc	aag	acc	tgc	ttc	agc	atg	gtg	cct	gcc	ctg	cag		410
Leu	Arg	Pro	Leu	Ala	Lys	Thr	Cys	Phe	Ser	Met	Val	Pro	Ala	Leu	Gln		
		80						85					90				
cag	gag	ctg	gac	agt	cgg	ccc	cag	ctg	cgc	tct	gtg	ctg	ctc	tgt	ggc		458
Gln	Glu	Leu	Asp	Ser	Arg	Pro	Gln	Leu	Arg	Ser	Val	Leu	Leu	Cys	Gly		
		95				100					105						
att	gag	gca	cag	gcc	tgc	atc	ttg	aac	acg	acc	ctg	gac	ctc	cta	gac		506
Ile	Glu	Ala	Gln	Ala	Cys	Ile	Leu	Asn	Thr	Thr	Leu	Asp	Leu	Leu	Asp		
		110				115					120						
cgg	ggg	ctg	cag	gtc	cat	gtg	gtg	gtg	gac	gcc	tgc	tcc	tca	cgc	agc		554
Arg	Gly	Leu	Gln	Val	His	Val	Val	Val	Asp	Ala	Cys	Ser	Ser	Arg	Ser		
					125					135				140			
cag	gtg	gac	cgt	ctg	gtg	gct	ctg	gcc	cgc	atg	aga	cag	agt	ggt	gcc		602

Gln Val Asp Arg Leu Val Ala Leu Ala Arg Met Arg Gln Ser Gly Ala	
145 150 155	
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Phe Leu Ser Thr Ser Glu Gly Leu Ile Leu Gln Leu Val Gly Asp Ala	
160 165 170	
gtc cac ccc cag ttc aag gag atc cag aaa ctc atc aag gag ccc gcc	698
Val His Pro Gln Phe Lys Glu Ile Gln Lys Leu Ile Lys Glu Pro Ala	
175 180 185	
cca gac agc gga ctg ctg ggc ctc ttc caa ggc cag aac tcc ctc ctc	746
Pro Asp Ser Gly Leu Leu Gly Leu Phe Gln Gly Gln Asn Ser Leu Leu	
190 195 200	
cac tgaactccaa ccctgccttg aggggaagacc accctcctgt caccgagacc	799
His	
205	
tcagtgggaag cccgttcccc ccattccctgg atcccaagag tgggtgcgatc caccaggagt	859
gccgccccct tgtggggggg ggcagggtgc tgccttccca ttggacagct gctcccggaa	919
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tcggccccgg gccacttcac gggggcgggaa ggggagggga agaagagctc cagactgtgg	1039
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Met Trp Leu Tyr Arg Asn	
1 5	
ccc tac gtg gag gcg gag tat ttc ccc acc aag ccg atg ttt gtt att	163
Pro Tyr Val Glu Ala Glu Tyr Phe Pro Thr Lys Pro Met Phe Val Ile	
10 15 20	
gca ttt ctc tct cca ctg tct ctg atc ttc ctg gcc aaa ttt ctc aag	211
Ala Phe Leu Ser Pro Leu Ser Leu Ile Phe Leu Ala Lys Phe Leu Lys	
25 30 35	
aag gca gac aca aga gac agc aga caa gcc tgc ctg gct gcc agc ctt	259
Lys Ala Asp Thr Arg Asp Ser Arg Gln Ala Cys Leu Ala Ala Ser Leu	
40 45 50	
gcc ctg gct ctg aat ggc gtc ttt acc aac aca ata aaa ctg atc gta	307
Ala Leu Ala Leu Asn Gly Val Phe Thr Asn Thr Ile Lys Leu Ile Val	
55 60 65 70	
ggg agg cca cgc cca gat ttc ttc tac cgc tgc ttc cct gat ggg cta	355
Gly Arg Pro Arg Pro Asp Phe Phe Tyr Arg Cys Phe Pro Asp Gly Leu	
75 80 85	
gcc cat tct gac ttg atg tgt aca ggg gat aag gac gtg gtg aat gag	403
Ala His Ser Asp Leu Met Cys Thr Gly Asp Lys Asp Val Val Asn Glu	
90 95 100	
ggc cga aag agc ttc ccc agt gga cat tct tcc ttt gca ttt gct ggt	451
Gly Arg Lys Ser Phe Pro Ser Gly His Ser Ser Phe Ala Phe Ala Gly	
105 110 115	
ctg gcc ttt gcg tcc ttc tac ctg gca ggg aag tta cac tgc ttc aca	499
Leu Ala Phe Ala Ser Phe Tyr Leu Ala Gly Lys Leu His Cys Phe Thr	
120 125 130	


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cca caa ggc cgt ggg aaa tct tgg agg ttc tgt gcc ttt ctg tca cct    547
Pro Gln Gly Arg Gly Lys Ser Trp Arg Phe Cys Ala Phe Leu Ser Pro
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cta ctt ttt gca gct gtg att gca ctg tcc cgc aca tgt gac tac aag    595
Leu Leu Phe Ala Ala Val Ile Ala Leu Ser Arg Thr Cys Asp Tyr Lys
          155          160          165
cat cac tgg caa gat ctg ctc aaa tgc acc aac act gcc aag    637
His His Trp Gln Asp Leu Leu Lys Cys Thr Asn Thr Ala Lys
          170          175          180
tgactaagggt agaaaagaaa aatgacagggt atcgatcatct gaaggacaga tgaatctttt    697
tctgccccctt cttcacaatg gaataataagg aacaattatg ggatgtcatc agaattggatg    757
ccataggacc tacagctccc tttctcttta ttgtgattat actttaataa tgacattgtc    817
ttttatgtgt atgttcctat attttcaatg tatctttttc cttcagtaaa cctgatattc    877
aaaaaaaaaa aaaaaaa    894

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 <213> Homo sapiens

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 <222> 221..670

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atctgcttag ttctacaaag tggagtttct gggcatcatt cttcatttct gtacacaaag    180
tgctgtgaag ctcaagaaga aatagctctg cacaggaacg atg tgc act gcc cta    235
          Met Cys Thr Ala Leu
          1          5
ctg ctt ctt tat cta aga tgg tgt ttc aac tta aaa ctt gtg aat gtg    283
Leu Leu Leu Tyr Leu Arg Trp Cys Phe Asn Leu Lys Leu Val Asn Val
          10          15          20
aaa tat gag cca aaa gac tct ctc ggc cct gaa atg acc ttt gta gca    331
Lys Tyr Glu Pro Lys Asp Ser Leu Gly Pro Glu Met Thr Phe Val Ala
          25          30          35
gat gct gcc aga ggc ccc ctg tta tcc tcc ctg gac tct cca gct aac    379
Asp Ala Ala Arg Gly Pro Leu Leu Ser Ser Leu Asp Ser Pro Ala Asn
          40          45          50
ctg atg tca act gcc agt gtg tgc atc tcc tta cct gag ggc tgt tct    427
Leu Met Ser Thr Ala Ser Val Cys Ile Ser Leu Pro Glu Gly Cys Ser
          55          60          65
ggg ggc agg agt cct tgc tac tca cag aaa tgg cca cca gaa gtg cca    475
Gly Gly Arg Ser Pro Cys Tyr Ser Gln Lys Trp Pro Pro Glu Val Pro
          70          75          80          85
gaa aaa tta acc tcc ctt ggc cag cag tcc tca acc agc tcc ctc act    523
Glu Lys Leu Thr Ser Leu Gly Gln Gln Ser Ser Thr Ser Ser Leu Thr
          90          95          100
gac act gat gtg cag gtg tct cct atg ctg gtt gct gga gtc aac cac    571
Asp Thr Asp Val Gln Val Ser Pro Met Leu Val Ala Gly Val Asn His
          105          110          115
agc agc agc ctt ctt gac aac ata ccc ttc act ggc tgc ctt cct ttc    619
Ser Ser Ser Leu Leu Asp Asn Ile Pro Phe Thr Gly Cys Leu Pro Phe
          120          125          130
cat ctc tct tct tca ctc ccc tac cta tgt ctc cta ggc tct ccc ttc    667
His Leu Ser Ser Ser Leu Pro Tyr Leu Cys Leu Leu Gly Ser Pro Phe
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 Lys
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 <212> DNA
 <213> Homo sapiens

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 atgtttcccg ggaagaactg ggataaagga aggggtcccag cacc atg gag gac ccg 176
 Met Glu Asp Pro
 1
 aac cct gaa gag aac atg aag cag cag gat tca ccc aag gag aga agt 224
 Asn Pro Glu Glu Asn Met Lys Gln Gln Asp Ser Pro Lys Glu Arg Ser
 5 10 15 20
 ccc cag agc cca gga ggc aac atc tgc cac ctg ggg gcc ccg aag tgc 272
 Pro Gln Ser Pro Gly Gly Asn Ile Cys His Leu Gly Ala Pro Lys Cys
 25 30 35
 acc cgc tgc ctc atc acc ttc gca gat tcc aag ttc cag gag cgt cac 320
 Thr Arg Cys Leu Ile Thr Phe Ala Asp Ser Lys Phe Gln Glu Arg His
 40 45 50
 atg aag cgg gag cac cca gcg gac ttc gtg gcc cag aag ctg cag ggg 368
 Met Lys Arg Glu His Pro Ala Asp Phe Val Ala Gln Lys Leu Gln Gly
 55 60 65
 gtc ctc ttc atc tgc ttc acc tgc gcc cgc tcc ttc ccc tcc tcc aaa 416
 Val Leu Phe Ile Cys Phe Thr Cys Ala Arg Ser Phe Pro Ser Ser Lys
 70 75 80
 gcc cta atc acc cac cag cgc agc cac ggt cca gcc gcc aag ccc acc 464
 Ala Leu Ile Thr His Gln Arg Ser His Gly Pro Ala Ala Lys Pro Thr
 85 90 95 100
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 Leu Pro Val Ala Thr Thr Thr Ala Gln Pro Thr Phe Pro Cys Pro Asp
 105 110 115
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 Cys Gly Lys Thr Phe Gly Gln Ala Val Ser Leu Arg Arg His Arg Gln
 120 125 130
 atg cat gag gtc cgt gcc cct cct ggc acc ttc gcc tgc aca gag tgc 608
 Met His Glu Val Arg Ala Pro Pro Gly Thr Phe Ala Cys Thr Glu Cys
 135 140 145
 ggt cag gac ttt gct cag gaa gca ggg ctg cat caa cac tac att cgg 656
 Gly Gln Asp Phe Ala Gln Glu Ala Gly Leu His Gln His Tyr Ile Arg
 150 155 160
 cat gcc cgg ggg gag ctc tgagtgcagc ttaagcctct ccacggtgac 704
 His Ala Arg Gly Glu Leu
 165 170
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 agattctcaa aaaaaaaaaa aaaaa 849

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<212> DNA
<213> Homo sapiens

<220>
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<222> 165..671

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atgtttcccg ggaagaactg ggataaagga aggggtcccag cacc atg gag gac ccg      176
                               Met Glu Asp Pro
                               1
aac cct gaa gag aac atg aag cag cag gat tca ccc aag gag aga agt      224
Asn Pro Glu Glu Asn Met Lys Gln Gln Asp Ser Pro Lys Glu Arg Ser
5                               10                               15                               20
ccc cag ccc agg agg caa cat ctg cca cct ggg ggc ccc gaa gtg cac      272
Pro Gln Pro Arg Arg Gln His Leu Pro Pro Gly Gly Pro Glu Val His
                               25                               30                               35
ccg ctg cct cat cac ctt cgc aga ttc caa gtt cca gga gcg tca cat      320
Pro Leu Pro His His Leu Arg Arg Phe Gln Val Pro Gly Ala Ser His
                               40                               45                               50
gaa gcg gga gca ccc agc gga ctt cgt ggc cca gaa gct gca ggg ggt      368
Glu Ala Gly Ala Pro Ser Gly Leu Arg Gly Pro Glu Ala Ala Gly Gly
                               55                               60                               65
cct ctt cat ctg ctt cac ctg cgc ccg ctc ctt ccc ctc ctc caa agc      416
Pro Leu His Leu Leu His Leu Arg Pro Leu Leu Pro Leu Leu Gln Ser
                               70                               75                               80
cct aat cac cca cca gcg cag cac ggt cca gcc gcc aag ccc acc ctg      464
Pro Asn His Pro Pro Ala Gln His Gly Pro Ala Ala Lys Pro Thr Leu
85                               90                               95                               100
ccg gtt gca acc act act gcc cag ccc acc ttc cct tgt cct gac tgt      512
Pro Val Ala Thr Thr Thr Ala Gln Pro Thr Phe Pro Cys Pro Asp Cys
                               105                               110                               115
ggc aag acc ttt ggg cag gct gtt tct ctg agg cgg cac cgc cag atg      560
Gly Lys Thr Phe Gly Gln Ala Val Ser Leu Arg Arg His Arg Gln Met
                               120                               125                               130
cat gag gtc cgt gcc cct cct ggc acc ttc gcc tgc aca gag tgc ggt      608
His Glu Val Arg Ala Pro Pro Gly Thr Phe Ala Cys Thr Glu Cys Gly
                               135                               140                               145
cag gac ttt gct cag gaa gca ggg ctg cat caa cac tac att cgg cat      656
Gln Asp Phe Ala Gln Glu Ala Gly Leu His Gln His Tyr Ile Arg His
                               150                               155                               160
gcc cgg ggg gag ctc tgagtgcagc ttaagcctct ccacgggtgac ggggtggctct      711
Ala Arg Gly Glu Leu
165
gtggctggta ggactcacc atgatatggg gtgcaggaac tctggggggc ctgaaggatt      771
tgcttcctc ccctgggaag gcagagggct cttaataaag aggaccaga agattctcaa      831
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<211> 1176
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> 28..1128

<400> 162

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			1				5									
acc	aac	tgc	agc	tgg	tgg	ccc	atc	tcc	gcg	ctg	gag	agc	gat	gcg	gcc	102
Thr	Asn	Cys	Ser	Trp	Trp	Pro	Ile	Ser	Ala	Leu	Glu	Ser	Asp	Ala	Ala	
10				15					20					25		
aag	cca	gcg	gag	gcc	ccc	gac	gct	ccc	gag	gcg	gcc	agc	ccc	gcc	cat	150
Lys	Pro	Ala	Glu	Ala	Pro	Asp	Ala	Pro	Glu	Ala	Ala	Ser	Pro	Ala	His	
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tgg	ccc	agg	gag	agc	ctg	gtt	ctg	tac	cac	tgg	acc	cag	tcc	ttc	agc	198
Trp	Pro	Arg	Glu	Ser	Leu	Val	Leu	Tyr	His	Trp	Thr	Gln	Ser	Phe	Ser	
			45					50					55			
tcg	cag	aag	gtg	cgg	ctg	gtg	atc	gcc	gag	aag	ggc	ctg	gtg	tgc	gag	246
Ser	Gln	Lys	Val	Arg	Leu	Val	Ile	Ala	Glu	Lys	Gly	Leu	Val	Cys	Glu	
		60					65					70				
gag	cgg	gac	gtg	agc	ctg	cca	cag	agc	gag	cac	aag	gag	ccc	tgg	ttc	294
Glu	Arg	Asp	Val	Ser	Leu	Pro	Gln	Ser	Glu	His	Lys	Glu	Pro	Trp	Phe	
		75				80					85					
atg	cgg	ctc	aac	ctg	ggc	gag	gag	gtg	ccc	gtc	atc	atc	cac	cgc	gac	342
Met	Arg	Leu	Asn	Leu	Gly	Glu	Glu	Val	Pro	Val	Ile	Ile	His	Arg	Asp	
90				95					100					105		
aac	atc	atc	agt	gac	tat	gac	cag	atc	att	gac	tat	gtg	gag	cgc	acc	390
Asn	Ile	Ile	Ser	Asp	Tyr	Asp	Gln	Ile	Ile	Asp	Tyr	Val	Glu	Arg	Thr	
			110					115						120		
ttc	aca	gga	gag	cac	gtg	gtg	gcc	ctg	atg	ccc	gag	gtg	ggc	agc	ctg	438
Phe	Thr	Gly	Glu	His	Val	Val	Ala	Leu	Met	Pro	Glu	Val	Gly	Ser	Leu	
		125					130						135			
cag	cac	gca	cgg	gtg	ctg	cag	tac	cgg	gag	ctg	ctg	gac	gca	ctg	ccc	486
Gln	His	Ala	Arg	Val	Leu	Gln	Tyr	Arg	Glu	Leu	Leu	Asp	Ala	Leu	Pro	
		140					145					150				
atg	gat	gcc	tac	acg	cat	ggc	tgc	atc	ctg	cat	ctc	gag	ctc	acc	acc	534
Met	Asp	Ala	Tyr	Thr	His	Gly	Cys	Ile	Leu	His	Leu	Glu	Leu	Thr	Thr	
		155				160					165					
gac	tcc	atg	atc	ccc	aag	tac	gcc	acg	gcc	gag	atc	cgc	aga	cat	tta	582
Asp	Ser	Met	Ile	Pro	Lys	Tyr	Ala	Thr	Ala	Glu	Ile	Arg	Arg	His	Leu	
170				175					180					185		
gcc	aat	gcc	acc	acg	gac	ctc	atg	aaa	ctg	gac	cat	gaa	gag	gag	ccc	630
Ala	Asn	Ala	Thr	Thr	Asp	Leu	Met	Lys	Leu	Asp	His	Glu	Glu	Glu	Pro	
			190					195					200			
cag	ctc	tcc	gag	ccc	tac	ctt	tct	aaa	caa	aag	aag	ctc	atg	gcc	aag	678
Gln	Leu	Ser	Glu	Pro	Tyr	Leu	Ser	Lys	Gln	Lys	Lys	Leu	Met	Ala	Lys	
		205						210				215				
atc	ttg	gag	cat	gat	gat	gtg	agc	tac	ctg	aag	aag	atc	ctc	ggg	gaa	726
Ile	Leu	Glu	His	Asp	Asp	Val	Ser	Tyr	Leu	Lys	Lys	Ile	Leu	Gly	Glu	
		220				225						230				
ctg	gcc	atg	gtg	ctg	gac	cag	att	gag	gcg	gag	ctg	gag	aag	agg	aag	774
Leu	Ala	Met	Val	Leu	Asp	Gln	Ile	Glu	Ala	Glu	Leu	Glu	Lys	Arg	Lys	
		235				240					245					
ctg	gag	aac	gag	ggg	cag	aaa	tgc	gag	ctg	tgg	ctc	tgt	ggc	tgt	gcc	822
Leu	Glu	Asn	Glu	Gly	Lys	Lys	Cys	Glu	Leu	Trp	Leu	Cys	Gly	Cys	Ala	
250				255					260					265		
ttc	acc	ctc	gct	gat	gtc	ctc	ctg	gga	gcc	acc	ctg	cac	cgc	ctc	aag	870
Phe	Thr	Leu	Ala	Asp	Val	Leu	Leu	Gly	Ala	Thr	Leu	His	Arg	Leu	Lys	
			270					275						280		
ttc	ctg	gga	ctg	tcc	aag	aaa	tac	tgg	gaa	gat	ggc	agc	cgg	ccc	aac	918
Phe	Leu	Gly	Leu	Ser	Lys	Lys	Tyr	Trp	Glu	Asp	Gly	Ser	Arg	Pro	Asn	

	285		290		295	
ctg cag tcc ttc ttt gag agg gtc cag aga cgc ttt gcc ttc cgg aaa						966
Leu Gln Ser Phe Phe Glu Arg Val Gln Arg Arg Phe Ala Phe Arg Lys						
	300		305		310	
gtc ctg ggt gac atc cac acc acc ctg ctg tcg gcc gtc atc ccc aat						1014
Val Leu Gly Asp Ile His Thr Thr Leu Leu Ser Ala Val Ile Pro Asn						
	315		320		325	
gct ttc cgg ctg gtc aag agg aaa ccc cca tcc ttc ttc ggg gcg tcc						1062
Ala Phe Arg Leu Val Lys Arg Lys Pro Pro Ser Phe Phe Gly Ala Ser						
	330		335		340	345
ttc ctc atg ggc tcc ctg ggt ggg atg ggc tac ttt gcc tac tgg tac						1110
Phe Leu Met Gly Ser Leu Gly Gly Met Gly Tyr Phe Ala Tyr Trp Tyr						
	350		355		360	
ctc aag aaa aaa tac atc tagggccagg cctggggcctt ggtgtctgac						1158
Leu Lys Lys Lys Tyr Ile						
	365					
aaaaaamaaa aaaaaaaaaa						1176

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 <213> Homo sapiens

<220>
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 <222> 135..194

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gcaccttccg gaaa atg gcg gct gcc agg ccc agc ctg ggc cga gtc ctc	170
Met Ala Ala Ala Arg Pro Ser Leu Gly Arg Val Leu	
1 5 10	
cca gga tcc tct cct gtt cct gtg tgacatgcag gagaagttcc gccacaacat	224
Pro Gly Ser Ser Pro Val Pro Val	
15 20	
cgctacttc ccacagatcg tctcagtggc tgcccgcgatg ctcaagggtgg cccgggtgct	284
tgagggtgcca gtcattgctga cggagcagta cccacaaggc ctgggcccga cgggtgcccga	344
gctgggggact gagggccttc ggccgctggc caagacctgc ttcagcatgg tgcctgccct	404
gcagcaggag ctggacagtc ggccccagct gcgctctgtg ctgctctgtg gcattgaggc	464
acaggcctgc atcttgaaca cgacctgga cctcctagac cgggggctgc aggtccatgt	524
ggtggtggac gcctgctcct cagcagccca ggtggaccgg ctggtggctc tggcccgcct	584
gagacagagt ggtgccttcc totccaccag cgaagggtc attctgcagc ttgtgggcga	644
tgccgtccac cccagttca aggagatcca gaaactcacc aaggagccc cccagacag	704
cggactgctg ggctcttcc aaggccagaa ctccctcctc cactgaactc caaccctgcc	764
ttgaggggaag accaccctcc tgtaaccggg acctcagtgg aagcccgctc ccccatccc	824
tggatcccaa gagtgggtgcg atccaccagg agtgccgccc ccttgggggg ggcagggtgc	884
tgccttccca ttggacagct gctcccggaa atgcaaatga gactcctgga aactgggtgg	944
gaattggctg agccaagatg gaggcggggc tcggccccgg gccacttcac ggggcgggaa	1004
ggggaggggga agaagagtct cagactgtgg gacacggact cgcagaataa acatatatgt	1064
ggcaaaaaaa aaaaaaaaaa	1084

<210> 164
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<220>

<221> CDS
<222> 173..847

<400> 164

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cgagttcatt actacaggaa aaactgttct cttctgtggc acagagaacc ctgcttcaaa      120
gcagaagtag cagttccgga gtccagctgg ctaaaactca tcccagagga ta atg gca      178
                                   Met Ala
                                   1
acc cat gcc tta gaa atc gct ggg ctg ttt ctt ggt ggt gtt gga atg      226
Thr His Ala Leu Glu Ile Ala Gly Leu Phe Leu Gly Gly Val Gly Met
                                   5
                                   10
                                   15
gtg ggc aca gtg gct gtc act atg cct cag tgg aga gtg tcg gcc      274
Val Gly Thr Val Ala Val Thr Val Met Pro Gln Trp Arg Val Ser Ala
                                   20
                                   25
                                   30
ttc att gaa aac aac atc gtg gtt ttt gaa aac ttc tgg gaa gga ctg      322
Phe Ile Glu Asn Asn Ile Val Val Phe Glu Asn Phe Trp Glu Gly Leu
                                   35
                                   40
                                   45
                                   50
tgg atg aat tgc gtg agg cag gct aac atc agg atg cag tgc aaa atc      370
Trp Met Asn Cys Val Arg Gln Ala Asn Ile Arg Met Gln Cys Lys Ile
                                   55
                                   60
                                   65
tat gat tcc ctg ctg gct ctt tct ccg gac cta cag gca gcc aga gga      418
Tyr Asp Ser Leu Leu Ala Leu Ser Pro Asp Leu Gln Ala Ala Arg Gly
                                   70
                                   75
                                   80
ctg atg tgt gct gct tcc gtg atg tcc ttc ttg gct ttc atg atg gcc      466
Leu Met Cys Ala Ala Ser Val Met Ser Phe Leu Ala Phe Met Met Ala
                                   85
                                   90
                                   95
atc ctt ggc atg aaa tgc acc agg tgc acg ggg gac aat gag aag gtg      514
Ile Leu Gly Met Lys Cys Thr Arg Cys Thr Gly Asp Asn Glu Lys Val
                                   100
                                   105
                                   110
aag gct cac att ctg ctg acg gct gga atc atc ttc atc atc acg ggc      562
Lys Ala His Ile Leu Leu Thr Ala Gly Ile Ile Phe Ile Ile Thr Gly
                                   115
                                   120
                                   125
                                   130
atg gtg gtg ctc atc cct gtg agc tgg gtt gcc aat gcc atc atc aga      610
Met Val Val Leu Ile Pro Val Ser Trp Val Ala Asn Ala Ile Ile Arg
                                   135
                                   140
                                   145
gat ttc tat aac tca ata gtg aat gtt gcc caa aaa cgt gag ctt gga      658
Asp Phe Tyr Asn Ser Ile Val Asn Val Ala Gln Lys Arg Glu Leu Gly
                                   150
                                   155
                                   160
gaa gct ctc tac tta gga tgg acc acg gca ctg gtg ctg att gtt gga      706
Glu Ala Leu Tyr Leu Gly Trp Thr Thr Ala Leu Val Leu Ile Val Gly
                                   165
                                   170
                                   175
gga gct ctg ttc tgc tgc gtt ttt tgt tgc aac gaa aag agc agt agc      754
Gly Ala Leu Phe Cys Cys Val Phe Cys Cys Asn Glu Lys Ser Ser Ser
                                   180
                                   185
                                   190
tac aga tac tcg ata cct tcc cat cgc aca acc caa aaa agt tat cac      802
Tyr Arg Tyr Ser Ile Pro Ser His Arg Thr Thr Gln Lys Ser Tyr His
                                   195
                                   200
                                   205
                                   210
acc gga aag aag tca ccg agc gtc tac tcc aga agt cag tat gtg      847
Thr Gly Lys Lys Ser Pro Ser Val Tyr Ser Arg Ser Gln Tyr Val
                                   215
                                   220
                                   225
tagttgtgta tgttttttta acttttactat aaagccatgc aaatgacaaa aatctatatt      907
actttctcaa aatggacccc aaagaaactt tgatttactg ttcttaactg cctaattcta      967
attacaggaa ctgtgcatca gctattttatg attctataag ctatttcagc agaatgagat      1027
attaaaccca atgctttgat tgttctagaa agtattgtaa tttgttttct aaggtggttc      1087
aagcatctac tctttttatc atttacttca aaatgacatt gctaaagact gcattattct      1147
actactgtaa tttctccacg acatagcatt atgtacatag atgagtgtaa catttatatc      1207
tcacatagag acatgcttat atggttttat ttaaaatgaa atgccagtcc attacactga      1267

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ataaatagaa ctcaactatt gcttttcagg gaaatcatgg ataggggttga agaagggttac 1327
tattaattgt ttaaaaaacag cttatggatt aatgtcctcc atttataatg aagattaaaaa 1387
tgaaggcttt aatcagcatt gtaaaggaaa ttgaatggct ttctgatatg ctgttttttta 1447
gcctaggagt tagaaatcct aacttccttta tcctcttctc ccagaggctt tttttttctt 1507
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tgcttttcca gggctatact cagaagaaag ataaaagtgt gatctaagaa aaagtgatgg 1627
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agaaatcata tatgtatgta tatatttttaa taagtatttg agtacagact ttgagggtttc 1747
atcaatataa ataaaagagc agaaaagtaa aaaaaaaaaa aaaaaa 1793

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<210> 165
<211> 1849
<212> DNA
<213> Homo sapiens

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<220>
<221> CDS
<222> 8..1141

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<220>
<221> misc_feature
<222> 1707
<223> n=a, g, c or t

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<400> 165
cgttgcc atg gat cct ggg gac gac tgg ctg gtg gaa tcc ttg cgc ttg 49
      Met Asp Pro Gly Asp Asp Trp Leu Val Glu Ser Leu Arg Leu
      1          5          10
tac cag gat ttc tat gca ttc gac ctg tca gga gcc act cga gtc ctt 97
Tyr Gln Asp Phe Tyr Ala Phe Asp Leu Ser Gly Ala Thr Arg Val Leu
15          20          25          30
gaa tgg att gat gac aaa gga gtc ttt gtt gct ggc tat gaa agc ctg 145
Glu Trp Ile Asp Asp Lys Gly Val Phe Val Ala Gly Tyr Glu Ser Leu
      35          40          45
aaa aag aat gaa att ctt cat ctg aaa tta cct ctc aga ctt tct gta 193
Lys Lys Asn Glu Ile Leu His Leu Lys Leu Pro Leu Arg Leu Ser Val
      50          55          60
aag gaa aac aag ggc tta ttc cca gaa aga gat ttc aaa gtg cgc cat 241
Lys Glu Asn Lys Gly Leu Phe Pro Glu Arg Asp Phe Lys Val Arg His
      65          70          75
gga gga ttt tca gac agg tct atc ttt gat cta aag cat gtg cca cat 289
Gly Gly Phe Ser Asp Arg Ser Ile Phe Asp Leu Lys His Val Pro His
      80          85          90
acc aga ttg ctg gtt acc agt ggc ctt cca ggt tgt tat ctg cag gtg 337
Thr Arg Leu Leu Val Thr Ser Gly Leu Pro Gly Cys Tyr Leu Gln Val
95          100          105          110
tgg cag gtt gca gag gac agt gat gtc att aaa gct gtc agc acc att 385
Trp Gln Val Ala Glu Asp Ser Asp Val Ile Lys Ala Val Ser Thr Ile
      115          120          125
gct gtg cat gag aaa gag gag agt ctc tgg cct agg gtg gcc gtc ttc 433
Ala Val His Glu Lys Glu Glu Ser Leu Trp Pro Arg Val Ala Val Phe
      130          135          140
tcc aca ttg gca ccc gga gtc ctc cat ggg gcg agg ctc cga agt ctg 481
Ser Thr Leu Ala Pro Gly Val Leu His Gly Ala Arg Leu Arg Ser Leu
      145          150          155
cag gtc gtt gat ctg gag tcc cgg aag acc acg tac acc tca gat gtc 529
Gln Val Val Asp Leu Glu Ser Arg Lys Thr Thr Tyr Thr Ser Asp Val
      160          165          170

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agt gac agt gag gag ctg agt agc ctg cag gtc cta gat gcg gac acc	577
Ser Asp Ser Glu Glu Leu Ser Ser Leu Gln Val Leu Asp Ala Asp Thr	
175 180 185 190	
ttt gcc ttc tgc tgt gct tcg ggc cgg ctg ggg ctt gtt gac acc cgg	625
Phe Ala Phe Cys Cys Ala Ser Gly Arg Leu Gly Leu Val Asp Thr Arg	
195 200 205	
cag aag tgg gca ccg ttg gag aat cgc agc cct ggc cct ggg tct ggt	673
Gln Lys Trp Ala Pro Leu Glu Asn Arg Ser Pro Gly Pro Gly Ser Gly	
210 215 220	
gga gag aga tgg tgt gct gaa gtt ggg agc tgg ggc cag ggc cct ggg	721
Gly Glu Arg Trp Cys Ala Glu Val Gly Ser Trp Gly Gln Gly Pro Gly	
225 230 235	
ccc agc att gcc agc ctt agc tca gat ggg cgt ctt tgt ctt ctt gac	769
Pro Ser Ile Ala Ser Leu Ser Ser Asp Gly Arg Leu Cys Leu Leu Asp	
240 245 250	
ccc cgg gat ctc tgc cat cct gtg agc tca gtc cag tgc cca gta tcc	817
Pro Arg Asp Leu Cys His Pro Val Ser Ser Val Gln Cys Pro Val Ser	
255 260 265 270	
gta cct agc cct gac cca gag ctg ctg cga gtg act tgg gcc cca ggc	865
Val Pro Ser Pro Asp Pro Glu Leu Leu Arg Val Thr Trp Ala Pro Gly	
275 280 285	
ctg aag aat tgc ttg gcc atc tca ggt ttt gat ggt aca gtc cag gtc	913
Leu Lys Asn Cys Leu Ala Ile Ser Gly Phe Asp Gly Thr Val Gln Val	
290 295 300	
tat gat gcc aca tct tgg gat gga aca cgg agc caa gat gga aca cgg	961
Tyr Asp Ala Thr Ser Trp Asp Gly Thr Arg Ser Gln Asp Gly Thr Arg	
305 310 315	
agc caa gta gaa cct ctc ttc act cac aga ggt cac atc ttc cta gat	1009
Ser Gln Val Glu Pro Leu Phe Thr His Arg Gly His Ile Phe Leu Asp	
320 325 330	
gga aat ggg atg gac cct gct cct ttg gtc acc acc cac acc tgg cat	1057
Gly Asn Gly Met Asp Pro Ala Pro Leu Val Thr Thr His Thr Trp His	
335 340 345 350	
ccc tgc aga cca agg act ttg tta tca gca aca aat gat gcc tct ctg	1105
Pro Cys Arg Pro Arg Thr Leu Leu Ser Ala Thr Asn Asp Ala Ser Leu	
355 360 365	
cat gtg tgg gac tgg gtg gac ctt tgt gcc ccc cgc tgacaccagc	1151
His Val Trp Asp Trp Val Asp Leu Cys Ala Pro Arg	
370 375	
atctttccat ctaggcctct agaaagggga ggagctgctg tagtagcaag ggtgctgatg	1211
taggactcaa gtgactacca gtccctgtta ccagctgtgt ggccttgggc aagtctgcc	1271
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tgatattgcg aagggttagaa gaaacgcatg gcataattac ttggtagcta ttgttagatc	1391
tgggagtgtg aaatggtagc gtttttgtccc tgtcttcaca ctatcatagg gagaatcaaa	1451
agagctaaca aatataaaca tgctttgtga atttttttaa agaaaaaaat gtaggggggc	1511
caataaacat gaaaaaatcc cagccctagt agcaattaag gaaatagcaa aacaggattt	1571
ctgctcctct tgaggggggtc tcatgggaac acaggtgcac tttccacac ttgtccccc	1631
agggtgactag gtccaagaga catttgcttt tggtggcccc acaaacattt ccttttgagg	1691
gcccatagtg aatatntaaa gtgtgctgga catggtggct catgcctgta atcccagcac	1751
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 <212> DNA
 <213> Homo sapiens

<220>

<221> CDS
<222> 136..264

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ggcacagaga accctgcttc aaagcagaag tagcagttcc ggagtccagc tggctaaaaac      120
tcattcccaga ggata atg gca acc cat gcc tta gaa atc gct ggg ctg ttt      171
               Met Ala Thr His Ala Leu Glu Ile Ala Gly Leu Phe
                   1             5             10
ctt ggt ggt gtt gga atg gtg ggc aca gtg gct gtc act gtc atg cct      219
Leu Gly Gly Val Gly Met Val Gly Thr Val Ala Val Thr Val Met Pro
                   15             20             25
cag tgg aga gtg tcg gcc ttc att gaa aac aac atc gtg gtt ttt      264
Gln Trp Arg Val Ser Ala Phe Ile Glu Asn Asn Ile Val Val Phe
                   30             35             40
taaaacttct gggaaggact gtggatgaat tgcgtgaggc aggctaacat caggatgcag      324
tgcaaaatct atgattccct gctggctctt tctccggacc tacaggcagc cagaggactg      384
atgtgtgctg cttccgtgat gtccctcttg gctttcatga tggccatcct tggcatgaaa      444
tgcaccagggt gcacggggga caatgagaag gtgaaggctc acattctgct gacggctgga      504
atcatcttca tcatcacggg catggtggtg ctcattccctg tgagctgggt tgccaatgcc      564
atcatcagag atttctataa ctcaatagtg aatggtgccc aaaaacgtga gcttggagaa      624
gctctctact taggatggac cacggcactg gtgctgattg ttggaggagc tctgttctgc      684
tgcggtttttt gttgcaacga aaagagcagt agctacagat actcgatacc ttcccatcgc      744
acaacccaaa aaagttatca caccggaaaag aagtcaccga gcgtctactc cagaagtcag      804
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tatattactt tctcaaaatg gaccccaaag aaactttgat ttactgttct taactgccta      924
atcttaatta caggaactgt gcatcagcta tttatgattc tataagctat ttcagcagaa      984
tgagatatta aaccgaatgc tttgattggt ctagaaagta tagtaatttg ttttctaagg      1044
tggktaagc atctactctt tttatcattt acttcaaaat gacattgcta aagactgcat      1104
tattttacta ctgtaatttc tccacgacat agcattatct acatagatga gtgtaacatt      1164
tatatctcac atagagacat gcttatatgg ttkcatttaa aatgaaatgc cagtccatta      1224
cactgaataa atagaactca actattgctt ttcagggaaa tcatggatag ggttgaagaa      1284
ggttactatt aattgtttta aaacagctta gggattaatg tcctccattt ataatgaaga      1344
ttaaatagaa ggctttaatc agcattgtaa aggaaattga atggctttct gatatgctgt      1404
tttttagcct aggagttaga aatcctaact tctttatcct cttctcccag aggctttttt      1464
tttcttgtgt attaaattaa cattttttaa aagcagatata tttgtcaagg ggctttgcat      1524
tcaaactgct tttccagggc tatactcaga agaaagataa aagtgtgatc taagaaaaag      1584
tgatggttttt aggaaagtga aaatatTTTT gtttttgtat ttgaagaaga atgatgcatt      1644
ttgacaagaa atcatatatg tatggatata ttttaataag tatttgagta cagactttga      1704
ggtttcatca atataaataa aagagcaaaa aaaaaaaaaa aaaa      1748

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<210> 167
<211> 1275
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> 14..1048

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                   1             5             10
tgc ggc cag gcg tgg ggt gcg tcg gtg ggc ggc cgc agc tgc gag gag      97
Cys Gly Gln Ala Trp Gly Ala Ser Val Gly Gly Arg Ser Cys Glu Glu
                   15             20             25
ctc act gcg gtc cta acc ccg ccg cag ctc ctc gga cgc agg ttt aac      145

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Leu	Thr	Ala	Val	Leu	Thr	Pro	Pro	Gln	Leu	Leu	Gly	Arg	Arg	Phe	Asn	
30						35					40					
ttc	ttt	att	caa	caa	aaa	tgc	gga	ttc	aga	aaa	gca	ccc	agg	aag	gtt	193
Phe	Phe	Ile	Gln	Gln	Lys	Cys	Gly	Phe	Arg	Lys	Ala	Pro	Arg	Lys	Val	
45					50					55					60	
gaa	cct	cga	aga	tca	gac	cca	ggg	aca	agt	ggg	gaa	gca	tac	aag	aga	241
Glu	Pro	Arg	Arg	Ser	Asp	Pro	Gly	Thr	Ser	Gly	Glu	Ala	Tyr	Lys	Arg	
				65					70						75	
agt	gct	ttg	att	cct	cct	gtg	gaa	gaa	aca	gtc	ttt	tat	cct	tct	ccc	289
Ser	Ala	Leu	Ile	Pro	Pro	Val	Glu	Glu	Thr	Val	Phe	Tyr	Pro	Ser	Pro	
			80				85						90			
tat	cct	ata	agg	agt	ctc	ata	aaa	cct	tta	ttt	ttt	act	gtt	ggg	ttt	337
Tyr	Pro	Ile	Arg	Ser	Leu	Ile	Lys	Pro	Leu	Phe	Phe	Thr	Val	Gly	Phe	
		95					100					105				
aca	ggc	tgt	gca	ttt	gga	tca	gct	att	tgg	caa	tat	gaa	tca	ctg		385
Thr	Gly	Cys	Ala	Phe	Gly	Ser	Ala	Ala	Ile	Trp	Gln	Tyr	Glu	Ser	Leu	
	110					115					120					
aaa	tcc	agg	gtc	cag	agt	tat	ttt	gat	ggg	ata	aaa	gct	gat	tgg	ttg	433
Lys	Ser	Arg	Val	Gln	Ser	Tyr	Phe	Asp	Gly	Ile	Lys	Ala	Asp	Trp	Leu	
125					130					135					140	
gat	agc	ata	aga	cca	caa	aaa	gaa	gga	gac	ttc	aga	aag	gag	att	aac	481
Asp	Ser	Ile	Arg	Pro	Gln	Lys	Glu	Gly	Asp	Phe	Arg	Lys	Glu	Ile	Asn	
				145					150					155		
aag	tgg	tgg	aat	aac	cta	agt	gat	ggc	cag	cgg	act	gtg	aca	ggg	att	529
Lys	Trp	Trp	Asn	Asn	Leu	Ser	Asp	Gly	Gln	Arg	Thr	Val	Thr	Gly	Ile	
			160					165					170			
ata	gct	gca	aat	gtc	ctt	gta	ttc	tgt	tta	tgg	aga	gta	cct	tct	ctg	577
Ile	Ala	Ala	Asn	Val	Leu	Val	Phe	Cys	Leu	Trp	Arg	Val	Pro	Ser	Leu	
		175					180					185				
cag	cgg	aca	atg	atc	aga	tat	ttc	aca	tcg	aat	cca	gcc	tca	aag	gtc	625
Gln	Arg	Thr	Met	Ile	Arg	Tyr	Phe	Thr	Ser	Asn	Pro	Ala	Ser	Lys	Val	
	190					195					200					
ctt	tgt	tct	cca	atg	ttg	ctg	tca	aca	ttc	agt	cat	ttc	tcc	tta	ttt	673
Leu	Cys	Ser	Pro	Met	Leu	Leu	Ser	Thr	Phe	Ser	His	Phe	Ser	Leu	Phe	
205					210					215					220	
cac	atg	gca	gca	aat	atg	tat	gtt	ttg	tgg	agc	ttc	tct	tcc	agc	ata	721
His	Met	Ala	Ala	Asn	Met	Tyr	Val	Leu	Trp	Ser	Phe	Ser	Ser	Ser	Ile	
				225					230					235		
gtg	aac	att	ctg	ggg	caa	gag	cag	ttc	atg	gca	gtg	tac	cta	tct	gca	769
Val	Asn	Ile	Leu	Gly	Gln	Glu	Gln	Phe	Met	Ala	Val	Tyr	Leu	Ser	Ala	
			240				245					250				
ggg	gtt	att	tcc	aat	ttt	gtc	agt	tac	gtg	ggg	aaa	gtt	gcc	aca	gga	817
Gly	Val	Ile	Ser	Asn	Phe	Val	Ser	Tyr	Val	Gly	Lys	Val	Ala	Thr	Gly	
		255					260					265				
aga	tat	gga	cca	tca	ctt	ggg	gca	gcc	ctg	aaa	gcc	att	atc	gcc	atg	865
Arg	Tyr	Gly	Pro	Ser	Leu	Gly	Ala	Ala	Leu	Lys	Ala	Ile	Ile	Ala	Met	
		270				275					280					
gat	aca	gca	gga	atg	atc	ctg	gga	tgg	aaa	ttt	ttt	gat	cat	gcg	gca	913
Asp	Thr	Ala	Gly	Met	Ile	Leu	Gly	Trp	Lys	Phe	Phe	Asp	His	Ala	Ala	
		285			290					295					300	
cat	ctt	ggg	gga	gct	ctt	ttt	gga	ata	tgg	tat	gtt	act	tac	ggg	cat	961
His	Leu	Gly	Gly	Ala	Leu	Phe	Gly	Ile	Trp	Tyr	Val	Thr	Tyr	Gly	His	
				305					310					315		
gaa	ctg	att	tgg	aag	aac	agg	gag	ccg	cta	gtg	aaa	atc	tgg	cat	gaa	1009
Glu	Leu	Ile	Trp	Lys	Asn	Arg	Glu	Pro	Leu	Val	Lys	Ile	Trp	His	Glu	
			320				325						330			
ata	agg	act	aat	ggc	ccc	aaa	aaa	gga	ggg	ggc	tct	aag	taaaa	actggg		1058
Ile	Arg	Thr	Asn	Gly	Pro	Lys	Lys	Gly	Gly	Gly	Ser	Lys				

335	340	345	
attggacagt	agtgggtgcat	ctgggtccttg	cgccttgaga
gagtgaccat	ggctatgctc	ccgtctggaa	gatgccagca
agctgtgtcc	cccagtcctg	gtcttttttag	aatgtgaatg
aggtttctat	ctagtttgca	aaaaaaaaa	aaaaaaa

<210> 168

<211> 1023

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> 70..777

<400> 168

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ggcccccg	atg aag aga	tct ggg aac	ccg gga gcc	gag gta acg	aac agc	111
Met	Lys	Arg	Ser	Gly	Asn	
Pro	Gly	Ala	Glu	Val	Thr	
Asn	Ser					
1	5	10				
tcg gtg gca	ggg cct gac	tgc tgc gga	ggc ctc ggc	aat att gat	ttt	159
Ser Val Ala	Gly Pro Asp	Cys Cys Gly	Gly Leu Gly	Asn Ile Asp	Phe	
15	20	25	30			
aga cag gca	gac ttc tgc	gtt atg acc	cgg ctg ctg	ggc tac gtg	gac	207
Arg Gln Ala	Asp Phe Cys	Val Met Thr	Arg Leu Leu	Gly Tyr Val	Asp	
35	40	45				
ccc ctg gat	ccc agc ttt	gtg gct gcc	gtc atc acc	atc acc ttc	aat	255
Pro Leu Asp	Pro Ser Phe	Val Ala Ala	Val Ile Thr	Ile Thr Phe	Asn	
50	55	60				
ccg ctc tac	tgg aat gtg	gtt gca cga	tgg gaa cac	aag acc cgc	aag	303
Pro Leu Tyr	Trp Asn Val	Val Ala Arg	Trp Glu His	Lys Thr Arg	Lys	
65	70	75				
ctg agc agg	gcc ttc gga	tcc ccc tac	ctg gcc tgc	tac tct cta	agc	351
Leu Ser Arg	Ala Phe Gly	Ser Pro Tyr	Leu Ala Cys	Tyr Ser Leu	Ser	
80	85	90				
atc acc atc	ctg ctc ctg	aac ttc ctg	cgc tgc cac	tgc ttc acg	cag	399
Ile Thr Ile	Leu Leu Leu	Asn Phe Leu	Arg Ser His	Cys Phe Thr	Gln	
95	100	105				
gcc atg ctg	agc cag ccc	agg atg gag	agc ctg gac	acc ccc gcg	gcc	447
Ala Met Leu	Ser Gln Pro	Arg Met Glu	Ser Leu Asp	Thr Pro Ala	Ala	
115	120	125				
tac agc ctg	gtc ctc gca	ctc ctg gga	ctg ggc gtc	gtg ctc gtg	ctc	495
Tyr Ser Leu	Val Leu Ala	Leu Leu Gly	Leu Gly Val	Val Leu Val	Leu	
130	135	140				
tcc agc ttc	ttt gca ctg	ggg ttc gct	gga act ttc	cta ggt gat	tac	543
Ser Ser Phe	Phe Ala Leu	Gly Phe Ala	Gly Thr Phe	Leu Gly Asp	Tyr	
145	150	155				
ttc ggg atc	ctc aag gag	gcg aga gtg	acc gtg ttc	ccc ttc aac	atc	591
Phe Gly Ile	Leu Lys Glu	Ala Arg Val	Thr Val Phe	Pro Phe Asn	Ile	
160	165	170				
ctg gac aac	ccc atg tac	tgg gga agc	aca gcc aac	tac ctg ggc	tgg	639
Leu Asp Asn	Pro Met Tyr	Trp Gly Ser	Thr Ala Asn	Tyr Leu Gly	Trp	
175	180	185				
gcc atc atg	cac gcc agc	ccc acg ggc	ctg ctc ctg	acg gtg ctg	gtg	687
Ala Ile Met	His Ala Ser	Pro Thr Gly	Leu Leu Leu	Thr Val Leu	Val	
195	200	205				
gcc ctc acc	tac ata gtg	gct ctc cta	tac gaa gag	ccc ttc acc	gct	735
Ala Leu Thr	Tyr Ile Val	Ala Leu Leu	Tyr Glu Glu	Pro Phe Thr	Ala	

210	215	220	
gag atc tac cgg cag aaa gcc tcc ggg tcc cac aag agg agc			777
Glu Ile Tyr Arg Gln Lys Ala Ser Gly Ser His Lys Arg Ser			
225	230	235	
tgattgagct gcaacagctt tgctgaaggc ctggccagcc tectggcctg ccccaagtgg			837
cagggcctgc gcagggcgag aatgggtgct gctgctcagg gctcgcccc ggctgtgggt			897
gccccagtgc cttggaacct gctgccttgg ggaccttga cgtgccgaca tatggccatt			957
gagctccaac ccacacattc ccattcacca ataaaggcac cctgacctca aaaaaaaaaa			1017
aaaaaa			1023

<210> 169
 <211> 1085
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> 38..400

<400> 169	
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Met Asn Thr Glu Ala Glu	
1 5	
caa cag ctt ctc cat cac gcc aga aat ggc aat gct gaa gaa gta aga	103
Gln Gln Leu Leu His His Ala Arg Asn Gly Asn Ala Glu Glu Val Arg	
10 15 20	
caa cta tta gag acc atg gcg agt aat gaa gtg att gct gac att aat	151
Gln Leu Leu Glu Thr Met Ala Ser Asn Glu Val Ile Ala Asp Ile Asn	
25 30 35	
tgc aaa gga aga agt aag tct aac ttg ggc tgg aca ccc cta cat ctg	199
Cys Lys Gly Arg Ser Lys Ser Asn Leu Gly Trp Thr Pro Leu His Leu	
40 45 50	
gca tgc tat ttt gga cac aga caa gtg gtc cag gat ctg ttg aag gct	247
Ala Cys Tyr Phe Gly His Arg Gln Val Val Gln Asp Leu Leu Lys Ala	
55 60 65 70	
ggt gca gaa gtg aat gtg ttg aat gac atg gga gac acg ccg ctt cat	295
Gly Ala Glu Val Asn Val Leu Asn Asp Met Gly Asp Thr Pro Leu His	
75 80 85	
cga gct gcc ttt aca gga cga aag gtg aaa atc att cta tgt tca atg	343
Arg Ala Ala Phe Thr Gly Arg Lys Val Lys Ile Ile Leu Cys Ser Met	
90 95 100	
ttt gta agt gag gta ttt gga gga gta gtt acc att gtt ttc tct gtt	391
Phe Val Ser Glu Val Phe Gly Gly Val Val Thr Ile Val Phe Ser Val	
105 110 115	
ata acc atc tgaccagcaa ccgaagaaag ccacacaaaa aaatgtatac	440
Ile Thr Ile	
120	
accagcactt tgggtcaaaa ggccacagga tcttttgagt ctgacagtga ggtccagtac	500
taagggtcatg gagaccccca ctctgtagca tccctgtgag gagatcattc cgtttctgct	560
tgtgtactcc agcaatgggg aactcctgat tattcttttt ttttaaaaaa aaatagcttc	620
attgaggtat aacttacatt gcataaactt cacctgtgat attgtgaaat atatatattgg	680
tctttgacct tgtacactaa agatgtacaa aaagatgact ggcaaccctt ggcttcagga	740
tgggggctgg tcaccagaaa gaccaaggca ggactagggg gttgggactt tcagccgaac	800
tttgcaacct ccagggaggg tagaggggct gaaggggaaa tggctcgcta atggccagtg	860
gtttcatcaa tcatgcctat ttaatggaac ctccataaaa acctgaaagg acagggttct	920
aggagctcct gggtagctga acacgtggag gttcttgaat gatcacaccc agggagggca	980
tgggtgctct gtgcccttcc tccatgcctt gctttatgta tctcttcac tgtatccttt	1040
gtaataaagc agtaaacatg ttttctgaa aaaaaaaaaa aaaaa	1085

<210> 170
 <211> 776
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> 63..572

<400> 170
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 ga atg cgg ctt caa ggg gct atc ttt gtg ctc ctg ccc cac ctg ggg 107
 Met Arg Leu Gln Gly Ala Ile Phe Val Leu Leu Pro His Leu Gly
 1 5 10 15
 ccc atc ctg gtc tgg ctg ttc act cgt gat cac atg tct ggt tgg tgt 155
 Pro Ile Leu Val Trp Leu Phe Thr Arg Asp His Met Ser Gly Trp Cys
 20 25 30
 gag ggc ccg agg atg ctg tcc tgg tgc cca ttc tac aaa gtc tta ttg 203
 Glu Gly Pro Arg Met Leu Ser Trp Cys Pro Phe Tyr Lys Val Leu Leu
 35 40 45
 ctt gta cag aca gcc atc tac tct gtc gtg ggc tat gcc tcc tac ctg 251
 Leu Val Gln Thr Ala Ile Tyr Ser Val Val Gly Tyr Ala Ser Tyr Leu
 50 55 60
 gtg tgg aag gac ctg gga ggg ggc ttg ggg tgg ccc ctg gcc ctg cct 299
 Val Trp Lys Asp Leu Gly Gly Gly Leu Gly Trp Pro Leu Ala Leu Pro
 65 70 75
 ctt ggc ctc tat gct gtt cag ctc acc atc agc tgg act gtc ctg gtt 347
 Leu Gly Leu Tyr Ala Val Gln Leu Thr Ile Ser Trp Thr Val Leu Val
 80 85 90 95
 ctc ttt ttc aca gtc cac aac cct ggt ctg gcc ctg ctg cac ctg ctg 395
 Leu Phe Phe Thr Val His Asn Pro Gly Leu Ala Leu Leu His Leu Leu
 100 105 110
 ctg ctg tat ggg ctg gtg gtg agc aca gca ctg atc tgg cat ccc atc 443
 Leu Leu Tyr Gly Leu Val Val Ser Thr Ala Leu Ile Trp His Pro Ile
 115 120 125
 aac aaa ctg gct gcc ctg tta ctg ctg ccc tac cta gcc tgg ctc acc 491
 Asn Lys Leu Ala Ala Leu Leu Leu Leu Pro Tyr Leu Ala Trp Leu Thr
 130 135 140
 gtg act tca gcc ctc acc tac cac ctg tgg agg gac agc ctt tgt cca 539
 Val Thr Ser Ala Leu Thr Tyr His Leu Trp Arg Asp Ser Leu Cys Pro
 145 150 155
 gtg cac cag cct cag ccc acg gag aag agt gac tgaggcccta gggcatggga 592
 Val His Gln Pro Gln Pro Thr Glu Lys Ser Asp
 160 165 170
 gaggagggac gccccaggtg gggaggaaga gtctgcaagc agggctgtgg agttaggggt 652
 ccccccaatg ggaccaccct cctgggtccc ctggtgccgt ttttccttag aaatcagaga 712
 aatgggaaag ggggggaaac tgattttaca cttaaataat aaaatcctat tagcaaaaaa 772
 aaaa 776

<210> 171
 <211> 1219
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> 160..867

<400> 171

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ggtttccgga ggacagccaa caagcgatgc tgccgccgcc gtttctgat tggttgtggg      120
tggctacctc ttcgttctga ttggccgcta gtgagcaag atg ctg agc aag ggt      174
                               Met Leu Ser Lys Gly
                               1       5

ctg aag cgg aaa cgg gag gag gag gag gag aag gaa cct ctg gca gtc      222
Leu Lys Arg Lys Arg Glu Glu Glu Glu Glu Lys Glu Pro Leu Ala Val
                               10       15       20

gac tcc tgg tgg cta gat cct ggc cac aca gcg gtg gca cag gca ccc      270
Asp Ser Trp Trp Leu Asp Pro Gly His Thr Ala Val Ala Gln Ala Pro
                               25       30       35

ccg gcc gtg gcc tct agc tcc ctc ttt gac ctc tca gtg ctc aag ctc      318
Pro Ala Val Ala Ser Ser Ser Leu Phe Asp Leu Ser Val Leu Lys Leu
                               40       45       50

cac cac agc ctg cag cag agt gag ccg gac ctg cgg cac ctg gtg ctg      366
His His Ser Leu Gln Gln Ser Glu Pro Asp Leu Arg His Leu Val Leu
                               55       60       65

gtc gtg aac act ctg cgg cgc atc cag gcg tcc atg gca ccc gcg gct      414
Val Val Asn Thr Leu Arg Arg Ile Gln Ala Ser Met Ala Pro Ala Ala
70                               75       80       85

gcc ctg cca cct gtg cct agc cca cct gca gcc ccc agt gtg gct gac      462
Ala Leu Pro Pro Val Pro Ser Pro Pro Ala Ala Pro Ser Val Ala Asp
                               90       95       100

aac tta ctg gca agc tcg gac gct gcc ctt tca gcc tcc atg gcc agc      510
Asn Leu Leu Ala Ser Ser Asp Ala Ala Leu Ser Ala Ser Met Ala Ser
                               105       110       115

ctc ctg gag gac ctc agc cac att gag ggc ctg agt cag gct ccc caa      558
Leu Leu Glu Asp Leu Ser His Ile Glu Gly Leu Ser Gln Ala Pro Gln
120                               125       130

ccc ttg gca gac gag ggg cca cca ggc cgt agc atc ggg gga gca gcg      606
Pro Leu Ala Asp Glu Gly Pro Pro Gly Arg Ser Ile Gly Gly Ala Ala
135                               140       145

ccc agc ctg ggt gcc ttg gac ctg ctg ggc cca gcc act ggc tgt cta      654
Pro Ser Leu Gly Ala Leu Asp Leu Leu Gly Pro Ala Thr Gly Cys Leu
150                               155       160       165

ctg gac gat ggg ctt gag ggc ctg ttt gag gat att gac acc tct atg      702
Leu Asp Asp Gly Leu Glu Gly Leu Phe Glu Asp Ile Asp Thr Ser Met
170                               175       180

tat gac aat gaa ctt tgg gca cca gcc tct gag ggc ctc aaa cca ggc      750
Tyr Asp Asn Glu Leu Trp Ala Pro Ala Ser Glu Gly Leu Lys Pro Gly
185                               190       195

cct gag gat ggg ccg ggc aag gag gaa gct ccg gag ctg gac gag gcc      798
Pro Glu Asp Gly Pro Gly Lys Glu Glu Ala Pro Glu Leu Asp Glu Ala
200                               205       210

gaa ttg gac tac ctc atg gat gtg ctg gtg ggc aca cag gca ctg gag      846
Glu Leu Asp Tyr Leu Met Asp Val Leu Val Gly Thr Gln Ala Leu Glu
215                               220       225

cga ccg ccg ggg cca ggg cgc tgagccctcg tgctggaatg gttgtctggt      897
Arg Pro Pro Gly Pro Gly Arg
230                               235

atctgaactg agcctgctgg ctggaccaac tgtcctcgaa aagacacagc tggcttcct      957
agtacagaga acagggcttg ggccactttg gagagacaga atctagtcct gggcaacttc      1017
acatccgtcc tctgtctca gggctggcag ggggagcctg gaattacccc ctagtgatgg      1077
aatgacaggg tctgggtggg acttaattcc ctggccctgg ggtcatagct tgggctgttc      1137
cttctctgat accgggaagag accccaatca gatttttcaa attaaagcca gtccctgggaa      1197
atctcaaaaa aaaaaaaaaa aa      1219
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<210> 172
 <211> 1487
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> 68..640

<400> 172
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 ggtgact atg aaa ggc tta tat ttc caa cag agt tcc aca gat gaa gaa 109
 Met Lys Gly Leu Tyr Phe Gln Gln Ser Ser Thr Asp Glu Glu
 1 5 10
 ata aca ttt gta ttt caa gaa aag gaa gat ctt cct gtt aca gag gat 157
 Ile Thr Phe Val Phe Gln Glu Lys Glu Asp Leu Pro Val Thr Glu Asp
 15 20 25 30
 aac ttt gtg aaa ctt caa gtt aaa gct tgt gct ctg agc cag ata aat 205
 Asn Phe Val Lys Leu Gln Val Lys Ala Cys Ala Leu Ser Gln Ile Asn
 35 40 45
 aca aag ctt ctg gca gaa atg aag atg aaa aag gat tta ttt cct gtt 253
 Thr Lys Leu Leu Ala Glu Met Lys Met Lys Lys Asp Leu Phe Pro Val
 50 55 60
 ggg aga gaa att gct gga att gta tta gat gtt gga agc aag gta tca 301
 Gly Arg Glu Ile Ala Gly Ile Val Leu Asp Val Gly Ser Lys Val Ser
 65 70 75
 ttc ttt caa cca gat gat gaa gta gtt gga att ttg ccc ctg gac tct 349
 Phe Phe Gln Pro Asp Asp Glu Val Val Gly Ile Leu Pro Leu Asp Ser
 80 85 90
 gaa gac cct gga ctt tgt gaa gtt gtt aga gta cat gag cat tac ttg 397
 Glu Asp Pro Gly Leu Cys Glu Val Val Arg Val His Glu His Tyr Leu
 95 100 105 110
 gtt cat aaa cca gaa aag gtc aca tgg acg gaa gca gca gga agc att 445
 Val His Lys Pro Glu Lys Val Thr Trp Thr Glu Ala Ala Gly Ser Ile
 115 120 125
 cgg gat gga gtg cgt gcc tat aca gct ctg cat tat ctt tct cat ctc 493
 Arg Asp Gly Val Arg Ala Tyr Thr Ala Leu His Tyr Leu Ser His Leu
 130 135 140
 tct cct gga aaa tca gtg ctg ata atg gat gga gca agt gca ttt ggt 541
 Ser Pro Gly Lys Ser Val Leu Ile Met Asp Gly Ala Ser Ala Phe Gly
 145 150 155
 aca ata gct att cag tta gca cat cat aga gga gcc aaa gta ttt caa 589
 Thr Ile Ala Ile Gln Leu Ala His His Arg Gly Ala Lys Val Phe Gln
 160 165 170
 cag cat gca gcc ttg aag ata agc agt gcc ttg aaa gat tca gac ctc 637
 Gln His Ala Ala Leu Lys Ile Ser Ser Ala Leu Lys Asp Ser Asp Leu
 175 180 185 190
 cca tagcccgagt gattgatgta tctaattggga aagttcatgt tgctgaaagc 690
 Pro
 tgttttggaag aaacagggtgg cctgggagta gatattgtcc tagatgctgg agtgagatta 750
 tatagtaaag atgatgaacc agctgtaaaa ctacaactac taccacataa acatgatatc 810
 atcacacttc ttggtgttgg aggccactgg gtaacaacag aagaaaacct tcagttggat 870
 cctccagata gccactgcct tttcctcaag ggagcaacgt tagctttcct gaatgatgaa 930
 gtttgggaatt tgtcaaatgt acaacaggga aaatatcttt gtatcttaaa ggatgtgatg 990
 gagaagtatt caactgggtgt tttcagacct cagttggatg aaccattcc actgtatgag 1050
 gcaaaagttt ccatggaagc tgttcagaaa aatcaaggaa gaaaaaagca agttgttcaa 1110
 ttttaatttt cttctttctc agacctcagt cggatgaaca tattccagta tttgaagcca 1170

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gaatttttctt tggaaattgt tgagaaaaac caaggaagat aaaacaagtt gcattttttaa 1230
gcacgttttct ctgctaagac aagatgctca gttgacacat ttgaaaagt tttgaaaaat 1290
tcttgtgcaa atgatcaaga taattctata attaacatct taagggaatt tttctaaaaa 1350
ccttttcatt gtttctatat attttgccc tgctataaaa ttccttccat gaagaaaact 1410
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aaaaaaaaaa aaaaaaa 1487

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<210> 173
<211> 1915
<212> DNA
<213> Homo sapiens

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<220>
<221> CDS
<222> 132..1298

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gcaccgcgcc c atg gca gag cca gac ccc tct cac cct ctg gag acc cag 170
          Met Ala Glu Pro Asp Pro Ser His Pro Leu Glu Thr Gln
          1          5          10
gca ggg aag gtg cag gag gct cag gac tca gat tca gac tct gag gga 218
Ala Gly Lys Val Gln Glu Ala Gln Asp Ser Asp Ser Asp Ser Glu Gly
          15          20          25
gga gcc gct ggt gga gaa gca gac atg gac ttc ctg cgg aac tta ttc 266
Gly Ala Ala Gly Gly Glu Ala Asp Met Asp Phe Leu Arg Asn Leu Phe
          30          35          40          45
tcc cag acg ctc agc ctg ggc agc cag aag gag cgt ctg ctg gac gag 314
Ser Gln Thr Leu Ser Leu Gly Ser Gln Lys Glu Arg Leu Leu Asp Glu
          50          55          60
ctg acc ttg gaa ggg gtg gcc cgg tac atg cag agc gaa cgc tgt cgc 362
Leu Thr Leu Glu Gly Val Ala Arg Tyr Met Gln Ser Glu Arg Cys Arg
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aga gtc atc tgt ttg gtg gga gct gga atc tcc aca tcc gca ggc atc 410
Arg Val Ile Cys Leu Val Gly Ala Gly Ile Ser Thr Ser Ala Gly Ile
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Pro Asp Phe Arg Ser Pro Thr Gly Leu Tyr Asp Asn Leu Glu Lys
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tac cat ctt ccc tac cca gag gcc atc ttt gag atc agc tat ttc aag 506
Tyr His Leu Pro Tyr Pro Glu Ala Ile Phe Glu Ile Ser Tyr Phe Lys
          110          115          120          125
aaa cat ccg gaa ccc ttc ttc gcc ctc gcc aag gaa ctc tat cct ggg 554
Lys His Pro Glu Pro Phe Phe Ala Leu Ala Lys Glu Leu Tyr Pro Gly
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cag ttc aag cca acc atc tgt cac tac ttc atg cgc ctg ctg aag gac 602
Gln Phe Lys Pro Thr Ile Cys His Tyr Phe Met Arg Leu Leu Lys Asp
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Lys Gly Leu Leu Leu Arg Cys Tyr Thr Gln Asn Ile Asp Thr Leu Glu
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cga ata gcc ggg ctg gaa cag gag gac ttg gtg gag gcg cac ggc acc 698
Arg Ile Ala Gly Leu Glu Gln Glu Asp Leu Val Glu Ala His Gly Thr
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ttc tac aca tca cac tgc gtc agc gcc agc tgc cgg cac gaa tac ccg 746
Phe Tyr Thr Ser His Cys Val Ser Ala Ser Arg His Glu Tyr Pro
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Leu Ser Trp Met Lys Glu Lys Ile Phe Ser Glu Val Thr Pro Lys Cys	
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Glu Asp Cys Gln Ser Leu Val Lys Pro Asp Ile Val Phe Phe Gly Glu	
225 230 235	
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Ser Leu Pro Ala Arg Phe Phe Ser Cys Met Gln Ser Asp Phe Leu Lys	
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Val Asp Leu Leu Leu Val Met Gly Thr Ser Leu Gln Val Gln Pro Phe	
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Gly Leu Gly Gly Met Asp Phe Asp Ser Lys Lys Ala Tyr Arg Asp	
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Val Ala Trp Leu Gly Glu Cys Asp Gln Gly Cys Leu Ala Leu Ala Glu	
320 325 330	
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Leu Leu Gly Trp Lys Lys Glu Leu Glu Asp Leu Val Arg Arg Glu His	
335 340 345	
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Ala Ser Ile Asp Ala Gln Ser Gly Ala Gly Val Pro Asn Pro Ser Thr	
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Ser Ala Ser Pro Lys Lys Ser Pro Pro Pro Ala Lys Asp Glu Ala Arg	
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Thr Thr Glu Arg Glu Lys Pro Gln	
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		Met Ser Leu Asn Leu Pro	Glu Ala Ser Leu Leu			
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Ser Arg Ala Ser Trp	Pro Glu Gln Ala Lys Glu Pro	Arg Arg Glu Gly				
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cac acg gac aaa caa cag	aca gaa gac gta ctg gcc gct	gga ctc cgc				387
His Thr Asp Lys Gln Gln Thr	Glu Asp Val Leu Ala Ala Gly	Leu Arg				
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Cys Leu Pro His Leu Pro	Ala Ile Cys Ala Arg Met	Ser Pro Ala				
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ttc agg gcc atg gat gtg	gag ccc cgc gca aaa ggc	gtc ctt ctg gag				483
Phe Arg Ala Met Asp Val	Glu Pro Arg Ala Lys Gly	Val Leu Leu Glu				
	60	65	70	75		
ccc ttt gtc cac cag gtc	ggg ggg cac tca tgc	gtg ctc cgc ttc aat				531
Pro Phe Val His Gln Val	Gly Gly His Ser Cys Val	Leu Arg Phe Asn				
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gag aca acc ctg tgc aag	ccc ctg gtc cca agg	gaa cat cag ttc tac				579
Glu Thr Thr Leu Cys Lys	Pro Leu Val Pro Arg	Glu His Gln Phe Tyr				
	95	100	105			
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Glu Thr Leu Pro Ala Glu	Met Arg Lys Phe Thr	Pro Gln Tyr Lys Gly				
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Val Val Ser Val Arg Phe	Glu Glu Asp Glu Asp	Asn Leu Cys Leu				
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Ile Ala Tyr Pro Leu Lys	Gly Asp His Gly Ile	Val Asp Ile Val Asp				
	140	145	150	155		
aat tca gac tgt gaa cca	aaa agt aag ctc cta	agg tgg aca aca aac				771
Asn Ser Asp Cys Glu Pro	Lys Ser Lys Leu Leu	Arg Trp Thr Thr Asn				
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aaa aaa cat cat gtc tta	gaa aca gaa aag acc	cct aag gac tgg gtg				819
Lys Lys His His Val Leu	Glu Thr Glu Lys Thr	Pro Lys Asp Trp Val				
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Arg Gln His Arg Lys Glu	Glu Glu Lys Met Lys	Ser His Lys Leu Glu Glu				
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Glu Phe Glu Trp Leu Lys	Lys Ser Glu Val Leu	Tyr Tyr Thr Val Glu				
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Lys Lys Gly Asn Ile Ser	Ser Ser Gln Leu Lys	His Tyr Asn Pro Trp Ser				
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Met Lys Cys His Gln Gln	Gln Leu Gln Arg Met	Lys Glu Asn Ala Lys				
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His Arg Asn Gln Tyr Lys	Phe Ile Leu Leu Glu	Asn Leu Thr Ser Arg				
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tat gag gtg cct tgt gtc	ctt gac ctc aag atg	ggc aca cga caa cat				1107
Tyr Glu Val Pro Cys Val	Leu Asp Leu Lys Met	Gly Thr Arg Gln His				
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Gln	Gln	Ser	Thr	Ser	Ala	Val	Ile	Gly	Val	Arg	Val	Cys	Gly	Met	Gln	
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Val	Tyr	Gln	Ala	Gly	Ser	Gly	Gln	Leu	Met	Phe	Met	Asn	Lys	Tyr	His	
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Gly	Arg	Lys	Leu	Ser	Val	Gln	Gly	Phe	Lys	Glu	Ala	Leu	Phe	Gln	Phe	
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Phe	His	Asn	Gly	Arg	Tyr	Leu	Arg	Arg	Glu	Leu	Leu	Gly	Pro	Val	Leu	
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Lys	Lys	Leu	Thr	Glu	Leu	Lys	Ala	Val	Leu	Glu	Arg	Gln	Glu	Ser	Tyr	
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Pro	Glu	Val	Val	Leu	Asp	Ser	Asp	Ala	Glu	Asp	Leu	Glu	Asp	Leu	Ser	
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Glu	Glu	Ser	Ala	Asp	Glu	Ser	Ala	Gly	Ala	Tyr	Ala	Tyr	Lys	Pro	Ile	
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Gly	Ala	Ser	Ser	Val	Asp	Val	Arg	Met	Ile	Asp	Phe	Ala	His	Thr	Thr	
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Cys	Arg	Leu	Tyr	Gly	Glu	Asp	Thr	Val	Val	His	Glu	Gly	Gln	Asp	Ala	
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Ser	Glu	Glu	Ser	Gly	Glu											
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cctggcagaa	tcaagatgag	gccctgtcat	gcctccccag	tgaggcctac	agtctgagca											180
gacagcatgg	cctgccactg	gcagtgaaca	cc atg tct	gca gga ggt	ggc cgg											233

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Leu Pro Ala Met Pro Thr Ala Arg Cys Ser Cys Ser Ser Leu Gln Ala						
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Gly Pro Arg Leu Phe Val Ile Gly Gly Val Ala Gln Gly Pro Ser Gln						
	330		335		340	
gcc gtg gag gca ctg tgt ctg cgt gat ggg gtc tgaaggcttg gtgggagctg						1294
Ala Val Glu Ala Leu Cys Leu Arg Asp Gly Val						
	345		350			
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Met Lys Gly Leu Tyr Phe Gln Gln Ser Ser Thr Asp Glu Glu	
1 5 10	
ata aca ttt gta ttt caa taaaaggaag atcttcctgt tacagaggat	157
Ile Thr Phe Val Phe Gln	
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      Met Lys Gly Leu Tyr Phe Gln Gln Ser Ser Thr Asp Glu Glu Ile
      1           5           10           15
aca ttt gta ttt caa gaa aag gaa gat ctt cct gtt aca gag gat aac 157
Thr Phe Val Phe Gln Glu Lys Glu Asp Leu Pro Val Thr Glu Asp Asn
      20           25           30
ttt gtg aaa ctt caa gtt aaa gct tgt gct ctg agc cag ata aat aca 205
Phe Val Lys Leu Gln Val Lys Ala Cys Ala Leu Ser Gln Ile Asn Thr
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Lys Leu Leu Ala Glu Met Lys Met Lys Lys Asp Leu Phe Pro Val Gly
      50           55           60
aga gaa att gct gga att gta tta gat gtt gga agc aag gta tca ttc 301
Arg Glu Ile Ala Gly Ile Val Leu Asp Val Gly Ser Lys Val Ser Phe
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Phe Gln Pro Asp Asp Glu Val Val Gly Ile Leu Pro Leu Asp Ser Glu
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gac cct gga ctt tgt gaa gtt gtt aga gta cat gag cat tac ttg gtt 397
Asp Pro Gly Leu Cys Glu Val Val Arg Val His Glu His Tyr Leu Val
      100          105          110
cat aaa cca gaa aag gtc aca tgg acg gaa gca gca gga agc att cgg 445
His Lys Pro Glu Lys Val Thr Trp Thr Glu Ala Ala Gly Ser Ile Arg
      115          120          125
gat gga gtg cgt gcc tat aca gct ctg cat tat ctt tct cat ctc tct 493
Asp Gly Val Arg Ala Tyr Thr Ala Leu His Tyr Leu Ser His Leu Ser
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cct gga aaa tca gtg ctg ata atg gat gga gca agt gca ttt ggt aca 541
Pro Gly Lys Ser Val Leu Ile Met Asp Gly Ala Ser Ala Phe Gly Thr
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Ile Ala Ile Gln Leu Ala His His Arg Gly Ala Lys Val Ile Ser Thr
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Ala Cys Ser Leu Glu Asp Lys Gln Cys Leu Glu Arg Phe Arg Pro Pro
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Gln Leu Leu Pro His Lys His Asp Ile Ile Thr Leu Leu Gly Val Gly	
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Gly His Trp Val Thr Thr Glu Glu Asn Leu Gln Leu Asp Pro Pro Asp	
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Lys Gly Cys Asp Gly Glu Val Ile Asn Trp Cys Phe Gln Thr Ser Val	
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<213> Homo sapiens

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<222> 109..585

<400> 178

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caggggcagg caacagagtg gcggccgcta cgccctgga acggggcc atg gag aag 117

Met Glu Lys

1

ctg cgg cga gtc ctg agc ggc cag gac gac gag gag cag ggc ctg act 165

Leu Arg Arg Val Leu Ser Gly Gln Asp Asp Glu Glu Gln Gly Leu Thr

5

10

15

gcg cag gtc ctg gat gcc tca tcc ctt agt ttc aac acc aga ttg aaa 213

Ala Gln Val Leu Asp Ala Ser Ser Leu Ser Phe Asn Thr Arg Leu Lys

20

25

30

35

tgg ttt gcc atc tgc ttc gta tgt ggc gtt ttc ttt tct att ctt gga 261

Trp Phe Ala Ile Cys Phe Val Cys Gly Val Phe Phe Ser Ile Leu Gly

40

45

50

act gga ttg ctg tgg ctt ccg ggc ggc ata aag ctt ttt gca gtg ttt 309

Thr Gly Leu Leu Trp Leu Pro Gly Gly Ile Lys Leu Phe Ala Val Phe

55

60

65

tat acc ctc ggc aat ctt gct gcg tta gcc agt aca tgc ttt tta atg 357

Tyr Thr Leu Gly Asn Leu Ala Ala Leu Ala Ser Thr Cys Phe Leu Met

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      70      75      80
gga cct gtg aag caa ctg aag aaa atg ttt gaa gca aca aga ttg ctt      405
Gly Pro Val Lys Gln Leu Lys Lys Met Phe Glu Ala Thr Arg Leu Leu
      85      90      95
gca aca att gtt atg ctt ttg tgt ttc ata ttt acc ctg tgt gct gct      453
Ala Thr Ile Val Met Leu Leu Cys Phe Ile Phe Thr Leu Cys Ala Ala
100      105      110      115
ctt tgg tgg cat aag aag gga ctg gct gtg tta ttc tgc ata ttg cag      501
Leu Trp Trp His Lys Lys Gly Leu Ala Val Leu Phe Cys Ile Leu Gln
      120      125      130
ttc ttg tca atg acc tgg tat agc ctg tgc tac atc cca tat gca agg      549
Phe Leu Ser Met Thr Trp Tyr Ser Leu Ser Tyr Ile Pro Tyr Ala Arg
      135      140      145
gat gca gtt att aaa tgc tgt tct ctc cta agt tgaaaatcag      595
Asp Ala Val Ile Lys Cys Cys Ser Ser Leu Leu Ser
      150      155
aaacattgtg gaaaagagca cttgaatgta tgggtactcta tgtttggtga agtttgcttt      655
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ctcattttgt atactggtaa aaactacatg cttgattaaa ccattaaatg cttgtaactt      775
taaattcatt atgtgtcatt aatatacttt tccaaagata agatttttaa tcaactgccag      835
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ttaaaggtag acctcgtgct gcaagataat taaacttttt tgctttttaa aaatgtctgc      955
atttttaaga ttttttttac tttaaatgtg aaacttattt taagctagaa amattgctta      1015
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aaaaataaaa aaaaaaaaaa agaaaaaaaaa aaaaaaaaaa      1113

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<213> Homo sapiens

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      1      5
cgg gcg gcg cgg aaa cgg gcg ggt ctg gcg gcc caa ccc cct gct gcc      100
Arg Ala Ala Arg Lys Arg Ala Gly Leu Ala Ala Gln Pro Pro Ala Ala
      10      15      20
agt cag ggc gca caa acc cca gga gag aag gcg gaa gca gca gcg act      148
Ser Gln Gly Ala Gln Thr Pro Gly Glu Lys Ala Glu Ala Ala Ala Thr
      25      30      35      40
cta aag gca gcc cca ggc tgg cta aag cgg ttc ctg gta tgg aaa cct      196
Leu Lys Ala Ala Pro Gly Trp Leu Lys Arg Phe Leu Val Trp Lys Pro
      45      50      55
agg ccc gcg agt gcc cgg gcc cag ccc ggc cta gtt cag gaa gcg gct      244
Arg Pro Ala Ser Ala Arg Ala Gln Pro Gly Leu Val Gln Glu Ala Ala
      60      65      70
cag ccc cag ggc agc aca tca gag aca cca tgg aac aca gcc att cct      292
Gln Pro Gln Gly Ser Thr Ser Glu Thr Pro Trp Asn Thr Ala Ile Pro
      75      80      85
ctg ccg tgc tgc tgg gac cag tct ttc ctg acc aat atc acc ttc ttg      340
Leu Pro Ser Cys Trp Asp Gln Ser Phe Leu Thr Asn Ile Thr Phe Leu
      90      95      100
aag gtt ctt ctc tgg ttg gtc ctg ctg gga ctg ttt gtg gaa ctg gaa      388

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Lys	Val	Leu	Leu	Trp	Leu	Val	Leu	Leu	Gly	Leu	Phe	Val	Glu	Leu	Glu		
105					110					115				120			
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Phe	Gly	Leu	Ala	Tyr	Phe	Val	Leu	Ser	Leu	Phe	Tyr	Trp	Met	Tyr	Val		
				125					130					135			
ggg	aca	cga	ggc	cct	gaa	gag	aag	aaa	gag	gga	gag	aag	agc	gcc	tac		484
Gly	Thr	Arg	Gly	Pro	Glu	Glu	Lys	Lys	Glu	Gly	Glu	Lys	Ser	Ala	Tyr		
			140					145					150				
tct	gtg	ttc	aat	cca	ggc	tgt	gaa	gcc	atc	cag	ggc	acc	ctg	act	gca		532
Ser	Val	Phe	Asn	Pro	Gly	Cys	Glu	Ala	Ile	Gln	Gly	Thr	Leu	Thr	Ala		
		155					160					165					
gag	cag	ttg	gag	cgc	gag	tta	cag	ttg	aga	ccc	ctg	gca	ggg	aga			577
Glu	Gln	Leu	Glu	Arg	Glu	Leu	Gln	Leu	Arg	Pro	Leu	Ala	Gly	Arg			
	170				175					180							
tagg	acccag	ctgt	gctgtc	atgc	agctaa	cctct	gatgt	ggc	cttcctc	accatt	ggct						637
atgg	atttga	tttc	caggtgt	atagg	actaa	gggc	cagcttg	cggg	tttagct	ctgt	gactgc						697
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tgaa	actctc	taaa	atacat	tcact	gtggg	tccg	acgcaa	tttata	aaaaa	ttat	gtactc						817
aaga	agggag	acct	gtttgt	ttcatt	ttctc	atct	gttttg	gagat	gatatt	taga	gacta						877
gaa	aggcact	gggg	agattc	tcag	cttaaa	acat	ccagca	gttt	gaagta	tgatt	aggta						937
cat	cagggt	gcatt	gtcaa	tg	ttctctt	aagt	ctttta	acatt	ttatag	caatt	ttttt						997
ttt	cccgag	ag	tttaggt	gca	agttttg	gg	tttcttg	ttg	tttttg	ttt	gtctcct						1057
gct	ttaattc	ttta	attttc	ag	tcattact	gg	tattgaaa	aata	aaatat	ctt	taaaaca						1117
tct	cctcttc	agaa	ataggt	ccct	cttcat	tg	cccatcac	cat	cttccac	tct	cctatta						1177
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gagg	gatttc	aca	agtgggt	atta	acggcc	ag	tcagcaa	ga	agtgttg	gtgt	gtacaa						1297
aggg	gagggc	tg	gaagtgt	aact	ccagac	cc	gttgctg	ctt	gagttgt	ttct	tatat						1357
ctaa	agcagc	agt	ccctaac	cttt	ttggca	cc	agggacca	gttt	tggtga	acac	agtttt						1417
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tct	cataagg	ag	cacgcaac	ctag	atccct	cgc	atgcgca	gtt	cacaata	cgg	ttctaag						1537
ggc	tttagag	ta	agcagctt	ttc	acctgt	ggg	cctctg	tg	agaaattc	tg	taaattgt						1597
gata	atcagg	ct	ggatttta	at	gtctgttt	tcc	agtacaa	tg	ttagagtt	tg	ggttcatt						1657
aaa	attaggt	aa	actcccat	tgg	gttaggg	ctt	ctctcat	tcc	attttgt	gg	ctaaccct						1717
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ttg	gccattg	gg	agtttg	gt	ccctcag	ag	ccatccgg	tca	agcagat	gg	tctgttct						1837
atc	tcacaga	aa	agtctttt	ctt	ccatgag	tt	ctgtctga	act	gaacatg	ta	aaaagtat						1897
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aaa																	1960

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<213> Homo sapiens

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<221> CDS

<222> 23..451

<400> 180

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		1				5					10						
tcc	aca	gtg	ctc	tct	tca	gtt	ccc	ctt	caa	atg	ctg	ttt	tat	ctc	agc		100
Ser	Thr	Val	Leu	Ser	Ser	Val	Pro	Leu	Gln	Met	Leu	Phe	Tyr	Leu	Ser		
			15				20					25					
gga	acg	tac	tac	gcc	ctg	tat	ttc	ctc	gcc	acg	ctc	ctg	atg	atc	acg		148
Gly	Thr	Tyr	Tyr	Ala	Leu	Tyr	Phe	Leu	Ala	Thr	Leu	Leu	Met	Ile	Thr		
			30				35					40					

tat aaa agt cag gtg ttc agc tat cct cac cgc tac ctg gtc ctc gat 196
 Tyr Lys Ser Gln Val Phe Ser Tyr Pro His Arg Tyr Leu Val Leu Asp
 45 50 55
 ctt gct ctg ctg ttt ctg atg ggg att cta gaa gca gtt cgg tta tac 244
 Leu Ala Leu Leu Phe Leu Met Gly Ile Leu Glu Ala Val Arg Leu Tyr
 60 65 70
 ctg ggc acc agg ggc aac ctg aca gag gct gag agg ccg ctg gcc gcc 292
 Leu Gly Thr Arg Gly Asn Leu Thr Glu Ala Glu Arg Pro Leu Ala Ala
 75 80 85 90
 agc ctg gcc ctc acg gct ggc acc gcc ctc ctc tct gcc cac ttc ctg 340
 Ser Leu Ala Leu Thr Ala Gly Thr Ala Leu Leu Ser Ala His Phe Leu
 95 100 105
 ctt tgg cag gcc cta gtg ttg tgg gcg gac tgg gcc ctc agc gcc acg 388
 Leu Trp Gln Ala Leu Val Leu Trp Ala Asp Trp Ala Leu Ser Ala Thr
 110 115 120
 ctc ctg gcc ctt cac ggc ctg gag gcc gtc ctg cag gtg gtt gcc atc 436
 Leu Leu Ala Leu His Gly Leu Glu Ala Val Leu Gln Val Val Ala Ile
 125 130 135
 gcg gcc ttc acc agg tagctacgga caccgaggat accccacact ggggccctcc 491
 Ala Ala Phe Thr Arg
 140
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 actatcagtt ctcccttaaaa agtatctaaag ctgttacagt agctttccct tcaattgatt 1331
 ctattgtgtg ttttctatgt ttggaataat tacacccaaa tatctagata ttttctcttc 1391
 accgcatttt gtaaataaag agatgtgtat gcctcaaaaa aaaaaaaaaa aa 1443

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 ccaaaactta caggcttaaa acaacaaaca tgtatcattt cttatgattc tgtgggttgg 180
 ctgggtgggt cttctagctg aggcaggatg gtctaggata gctacatcca c atg tct 237
 Met Ser
 1
 ggg gtc cca gct gag atg act ggg gct gtt gag gcc ttt ctc cct gtg 285
 Gly Val Pro Ala Glu Met Thr Gly Ala Val Glu Ala Phe Leu Pro Val
 5 10 15
 gtg tca tcc tcc aga agg ctg ccc aga ttt gtc cat atg gta gca gga 333

[illegible]

<400> 182

207

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Gly Trp Ser Gln Gly His Arg Ala Arg Gly Arg Gly Gly Val Ser Leu
      105                      110                      115
aga gac aac acc ttc ttt cag gaa gcc agt gag ggc cag gga cag tgg      1159
Arg Asp Asn Thr Phe Phe Gln Glu Ala Ser Glu Gly Gln Gly Gln Trp
      120                      125                      130
ctc atg cct gta atc cca gca ttt taggaggctg agacaggtag atcacttgag      1213
Leu Met Pro Val Ile Pro Ala Phe
      135                      140
gtcaggtggt cgagaccagc ctggccaacg tgggtgaaacc tcgtctctac taaaaaatac      1273
aaaaaattaa ctgggcgtgg tggcacacgc ctgtaatccc agctacatat gaggctgagg      1333
caagagaata acttgaaccc aggaggcgga ggggtgcagtg agctgagatc ctgccgctgc      1393
actccagcct ggggtgacaga gcacactccg tctcaaaaaa ggaaagctga tgagaaattg      1453
ggcatcccgg aattcacacc caaaccatca gctggagctc tgagactggt ggggtgggaa      1513
ttcttccaag atgagaagca agccaggagg gctcaggtcc tgggatgggc agggctttga      1573
tcaaaagaac acaggaagtg atttgctact tgaaagaaag gcaaccctc cccaaggaag      1633
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atgggggttt accatgttgg ccaggctggc cttgaactcc tgacctcagg tgatccgccc      180
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agagt atg tta tca att ctc aag cct agg aga agt cag gag tgg aga aca      530
      Met Leu Ser Ile Leu Lys Pro Arg Arg Ser Gln Glu Trp Arg Thr
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gct ctg aga aga tac tgt tgt cca act gat ctc cag gca cca cgg agt      578
Ala Leu Arg Arg Tyr Cys Cys Pro Thr Asp Leu Gln Ala Pro Arg Ser
      20          25          30
ccg gtc cct cca atc agg aag gtc gga atc tct gat gtc atc gtt cat      626
Pro Val Pro Pro Ile Arg Lys Val Gly Ile Ser Asp Val Ile Val His
      35          40          45
gcc aac ctg gca acc agt ttg aaa aaa aac aca tgt aac tgc cag gct      674
Ala Asn Leu Ala Thr Ser Leu Lys Lys Asn Thr Cys Asn Cys Gln Ala
      50          55          60
gat ctc ttg tcc tgg aga tcc tgg gtg aat ggt atc tcc tgc cac tgt      722
Asp Leu Leu Ser Trp Arg Ser Trp Val Asn Gly Ile Ser Cys His Cys
      65          70          75
ccc aac ctc aga cca ttg tcc aaa agc atc ttc agg gac tcc aca tcc      770
Pro Asn Leu Arg Pro Leu Ser Lys Ser Ile Phe Arg Asp Ser Thr Ser
      80          85          90          95
ctc tgt tcc ctg tcc cag cag agg ctg tgt cct ctc cac tca aag cct      818
Leu Cys Ser Leu Ser Gln Gln Arg Leu Cys Pro Leu His Ser Lys Pro
      100          105          110

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Glu Ala Cys Trp Gly Leu Phe Val Ser Val His Ala His Phe Arg Val
115 120 125
cag gct ggt ggg aga ggg aac aga gtg gga aag aaa act agg gta agc 914
Gln Ala Gly Gly Arg Gly Asn Arg Val Gly Lys Lys Thr Arg Val Ser
130 135 140
aga aac gat gaa acc tta taagagtgag attatcatgt gcaagagtga 962
Arg Asn Asp Glu Thr Leu
145
gattatcatg tacaagagat cccaggaaat actgactttg atgaaaaagt cacatcagag 1022
cactcagttt tggcagagct ttttctgccg aatgtttact cacattcact gtccgagatt 1082
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aaaa 1686

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ccattagatc atttcacaa atg tat ctg cca cca aac agg tca gag ctt tgc 112
Met Tyr Leu Pro Pro Asn Arg Ser Glu Leu Cys
1 5 10
aac ttt gct ttg tct ctt aac ctc tat ggc aaa ggg ttt ttt agc ctg 160
Asn Phe Ala Leu Ser Leu Asn Leu Tyr Gly Lys Gly Phe Phe Ser Leu
15 20 25
gtg gaa aag cat aac agc agg gat tta gaa gat aga gct agt tct ggc 208
Val Glu Lys His Asn Ser Arg Asp Leu Glu Asp Arg Ala Ser Ser Gly
30 35 40
cca tca ctt tca tct cca tca cac ccg gac tgg ggt tat ata gtt ctg 256
Pro Ser Leu Ser Ser Pro Ser His Pro Asp Trp Gly Tyr Ile Val Leu
45 50 55
att tta gtg gca acc ctg ggg gaa ctt gat acc cag gta ggt ggt cac 304
Ile Leu Val Ala Thr Leu Gly Glu Leu Asp Thr Gln Val Gly Gly His
60 65 70 75
tgatcagtag ttgggagagg taggaattgg tgagtacagg taattagagg aaagtcttgt 364
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 aaaggactct ggattggttg gcagtctgct ttttttttcc caaggtgatc actttactgt 180
 agaagaa atg agg tta aca gaa aag agt gag gga gaa caa caa ctc aag 229
 Met Arg Leu Thr Glu Lys Ser Glu Gly Glu Gln Gln Leu Lys
 1 5 10
 ccc aac aac tct aat gca ccc aat gaa gat caa gaa gaa gaa atc caa 277
 Pro Asn Asn Ser Asn Ala Pro Asn Glu Asp Gln Glu Glu Glu Ile Gln
 15 20 25 30
 cag tca gaa cag cat act cca gca agg cag cga aca caa aga gca gac 325
 Gln Ser Glu Gln His Thr Pro Ala Arg Gln Arg Thr Gln Arg Ala Asp
 35 40 45
 aca cag cca tcc aga tgt cga ttg cct tca cgt agg aca cct aca aca 373
 Thr Gln Pro Ser Arg Cys Arg Leu Pro Ser Arg Arg Thr Pro Thr Thr
 50 55 60
 tcc agc gac aga acg atc aac ctt ctt gaa gtc ctt ccg tgg cct act 421
 Ser Ser Asp Arg Thr Ile Asn Leu Leu Glu Val Leu Pro Trp Pro Thr
 65 70 75
 gag tgg att ttc aac ccc tat cga ttg cct gct ctt ttt gag ctt tat 469
 Glu Trp Ile Phe Asn Pro Tyr Arg Leu Pro Ala Leu Phe Glu Leu Tyr
 80 85 90
 cct gaa ttt ctt ctg gtg ttt aaa gaa gcc ttc cat gac ata tcc cat 517
 Pro Glu Phe Leu Leu Val Phe Lys Glu Ala Phe His Asp Ile Ser His
 95 100 105 110
 tgt ctg aaa gcc cag atg gaa aag atc gga ctg ccc atc ata ctc cac 565
 Cys Leu Lys Ala Gln Met Glu Lys Ile Gly Leu Pro Ile Ile Leu His
 115 120 125
 ctc ttc gca ctc tcc acc ctc tac ttc tac aag ttt ttc ctt cct aca 613
 Leu Phe Ala Leu Ser Thr Leu Tyr Phe Tyr Lys Phe Phe Leu Pro Thr
 130 135 140
 att ctt tcc ctt tct ttc ttt att ctt ctt gta ctt ctg ctt ctg ctt 661
 Ile Leu Ser Leu Ser Phe Phe Ile Leu Leu Val Leu Leu Leu Leu Leu
 145 150 155
 ttt att att gtc ttc att ctg atc ttc ttc tgattctttt gtttcaataa 711
 Phe Ile Ile Val Phe Ile Leu Ile Phe Phe
 160 165
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 Met Pro Arg Ser Ser Arg Ser
 1 5

cct ggg gac cca ggc gcc cta ctc gaa gat gtg gcc cac aat ccc aga	162
Pro Gly Asp Pro Gly Ala Leu Leu Glu Asp Val Ala His Asn Pro Arg	
10 15 20	
ccc cgg agg att gcc cag cga ggc cgg aac acc agc agg atg gca gag	210
Pro Arg Arg Ile Ala Gln Arg Gly Arg Asn Thr Ser Arg Met Ala Glu	
25 30 35	
gac acc tcc cca aac atg aat gac aac atc ctg ttg cct gtc cgc aac	258
Asp Thr Ser Pro Asn Met Asn Asp Asn Ile Leu Leu Pro Val Arg Asn	
40 45 50 55	
aat gac caa gcc cta ggc ctg act cag tgc atg ctg gga tgt gtg tcc	306
Asn Asp Gln Ala Leu Gly Leu Thr Gln Cys Met Leu Gly Cys Val Ser	
60 65 70	
tgg ttc acc tgt ttt gcc tgc tcc ctg aga act cag gcc cag cag gtt	354
Trp Phe Thr Cys Phe Ala Cys Ser Leu Arg Thr Gln Ala Gln Gln Val	
75 80 85	
ctg ttt aac acg tgc aga gac aga gtt tca cca tgt tgc cca ggc tgg	402
Leu Phe Asn Thr Cys Arg Asp Arg Val Ser Pro Cys Cys Pro Gly Trp	
90 95 100	
tct caa act cca gtg atc ctc cca cct cag cct tcc gaa gtg ctg gga	450
Ser Gln Thr Pro Val Ile Leu Pro Pro Gln Pro Ser Glu Val Leu Gly	
105 110 115	
tta cag atg caa gct gct gtg cca gaa gct cat gga gaa gac agg cat	498
Leu Gln Met Gln Ala Ala Val Pro Glu Ala His Gly Glu Asp Arg His	
120 125 130 135	
tct gct cct ctg tgc ttt cgg tgt gtc cca ggg ccc tgc cca gtc cca	546
Ser Ala Pro Leu Cys Phe Arg Cys Val Pro Gly Pro Cys Pro Val Pro	
140 145 150	
ggg gga ggt atc cct ggg ccc tgg cac tgattatagg acactgggca	593
Gly Gly Gly Ile Pro Gly Pro Trp His	
155 160	
agacactgca ctgccacgtg actcagtttc cccatctgcc tgatgggtgt tgctgtgaga	653
attatgaaat gaaatgatga ccatgaaaat attgtagaag ccaagaaatg cttcagaagt	713
tataaagctc tccccaacc gtgttaaaaa aaaaaaaaaa	753

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 <212> DNA
 <213> Homo sapiens

<220>
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 <222> 181..462

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ctgtgccaac acagcctgat ggcttcttgt ttcaggaaac atccagaatt acaactggcc	120
attgagttat tacatatcaa ttgaacaagg tagttttaaa atgaaagaaa atcttgcaac	180
atg aat aaa gag ata gac tct ttg aat ctg gca tac agc ttt ccc ttc	228
Met Asn Lys Glu Ile Asp Ser Leu Asn Leu Ala Tyr Ser Phe Pro Phe	
1 5 10 15	
ctt ctt cct gct ttc ctg gac aca ccg tgg aca gac cca ttt ccc tct	276
Leu Leu Pro Ala Phe Leu Asp Thr Pro Trp Thr Asp Pro Phe Pro Ser	
20 25 30	
gga ttc atg gta agg tcc cga gtg ctt ctg ata cag ctg ctg agc aga	324
Gly Phe Met Val Arg Ser Arg Val Leu Leu Ile Gln Leu Leu Ser Arg	
35 40 45	
ccc cgc tca tct cag gag tcc cga gga cac tcg ctt ccc tgc agc ccg	372
Pro Arg Ser Ser Gln Glu Ser Arg Gly His Ser Leu Pro Cys Ser Pro	

50	55	60	
tcc gcc ctc cat aag cct ggg ggc atc tgc cct gca gca ctg ggg agg			420
Ser Ala Leu His Lys Pro Gly Gly Ile Cys Pro Ala Ala Leu Gly Arg			
65	70	75	80
agc cac ctc ctt gtc tgg gaa cag cca agc ctc cgt gac agc			462
Ser His Leu Leu Val Trp Glu Gln Pro Ser Leu Arg Asp Ser			
85	90		
tgaggattct tgtggattgt tctttctgta actggacagc acatccggaa ttccttgcca			522
tagctctgtg ccttgctggg gtctgaggtt cacagggtcag atgctgctgt ctggtccttc			582
ccaattgcgg cgtgaattcc ttcacacctca ccagtagctt cttgctctcc ccaagggagg			642
cacgtgctta gtagggagag aggcctacca aggttgccat ctgccatggg ctcaattgtg			702
cccccaaccc ccttgcaaat tatatatattga agtccccaaa aaaaaaaaaa aa			754

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 <211> 998
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> 6..290

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Met Lys Ala Ser Gly Pro Asp Leu Ser Asp Gly Leu His Cys Pro	
1 5 10 15	
agt cta att aga cat tta aga acc ttc tct gca gct gct gcc tta gcc	98
Ser Leu Ile Arg His Leu Arg Thr Phe Ser Ala Ala Ala Ala Leu Ala	
20 25 30	
cca aga tac cca acc aga ctt ccc agt tca ctg ctt cta tgg cac ctc	146
Pro Arg Tyr Pro Thr Arg Leu Pro Ser Ser Leu Leu Leu Trp His Leu	
35 40 45	
tgc cag tgc ctc cat ctc ctc tat gca gtt tct acc tca tgc aac agc	194
Cys Gln Cys Leu His Leu Leu Tyr Ala Val Ser Thr Ser Cys Asn Ser	
50 55 60	
cat ggg aag aga tcg gct gcc tgg gca atg acc aga aca gaa gac aca	242
His Gly Lys Arg Ser Ala Ala Trp Ala Met Thr Arg Thr Glu Asp Thr	
65 70 75	
gat gcg cta aca gat tcc ttc gat gac agt ttc atc agt tct gca gat	290
Asp Ala Leu Thr Asp Ser Phe Asp Asp Ser Phe Ile Ser Ser Ala Asp	
80 85 90 95	
taaagacttt caccagaaaa aaaaattacc tgattttgcc ctgaggcagc caggaggaggc	350
tttgtccttg acaatcccac tgacttattt aacaggtagc tcaaaaccca acaaaaaactg	410
gaggaggctg ctccactgca gggatggttt caattcggtg actggagtat tgtactctcc	470
ttgcaccctg gctcatcccc acaaaagacc tttcaaagaa aacacttaat tacctccttg	530
cacaagccct gtaagcccta aggtgaaaag aaactcagca gacaagggtcc acagagaagg	590
agaaggcaca attcagtagg gacctacgct cagcaccagg ataaagaaac tgtccattcc	650
tgccacctcc taggaagcta aaagaattaa ggggaggcgg ggcacggtgg ctcacgcctg	710
taatcccagc actttggggag gccgaggcgg gtggatcatg aggtcaggag atcgagacca	770
tcctggctaa catggtgaaa ccccatctct actaaaaata caaaaaatta gccgggcgtg	830
gtggcggggc ccctgtagtc ccagctactc gggaggctga nggcaggaga atggtgtgaa	890
cctgggaggc ggagcttgca gtgagccgag attgcgcctt gctccactcc agcctgagcg	950
acagagcgag actccgtctc aaaaaaaaaa argaaaaaaaa aaaaaaaaaa	998

<210> 189
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 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> 115..411

<400> 189
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 ggacaggaag aaccacagat accagatacg ggtactgttg taactctgtt ctcc atg 117
 Met
 1
 aaa aaa aag gaa gaa aca aca ctt tca gag atg gag cct gtt gag cca 165
 Lys Lys Lys Glu Glu Thr Thr Leu Ser Glu Met Glu Pro Val Glu Pro
 5 10 15
 cag tac caa cta gtc aat gct gaa tcg act tct ccc ttt cta cat tgc 213
 Gln Tyr Gln Leu Val Asn Ala Glu Ser Thr Ser Pro Phe Leu His Cys
 20 25 30
 ctg aga gaa gtc att ggg gaa tac tct gta cac gaa ttt tca ctg ttg 261
 Leu Arg Glu Val Ile Gly Glu Tyr Ser Val His Glu Phe Ser Leu Leu
 35 40 45
 ggg aaa aca gag agt caa ggg att gga ttg tgg att gca ttg gtg gtt 309
 Gly Lys Thr Glu Ser Gln Gly Ile Gly Leu Trp Ile Ala Leu Val Val
 50 55 60 65
 ttc ctc agt ttc ctc atc ttc tcc aca agt ttc tac ata tcg aat gca 357
 Phe Leu Ser Phe Leu Ile Phe Ser Thr Ser Phe Tyr Ile Ser Asn Ala
 70 75 80
 gag cag ccc ttc ttc aaa gaa cct cct acg gaa gct gct aag gaa ctc 405
 Glu Gln Pro Phe Phe Lys Glu Pro Pro Thr Glu Ala Ala Lys Glu Leu
 85 90 95
 agt ctg tagctctgcg tggagccatg tgtaaact gaactgagac ctgccacctc 461
 Ser Leu
 ctactaccta agggccatt ttcactgat atcatcccc agaaacaaac tcatgatgac 521
 ttccatgttt tttttagatt agatacatgg agaattttcc tttcccttag aattaaaatc 581
 ctgcattcta aaaaaaaaaa aaaa 605

<210> 190
 <211> 526
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> 3..368

<400> 190
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 Ile Arg Ala Thr Met Val Ala Arg Val Trp Ser Leu Met Arg Phe
 1 5 10 15
 ctc atc aag gga agt gtg gct ggg ggc gcc gtc tac ctg gtg tac gac 95
 Leu Ile Lys Gly Ser Val Ala Gly Gly Ala Val Tyr Leu Val Tyr Asp
 20 25 30
 cag gag ctg ctg ggg ccc agc gac aag agc cag gca gcc cta cag aag 143
 Gln Glu Leu Leu Gly Pro Ser Asp Lys Ser Gln Ala Ala Leu Gln Lys
 35 40 45

gct ggg gag gtg gtc ccc ccc gcc atg tac cag ttc agc cag tac gtg	191
Ala Gly Glu Val Val Pro Pro Ala Met Tyr Gln Phe Ser Gln Tyr Val	
50 55 60	
tgt cag cag aca ggc ctg cag ata ccc cag ctc cca gcc cct cca aag	239
Cys Gln Gln Thr Gly Leu Gln Ile Pro Gln Leu Pro Ala Pro Pro Lys	
65 70 75	
att tac ttt ccc atc cgt gac tcc tgg aat gca ggc atc atg acg gtg	287
Ile Tyr Phe Pro Ile Arg Asp Ser Trp Asn Ala Gly Ile Met Thr Val	
80 85 90 95	
atg tca gct ctg tgc gtg gcc ccc tcc aag gcc cgc gag tac tcc aag	335
Met Ser Ala Leu Ser Val Ala Pro Ser Lys Ala Arg Glu Tyr Ser Lys	
100 105 110	
gag ggc tgg gag tat gtg aag gcg cgc acc aag tagcgagtca gcaggggccg	388
Glu Gly Trp Glu Tyr Val Lys Ala Arg Thr Lys	
115 120	
cctgccccgg ccagaacggg cagggctgcc actgacctga agactccgga ctgggacccc	448
actccgaggg cagctcccg ccttgccggc ccaataaagg acttcagaag tgaaaaaaaa	508
ataaaaaaaaa aaaaaaaa	526

<210> 191

<211> 910

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> 174..527

<400> 191

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tcccttgctt gtgggcatat gtgggtcata tttccctccc atcaccctct gcacgccacc	120
cccatcaccg ccacagaccc ccagcccttc agttgccttg cacctccttg gtg atg	176
Met	
1	

cag ccg tcc ttg tta agg tca tac agg ttg aag gcc caa tta agc ctg	224
Gln Pro Ser Leu Leu Arg Ser Tyr Arg Leu Lys Ala Gln Leu Ser Leu	
5 10 15	

tca tct aca gtt ccc cga aga atc acg gac aaa cca gcc aca aag tcc	272
Ser Ser Thr Val Pro Arg Arg Ile Thr Asp Lys Pro Ala Thr Lys Ser	
20 25 30	

tgg gaa gga ggc agg agg gag ctg tgt cct cgg gta ctc ttc acc caa	320
Trp Glu Gly Gly Arg Arg Glu Leu Cys Pro Arg Val Leu Phe Thr Gln	
35 40 45	

ctc ctt ctc tgg gtt tgg cct gga gat cct ggc cct gaa ctc cag gaa	368
Leu Leu Leu Trp Val Trp Pro Gly Asp Pro Gly Pro Glu Leu Gln Glu	
50 55 60 65	

aca ggc ttc cct ggc cca cct cgc cca gct cac ctc aaa act gac cga	416
Thr Gly Phe Pro Pro Pro Arg Pro Ala His Leu Lys Thr Asp Arg	
70 75 80	

gcc atc atg gtt ggt gtc aaa ggc att gaa gag aaa agt ggc ata ggt	464
Ala Ile Met Val Gly Val Lys Gly Ile Glu Glu Lys Ser Gly Ile Gly	
85 90 95	

gct gga gtc tgc agg gtg agt gtg gag aag ttg gct tcc aca cag gag	512
Ala Gly Val Cys Arg Val Ser Val Glu Lys Leu Ala Ser Thr Gln Glu	
100 105 110	

agg act tcc tcc ctc taaggagctc cccatacccc ccatcacctt ggcattccca	567
Arg Thr Ser Ser Leu	
115	

gctcctccag	aatccctccc	tcctcagcc	tagagaagga	caactgcttc	cccttgggcc	627
ttgtcccctc	acctccttga	ggaaagaact	gggagtaaat	ctgcttgaag	ttctcctcat	687
tgacaattcc	gctgggacat	tcctggaagg	agagggcacc	aggctgaggg	cagagacaaa	747
atccccttcc	gttcaccgcc	cccaccctcc	atggcccaag	actcccaggg	aggggggataa	807
tcttcaagcc	tccagaggac	tcaccacgtg	gctcatgtga	tgggagggaa	gacttctttc	867
ccagtgcaca	aataaaaaaac	atggaacgaa	aaaaaaaaaaa	aaa		910

<210> 192
 <211> 668
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> 57..203

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						Met										
						1										
gag	ctc	gag	gcc	atg	agc	aga	tat	acc	agc	cca	gtg	aac	cca	cct	gtc	107
Glu	Leu	Glu	Ala	Met	Ser	Arg	Tyr	Thr	Ser	Pro	Val	Asn	Pro	Pro	Val	
			5					10					15			
ttc	ccc	cat	ctg	acc	gtg	gtg	ctt	ttg	gcc	att	ggc	atg	ttc	ttc	acc	155
Phe	Pro	His	Leu	Thr	Val	Val	Leu	Leu	Ala	Ile	Gly	Met	Phe	Phe	Thr	
			20				25				30					
gcc	tgg	ttc	ttc	gtg	tat	cct	ttc	act	gag	cag	cca	gag	gac	cag	cat	203
Ala	Trp	Phe	Phe	Val	Tyr	Pro	Phe	Thr	Glu	Gln	Pro	Glu	Asp	Gln	His	
	35				40					45						
tagtgatgtg	ggaagctcag	ggagaaacca	cgctaggtac	atggaccccg	ccggttttgt											263
acattggatt	ggggctgaga	gaagattgcc	gtgggctggg	ctctctgcac	tccacagtcc											323
accccttcgc	tttgccttaa	ctgctgtgcc	cagttacgag	gtcacctcta	ccaagtacac											383
togtgatata	tataaagagc	tcctcatctc	attagtggcc	tcaactctta	tgggcttttg											443
agtcctcttc	ctgctgctct	gggttggcat	ctacgtgtga	gcaccaagg	gtaacaacca											503
gatggcttca	ctgaaacctg	cttttgtaaa	ttactttttt	ttactgttgc	tggaagtgtc											563
ccacctgctg	ctcataataa	atgcagatgt	atagcaaaaa	aaaaaaaaaaa	aaaaaaaaaaa											623
aaaaaaaaaaa	aaaaaaaaaaa	aaaaaaaaaat	aaaaaaaaaaa	aaaaaa												668

<210> 193
 <211> 637
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> 68..334

<400> 193																
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cccaggc	atg	ctg	gct	ctc	ttc	cac	ttc	cac	ctt	cca	cca	tgg	gat	gac		109
	Met	Leu	Ala	Leu	Phe	His	Phe	His	Leu	Pro	Pro	Trp	Asp	Asp		
	1				5					10						
gca	gta	aga	agg	cca	tca	gta	gat	gcc	agt	ccc	tca	acc	ttg	aac	ttt	157
Ala	Val	Arg	Arg	Pro	Ser	Val	Asp	Ala	Ser	Pro	Ser	Thr	Leu	Asn	Phe	
	15				20				25				30			
cca	gac	gca	gaa	ctt	tat	gcc	tcc	att	ttc	ctc	tgc	tgc	atg	gcc	cca	205
Pro	Asp	Ala	Glu	Leu	Tyr	Ala	Ser	Ile	Phe	Leu	Cys	Cys	Met	Ala	Pro	
			35				40						45			

gga gag att tta att agc ttt cta acc ttg gtc cag att gca cat gca	253
Gly Glu Ile Leu Ile Ser Phe Leu Thr Leu Val Gln Ile Ala His Ala	
50 55 60	
aat ggt aga gga tgc aac acc ccc gct tgt gga gct gcc gct tgt gtc	301
Asn Gly Arg Gly Cys Asn Thr Pro Ala Cys Gly Ala Ala Ala Cys Val	
65 70 75	
tgg cat gaa aat tca caa gaa gag agg aaa tac tgaggagaaa atggcagatt	354
Trp His Glu Asn Ser Gln Glu Glu Arg Lys Tyr	
80 85	
gtgtttgctg aatttgattg acgaagaagt caccatgaaa atcacagtga accatttgga	414
aagcaaaactg ccaaaaaaat aatagtttagt catgctctca ggctgggttgt tttggctgtt	474
gtgggtttct tgcatttcca gatgattgca aagagctgtt tctcaatttc tgcaacaagt	534
gccagctgaa attttggtac cagtttcatt aaatatgtat aacaaaakaa aaaaaaaaaa	594
aaaaaaaaa aaaaaaaaaa aaaaaaagaa aaaaaaaaaa aaa	637

<210> 194
 <211> 706
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
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cacagaaacc cagggccgaa gcaaagtccc aatcccagag aggctggggc acacctacaa	120
ctgaaaggag gcttagaaat ccttcagaga ccacctatc gggtctctc cacctggaca	180
gg atg agc cag caa cac aga agg aag agg cct tcc tcc gaa aga aaa	227
Met Ser Gln Gln His Arg Arg Lys Arg Pro Ser Ser Glu Arg Lys	
1 5 10 15	
agc aca aga aag atg gac aca tgg cag agt ctt aaa gtc aaa gaa gta	275
Ser Thr Arg Lys Met Asp Thr Trp Gln Ser Leu Lys Val Lys Glu Val	
20 25 30	
ttc tgt aag cat aat tct tcc tat gaa tgc ctt ctc tat aaa gag gtt	323
Phe Cys Lys His Asn Ser Ser Tyr Glu Cys Leu Leu Tyr Lys Glu Val	
35 40 45	
gaa gca aga cag gtt tct aag aca gcc acc gat ggg tcc tac ctc ctc	371
Glu Ala Arg Gln Val Ser Lys Thr Ala Thr Asp Gly Ser Tyr Leu Leu	
50 55 60	
gta ttc aca tcc tat gta atc tcc tcc cca gtg tgg act gga cct ggt	419
Val Phe Thr Ser Tyr Val Ile Ser Ser Pro Val Trp Thr Gly Pro Gly	
65 70 75	
gac ttg ctt cca gtg aat aga ata tagcaaaagt gattgatgtc acctccaaga	473
Asp Leu Leu Pro Val Asn Arg Ile	
80 85	
ttcagctata gaagactatg actatgactt tcctcttggc tagcattctc gctaaccctt	533
cctgcttgct tgtactgagc tgccctatga agaggcccat gtaggggtggc ctgggtgggg	593
gtgatctgtg gccaacagcc agcaaggaac taaatcctgt ttacaaccac atgagcttgg	653
aaggagatcc ttccccagta aagccaggag atgaatacaa aaaaaaaaaa aaa	706

<210> 195
 <211> 670
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS

<222> 94..228

<400> 195

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catctccatc cccaatccta aagaaggaaa tcg atg cca cgg tcc tca agg agc 114
                               Met Pro Arg Ser Ser Arg Ser
                               1           5
cct ggg gac cca ggc gcc cta ctc gaa gat ggc cca caa tcc cag acc 162
Pro Gly Asp Pro Gly Ala Leu Leu Glu Asp Gly Pro Gln Ser Gln Thr
      10           15           20
ccg gag gat tgc cca gcg agg ccg gaa cac cag cag gat ggc aga gga 210
Pro Glu Asp Cys Pro Ala Arg Pro Glu His Gln Gln Asp Gly Arg Gly
      25           30           35
cac ctc ccc aaa cat gaa tgacaacatc ctgttgctg tccgcaacaa 258
His Leu Pro Lys His Glu
40           45
tgaccaagcc ctaggcctga ctcagtgcac gctgggatgt gtgtcctggt tcacctgttt 318
tgctgtctcc ctgagaactc aggccagca ggttctgttt aacacgtgca gatgcaagct 378
gctgtgccag aagctcatgg agaagacagg cattctgctc ctctgtgctt tcggtgtgctc 438
ccagggccct gccagtcctc aggtggaagg tatccctggg ccctggcact gattatagga 498
cactgggcaa gacactgcac cgccacgtga ctcagtttcc ccctctgcct gatgggtgtt 558
gctgtgagaa ttatgaaatg aaatgatgac catgaaaata ttgtagaagc caagaaatgc 618
ttcagaagtt ataaagctct ccccaaaccg tgttatgaaa aaaaaaaaaa aa 670
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<210> 196

<211> 510

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> 133..327

<400> 196

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ctccaataacc caaaccaggg gtagttgcct aatccatcct catgtggata gctctttact 120
taggaaacct tg atg gct tat ttg gat gac aaa ggt tcc ctt ttg gcg ata 171
                               Met Ala Tyr Leu Asp Asp Lys Gly Ser Leu Leu Ala Ile
                               1           5           10
cat agc cat gcg aga caa cat agc cat gaa aca aac caa gtc cac cag 219
His Ser His Ala Arg Gln His Ser His Glu Thr Asn Gln Val His Gln
      15           20           25
tgg ctt cct agg aac aca ttt gct ttc ctg ata aaa gag gac aga tgc 267
Trp Leu Pro Arg Asn Thr Phe Ala Phe Leu Ile Lys Glu Asp Arg Cys
      30           35           40           45
agt tgc aga agt acc tgt gcc tct ttt tct ttt tct tct tct ttt tct 315
Ser Cys Arg Ser Thr Cys Ala Ser Phe Ser Phe Ser Ser Ser Phe Ser
      50           55           60
ttt tta atc tct taaatgcaga tataagaact ggtactgaag cagccatctt 367
Phe Leu Ile Ser
      65
gtgaccataa ggaagaagcc aagaacatca gaaccagtgg cctagccatt gcacagtcac 427
ctaaacacac ctctggactt gttattatgt aaaaaaaaaa aaacacctgc tcttggtatt 487
tgcaatccaa aaaaaaaaaa aaa 510
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<210> 197

<211> 500

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> 22..357

<400> 197

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                        1      5      10
aaa aaa aca aat aca tac gaa gaa agt aat gca gga aat gaa gga caa      99
Lys Lys Thr Asn Thr Tyr Glu Glu Ser Asn Ala Gly Asn Glu Gly Gln
                        15      20      25
aaa gaa gct ata agc att tgt att tgc aga aga gat ggt tta ctt cct      147
Lys Glu Ala Ile Ser Ile Cys Ile Cys Arg Arg Asp Gly Leu Leu Pro
                        30      35      40
ctg tgg gta acc agg tta tca gat ttg gtg ttt tcc aaa gaa aag gca      195
Leu Trp Val Thr Arg Leu Ser Asp Leu Val Phe Ser Lys Glu Lys Ala
                        45      50      55
cat ggc atg att cca ctt ctt ggc tcc cat agg gaa aag aag aca agt      243
His Gly Met Ile Pro Leu Leu Gly Ser His Arg Glu Lys Lys Thr Ser
                        60      65      70
aaa gag atg aag act tct tcc agg aac ctg agg tac ttc att gtc tgc      291
Lys Glu Met Lys Thr Ser Ser Arg Asn Leu Arg Tyr Phe Ile Val Cys
                        75      80      85      90
aga gat gcc tca tcc tac acc cct cag tca ctc ata tct gga tac att      339
Arg Asp Ala Ser Ser Tyr Thr Pro Gln Ser Leu Ile Ser Gly Tyr Ile
                        95      100      105
gga cct tgt caa cat caa taatggacat acctctgata tttgaactct      387
Gly Pro Cys Gln His Gln
                        110
gaatctcact ctgtgaccac aactttgtat ctttctaagt ctttaatctt caacctcaca      447
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<211> 667

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> 4..333

<400> 198

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      Met Val Phe Gly Ala Met Val Leu Leu Val Gly Leu Glu Glu Leu
      1      5      10      15
acc aat atc cgc aac gtg gag aga ctg aag aag gac ttg agg gcc agt      96
Thr Asn Ile Arg Asn Val Glu Arg Leu Lys Lys Asp Leu Arg Ala Ser
      20      25      30
tat tgc ctc atc gac agc ttc ctg ggg gac tcg gag ctc atc ggg gac      144
Tyr Cys Leu Ile Asp Ser Phe Leu Gly Asp Ser Glu Leu Ile Gly Asp
      35      40      45
ctg acc cag tgt gtg gac tgc gtg att cct cca gag ggg tcc ctc ttg      192
Leu Thr Gln Cys Val Asp Cys Val Ile Pro Pro Glu Gly Ser Leu Leu
      50      55      60
cag atc tct agc tac ctc tac tta aat act gct ctt gtg gac ttg cct      240
Gln Ile Ser Ser Tyr Leu Tyr Leu Asn Thr Ala Leu Val Asp Leu Pro
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65	70	75	
ggt gtg gcg gcc tcc cag gca tgt gac tct cag cag gtg act tgg ctt			288
Gly Val Ala Ala Ser Gln Ala Cys Asp Ser Gln Gln Val Thr Trp Leu			
80	85	90	95
ctc tac gtt gct aat ggt gcc tac tcg gca tgt aac agg cct gga			333
Leu Tyr Val Ala Asn Gly Ala Tyr Ser Ala Cys Asn Arg Pro Gly			
100	105	110	
tgaacggtag ctgctgcggt tacattatta gcttcagttt gcccgccag gctagatgtt			393
taatcagatt tcacagactt cacagtgtga gttggggatg tgacttcgta tgaaagtga			453
ggaactcagg ctgagagagg gtgagacgta ggagcatggc cactgcgcga gctcggggct			513
ggctgtgggt ttctcccat tccctgccc tctgggaagt cgctgccacc ccctacgctt			573
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ataaaaaaac aaaaggccga aaaaaaaaaa aaaa			667

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 <211> 514
 <212> DNA
 <213> Homo sapiens

<220>
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 <222> 1..363

<400> 199	
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Thr Ser Ser Ser Gly Ala Glu Val Thr Met Ala Ala Ala Leu Ala Arg	
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ctt ggt ctg cgg cct gtc aaa cag gtt cgg gtt cag ttc tgt ccc ttc	96
Leu Gly Leu Arg Pro Val Lys Gln Val Arg Val Gln Phe Cys Pro Phe	
20 25 30	
gag aaa aac gtg gaa tcg acg agg acc ttc ctg cag acg gtg agc agt	144
Glu Lys Asn Val Glu Ser Thr Arg Thr Phe Leu Gln Thr Val Ser Ser	
35 40 45	
gag aag gtc cgc tcc act aat ctc aac tgc tca gtg att gcg gac gtg	192
Glu Lys Val Arg Ser Thr Asn Leu Asn Cys Ser Val Ile Ala Asp Val	
50 55 60	
agg cat gac ggc tcc gag ccc tgc gtg gac gtg ctg ttc gga gac ggg	240
Arg His Asp Gly Ser Glu Pro Cys Val Asp Val Leu Phe Gly Asp Gly	
65 70 75 80	
cat cgc ctg att atg cgc ggc gct cat ctc acc gct ctg gaa atg ctc	288
His Arg Leu Ile Met Arg Gly Ala His Leu Thr Ala Leu Glu Met Leu	
85 90 95	
acc gcc ttc gcc tcc cac atc cgg gcc agg gac gcg gcg ggc agc ggg	336
Thr Ala Phe Ala Ser His Ile Arg Ala Arg Asp Ala Ala Gly Ser Gly	
100 105 110	
gac aag ccg ggc gct gat act ggt cgc tgacagcgcc aaagagacca	383
Asp Lys Pro Gly Ala Asp Thr Gly Arg	
115 120	
acaagatgat ttgcgtggac taggacactt aacctaagaa gagtttcaact taatcattca	443
aatcactatc tgaagggtca cggagcgcaa aataaagttt aaaaccctgc taccaaaaaa	503
aaaaaaaaa a	514

<210> 200
 <211> 462
 <212> DNA
 <213> Homo sapiens

<220>

<221> CDS
<222> 41..337

<400> 200
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Met Leu Ala Arg Ala
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act ttc cgc gcc gcc tcg gcc cca act ctc gtc gcc cgc cgc ggc ttc 103
Thr Phe Arg Ala Ala Ser Ala Pro Thr Leu Val Ala Arg Arg Gly Phe
10 15 20
cag tcg acc cgc gcg caa atg gcc agc cca tac cac tac ccc gag ggt 151
Gln Ser Thr Arg Ala Gln Met Ala Ser Pro Tyr His Tyr Pro Glu Gly
25 30 35
cct cgc agc aac ttg cca ttc gac ccg ctg aag aag ggc ttt gct ttc 199
Pro Arg Ser Asn Leu Pro Phe Asp Pro Leu Lys Lys Gly Phe Ala Phe
40 45 50
aag tac tgg ggc ttt atg ggc acc gga ttc gcc ctt ccc ttc ctc ctt 247
Lys Tyr Trp Gly Phe Met Gly Thr Gly Phe Ala Leu Pro Phe Leu Leu
55 60 65
gct gtc tgg caa aca gaa caa gcc gta aat gcg ctg aga cac ggc gtg 295
Ala Val Trp Gln Thr Glu Gln Ala Val Asn Ala Leu Arg His Gly Val
70 75 80 85
gac atg cgt atc ggg atc ccg ggg aac acg gca ttt gta gat 337
Asp Met Arg Ile Gly Ile Pro Gly Asn Thr Ala Phe Val Asp
90 95
taggtggagg gcccgcatac ggctatacta gacatcacag catcaatttc attgtctgtc 397
ccccaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa
457
aaaaaa 462

<210> 201
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<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> 1..549

<400> 201
aga gag gga gcc cga gcc agg cca tct cca acc atg tcc gac gag gcc 48
Arg Glu Gly Ala Arg Ala Arg Pro Ser Pro Thr Met Ser Asp Glu Ala
1 5 10 15
tcg gcc atc act tcc tac gag aag ttt cta acc ccc gag gag ccc ttc 96
Ser Ala Ile Thr Ser Tyr Glu Lys Phe Leu Thr Pro Glu Glu Pro Phe
20 25 30
cca ctc ctg gga cct cct cgc ggg gtg ggc acc tgc ccg agc gag gag 144
Pro Leu Leu Gly Pro Pro Arg Gly Val Gly Thr Cys Pro Ser Glu Glu
35 40 45
ccg ggc tgc ctg gac atc agc gac ttc ggc tgc cag ctg tcc tcc tgc 192
Pro Gly Cys Leu Asp Ile Ser Asp Phe Gly Cys Gln Leu Ser Ser Cys
50 55 60
cat cgc acc gac ccg ctc cac cgc ttc cac acc aac agg tgg aac cta 240
His Arg Thr Asp Pro Leu His Arg Phe His Thr Asn Arg Trp Asn Leu
65 70 75 80
act tct tgt gga aca agt gtt gcc agc tca gaa ggc agt gag gag ctg 288
Thr Ser Cys Gly Thr Ser Val Ala Ser Ser Glu Gly Ser Glu Glu Leu
85 90 95
ttt tca tct gtg tct gtt gga gat caa gat gat tgc tat tcc ctg tta 336

<210> 203
 <211> 408
 <212> DNA
 <213> Homo sapiens

<220>
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 <222> 1..315

<400> 203
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 Ile Gly Pro Arg Ala Pro Ser Pro Ser Phe Ser Val Arg Asp Val Glu
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 ctg agc gac cca gcc cgc gag cga ggt gag atg ccg gtg gcc gtg ggt 96
 Leu Ser Asp Pro Ala Arg Glu Arg Gly Glu Met Pro Val Ala Val Gly
 20 25 30
 ccc tac gga cag tcc cag cca agc tgc ttc gac cgt gtc aaa atg ggc 144
 Pro Tyr Gly Gln Ser Gln Pro Ser Cys Phe Asp Arg Val Lys Met Gly
 35 40 45
 ttc gtg atg ggt tgc gcc gtg ggc atg gcg gcc ggg gcg ctc ttc ggc 192
 Phe Val Met Gly Cys Ala Val Gly Met Ala Ala Gly Ala Leu Phe Gly
 50 55 60
 acc ttt tcc tgt ctc agg atc gga atg cgg ggt cga gag ctg atg ggc 240
 Thr Phe Ser Cys Leu Arg Ile Gly Met Arg Gly Arg Glu Leu Met Gly
 65 70 75 80
 ggc att ggg aaa acc atg atg cag agt ggc ggc acc ttt ggc aca ttc 288
 Gly Ile Gly Lys Thr Met Met Gln Ser Gly Gly Thr Phe Gly Thr Phe
 85 90 95
 atg gcc att ggg atg ggc atc cga tgc taaccatggt tgccaactac 335
 Met Ala Ile Gly Met Gly Ile Arg Cys
 100 105
 atctgtccct tcccatcaat ccagagccat gtactaataa aagaaagtct ttgagcaaaa 395
 aaaaaaaaaa aaa 408

<210> 204
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 <212> DNA
 <213> Homo sapiens

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 <222> 94..582

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 Met Pro Arg Ser Ser Arg Ser
 1 5
 cct ggg gac cca ggc gcc cta ctc gaa gat gtg gcc cac aat ccc aga 162
 Pro Gly Asp Pro Gly Ala Leu Glu Asp Val Ala His Asn Pro Arg
 10 15 20
 ccc cgg agg att gcc cag cga ggc cgg aac acc agc agg atg gca gag 210
 Pro Arg Arg Ile Ala Gln Arg Gly Arg Asn Thr Ser Arg Met Ala Glu
 25 30 35
 gac acc tcc cca aac atg aat gac aac atc ctg ttg cct gtc cgc aac 258
 Asp Thr Ser Pro Asn Met Asn Asp Asn Ile Leu Leu Pro Val Arg Asn
 40 45 50 55

aat gac caa gcc cta ggc ctg act cag tgc atg ctg gga tgt gtg tcc	306
Asn Asp Gln Ala Leu Gly Leu Thr Gln Cys Met Leu Gly Cys Val Ser	
60 65 70	
tgg ttc acc tgt ttt gcc tgc tcc ctg aga act cag gcc cag cag gtt	354
Trp Phe Thr Cys Phe Ala Cys Ser Leu Arg Thr Gln Ala Gln Gln Val	
75 80 85	
ctg ttt aac acg tgc aga tgc aag ctg ctg tgc cag aag ctc atg gag	402
Leu Phe Asn Thr Cys Arg Cys Lys Leu Leu Cys Gln Lys Leu Met Glu	
90 95 100	
aag aca ggc att ctg ctc ctc tgt gct ttc ggt gtg tcc cag ggc cct	450
Lys Thr Gly Ile Leu Leu Leu Cys Ala Phe Gly Val Ser Gln Gly Pro	
105 110 115	
gcc cag tcc cag gtg gag gta tcc ctg ggc cct ggc act gat tat agg	498
Ala Gln Ser Gln Val Glu Val Ser Leu Gly Pro Gly Thr Asp Tyr Arg	
120 125 130 135	
aca ctg ggc aag aca ctg cac tgc cac gtg act cag ttt ccc cat ctg	546
Thr Leu Gly Lys Thr Leu His Cys His Val Thr Gln Phe Pro His Leu	
140 145 150	
cct gat ggg tgt tgc tgt gag aat tat gaa atg aaa tgatgacat	592
Pro Asp Gly Cys Cys Cys Glu Asn Tyr Glu Met Lys	
155 160	
gaaaatattg tagaagccaa gaaatgcttc agaagttata aagctctccc caaacgcgaa	652
aaaaaaaaaaa aaa	665

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<211> 1008

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> 540..923

<400> 205

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ccaaggcagc atttcagaag gtgatccacg gcaaagccgt cccttcaaata ccgtctttgt	180
gcccaactgcc atagtcaacc ccgtgagaag cacagccggc cctgggactt taggacaagg	240
gtctcttcgg aaagggcgga gcagcatgag aaagagtaag tgggtggcaga gagatggatc	300
cctgcagaga cccctccagt ccgggatccc cactctcgtg gtaggctccc tcagacgcag	360
cccaccatg gtccttcggc ctacagcagtt ccaattctac cagccacagg ggatcacctc	420
ctccccctca gccgtggtgg tggagatggg gtccaagcct gccctcacgg gggagccggc	480
cctcacgtgc atcagcaggg gcagtgaggc ggatccactc cgcggccagc tccctcatt	539
atg gaa gac aaa gaa atc ccc atc aag agt gag cct ctg cca aaa ccg	587
Met Glu Asp Lys Lys Ile Pro Ile Lys Ser Glu Pro Leu Pro Lys Pro	
1 5 10 15	
ccc gca tct gcc cca cca tcc atc ctg gtg aaa cca gaa aac tca aga	635
Pro Ala Ser Ala Pro Pro Ser Ile Leu Val Lys Pro Glu Asn Ser Arg	
20 25 30	
aat gga atc gaa aag caa gtc aaa acc gtg aga ttt cag aat tac agc	683
Asn Gly Ile Glu Lys Gln Val Lys Thr Val Arg Phe Gln Asn Tyr Ser	
35 40 45	
cct cct ccc acc aaa cat tac acc tcc cat ccc acc tcc gga aag cct	731
Pro Pro Pro Thr Lys His Tyr Thr Ser His Pro Thr Ser Gly Lys Pro	
50 55 60	
gaa cag cca gcc acc ctc aag gcg tcc cag cct gaa gca gcg tcc ttg	779
Glu Gln Pro Ala Thr Leu Lys Ala Ser Gln Pro Glu Ala Ala Ser Leu	
65 70 75 80	

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ggc cca gag atg acc gtc cta ttt gcc cac cga agt ggc tgc cac tcc      827
Gly Pro Glu Met Thr Val Leu Phe Ala His Arg Ser Gly Cys His Ser
      85      90      95
gga cag cag aca gac ctc cgg aga aag tca gct ctt gcc aag gcc aca      875
Gly Gln Gln Thr Asp Leu Arg Arg Lys Ser Ala Leu Ala Lys Ala Thr
      100      105      110
acc ctg gtg tcc act gcc tca ggc acg cag acc gtg ttt ccc agc aaa      923
Thr Leu Val Ser Thr Ala Ser Gly Thr Gln Thr Val Phe Pro Ser Lys
      115      120      125
tgaacctacg ggtggctttt cctagacccc aaagaggtga attgcattta aatacagtct      983
gcctyactg aaaaaaaaaa aaaaaa      1008

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 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> 77..364

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      Met Leu Thr Arg Val Glu Glu Gln Lys Lys Met Val
      1      5      10
aag gcc tgc agg tat agg tgt tca gca tgt cat ctg aaa tat tcc cca      160
Lys Ala Cys Arg Tyr Arg Cys Ser Ala Cys His Leu Lys Tyr Ser Pro
      15      20      25
cag agg caa aaa gaa agg aaa tta tct ctg aaa agg ggg agg aca agt      208
Gln Arg Gln Lys Glu Arg Lys Leu Ser Leu Lys Arg Gly Arg Thr Ser
      30      35      40
cag cag aat atg tca atg ttt tgg ttg aag aag ctg ctt gaa tct ggg      256
Gln Gln Asn Met Ser Met Phe Trp Leu Lys Lys Leu Leu Glu Ser Gly
      45      50      55      60
ctt ttc tgt gcc atg tgt tct ccc agg gcc agc aca aag aag ggc ttt      304
Leu Phe Cys Ala Met Cys Ser Pro Arg Ala Ser Thr Lys Lys Gly Phe
      65      70      75
tgg tgc agg ccc aag acc acc ata atc atc att gat tat tcc tct cca      352
Trp Cys Arg Pro Lys Thr Thr Ile Ile Ile Ile Asp Tyr Ser Ser Pro
      80      85      90
cgc cag tgt ctc taaataaaact ttctcttctt tctctgaaaa aaaaaaaaaa      404
Arg Gln Cys Leu
      95
aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaagaaaa aaaaaaaaaa a      455

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<210> 207
 <211> 749
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> 65..544

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<400> 207
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tacc atg ggg aaa atc gcg ctg caa ctc aaa gcc acg ctg gag aac atc      109

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	Met	Gly	Lys	Ile	Ala	Leu	Gln	Leu	Lys	Ala	Thr	Leu	Glu	Asn	Ile	
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acc aac ctc cgg ccc gtg ggc gag gac ttc cgg tgg tac ctg aag atg																157
Thr Asn Leu Arg Pro Val Gly Glu Asp Phe Arg Trp Tyr Leu Lys Met																
					20					25					30	
aaa tgt ggc aac tgt ggt gag att tcg gac aag tgg cag tac atc cgg																205
Lys Cys Gly Asn Cys Gly Glu Ile Ser Asp Lys Trp Gln Tyr Ile Arg																
				35					40					45		
ctg atg gac agt gtg gca ctg aag ggg ggc cgt ggc agt gct tcc atg																253
Leu Met Asp Ser Val Ala Leu Lys Gly Gly Arg Gly Ser Ala Ser Met																
				50				55					60			
gtc cag aag tgc aag ctg tgt gca aga gaa aat tcc atc gag att tta																301
Val Gln Lys Cys Lys Leu Cys Ala Arg Glu Asn Ser Ile Glu Ile Leu																
				65				70					75			
agc agc acc atc aag cct tac aat gct gaa gac aat gag aac ttc aag																349
Ser Ser Thr Ile Lys Pro Tyr Asn Ala Glu Asp Asn Glu Asn Phe Lys																
				80				85					90		95	
aca ata gtg gag ttt gag tgc cgg ggc ctt gaa cca gtt gat ttc cag																397
Thr ile Val Glu Phe Glu Cys Arg Gly Leu Glu Pro Val Asp Phe Gln																
				100						105					110	
ccg cas gwg rtw ttg ctg ctg aag gtg tgg agt cag gga cag cct tca																445
Pro Xaa Xaa Xaa Leu Leu Leu Lys Val Trp Ser Gln Gly Gln Pro Ser																
				115						120					125	
gtg aca tta atc tgc agg aga agg act ggg act gac tat gat gaa aag																493
Val Thr Leu Ile Cys Arg Arg Arg Thr Gly Thr Asp Tyr Asp Glu Lys																
				130				135					140			
gcc cag gag tct gtg gga atc tat gag gtc acc cac cag ttt gtg aag																541
Ala Gln Glu Ser Val Gly Ile Tyr Glu Val Thr His Gln Phe Val Lys																
				145				150					155			
tgc tgatccctct tccttcccag ttgcccttaa gaactgagaa aggacaaagt																594
Cys																
				160												
actctaagca gcagagccca cagaggctcg ttcctttgac ccttgtctcc tgggtggctat																654
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agccctgtt cacgctacaa aaaaaaaaaa aaaaa																749

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 <213> Homo sapiens

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 <222> 117..467

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	Met
	1
gac tcc ctg gct gct gga gag ttg aat gcc agc cac cag cca tgg gtg	167
Asp Ser Leu Ala Ala Gly Glu Leu Asn Ala Ser His Gln Pro Trp Val	
	5
	10
cca gag ttt gta gcc tat tgg agg aaa aca cac caa gat cac ctc tgc	215
Pro Glu Phe Val Ala Tyr Trp Arg Lys Thr His Gln Asp His Leu Cys	
	20
	25
	30
agc ctg cac agc cgg gcc ttt gga ctc ctg gat gct aga gtg acc tgg	263
Ser Leu His Ser Arg Ala Phe Gly Leu Leu Asp Ala Arg Val Thr Trp	

35	40	45	
gcg ctg agg agg gcc ccc gag cca gta cca gga aag gat aga ctc ctg			311
Ala Leu Arg Arg Ala Pro Glu Pro Val Pro Gly Lys Asp Arg Leu Leu			
50	55	60	65
ctt gca gca ttc cca gca gag gca tcg cct gtg gac acc gcg tct gtg			359
Leu Ala Ala Phe Pro Ala Glu Ala Ser Pro Val Asp Thr Ala Ser Val			
70	75	80	
tct gta tat ggc aga gct ccc aga tat atg cac aag gga gtg aaa aaa			407
Ser Val Tyr Gly Arg Ala Pro Arg Tyr Met His Lys Gly Val Lys Lys			
85	90	95	
tgt gtt tgc acc cca gtc tct aaa aat tca aca gcc tgg tta ctt ctg			455
Cys Val Cys Thr Pro Val Ser Lys Asn Ser Thr Ala Trp Leu Leu Leu			
100	105	110	
ggg ggt ata tcg taggtggcct taatacgtgt tatttgctca tctgtatttc			507
Gly Gly Ile Ser			
115			
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 <222> 893..1897

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gcccttgagt ggcgggggtgg acagcgcagc caccgcctgc ctcactact cc atg tgc	898		
	Met Cys		
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tgc cag gtc tgc gag gcc gtg agg agt gga aat gag gaa gtg ctg gct	946		
Cys Gln Val Cys Glu Ala Val Arg Ser Gly Asn Glu Glu Val Leu Ala			
5	10	15	
gat gtc cgc acc atc gtg aac cag atc agc tac acc ccc cag gat ccc	994		
Asp Val Arg Thr Ile Val Asn Gln Ile Ser Tyr Thr Pro Gln Asp Pro			
20	25	30	
cga gac ctc tgt gga cgc ata ctg acc acc tgc tac atg gcc agc aag	1042		
Arg Asp Leu Cys Gly Arg Ile Leu Thr Thr Cys Tyr Met Ala Ser Lys			
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aac tcc tcc cag gag acg tgc acc cgg gcc aga gag ttg gcc cag cag	1090		
Asn Ser Ser Gln Glu Thr Cys Thr Arg Ala Arg Glu Leu Ala Gln Gln			
55	60	65	

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Ile Gly Ser His His Ile Ser Leu Asn Ile Asp Pro Ala Val Lys Ala	
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Val Met Gly Ile Phe Ser Leu Val Thr Gly Lys Ser Pro Leu Phe Ala	
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Ala His Gly Gly Ser Ser Arg Glu Asn Leu Ala Leu Gln Asn Val Gln	
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gct cga ata cgg atg gtc ctc gcc tat ctg ttt gct cag ttg agc ctc	1282
Ala Arg Ile Arg Met Val Leu Ala Tyr Leu Phe Ala Gln Leu Ser Leu	
115 120 125 130	
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Trp Ser Arg Gly Val His Gly Gly Leu Leu Val Leu Gly Ser Ala Asn	
135 140 145	
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Val Asp Glu Ser Leu Leu Gly Tyr Leu Thr Lys Tyr Asp Cys Ser Ser	
150 155 160	
gcg gac atc aac ccc ata ggc ggg atc agc aag acg gac ctc agg gcc	1426
Ala Asp Ile Asn Pro Ile Gly Gly Ile Ser Lys Thr Asp Leu Arg Ala	
165 170 175	
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Phe Val Gln Phe Cys Ile Gln Arg Phe Gln Leu Pro Ala Leu Gln Ser	
180 185 190	
atc ctg ttg gcg ccg gcc acc gca gag ctg gag ccc ttg gct gat gga	1522
Ile Leu Leu Ala Pro Ala Thr Ala Glu Leu Glu Pro Leu Ala Asp Gly	
195 200 205 210	
cag gtg tcc cag acc gac gag gaa gat atg ggg atg aca tat gcg gag	1570
Gln Val Ser Gln Thr Asp Glu Glu Asp Met Gly Met Thr Tyr Ala Glu	
215 220 225	
ctc tgc gtc tat ggg aaa ctc agg aag gtg gcc aag atg ggg ccc tac	1618
Leu Ser Val Tyr Gly Lys Leu Arg Lys Val Ala Lys Met Gly Pro Tyr	
230 235 240	
agc atg ttc tgc aaa ctc ctc ggc atg tgg aga cac atc tgc acc ccg	1666
Ser Met Phe Cys Lys Leu Leu Gly Met Trp Arg His Ile Cys Thr Pro	
245 250 255	
aga cag gtc gct gac aaa gtg aag cgg ttt ttc tcc aag tac tcc atg	1714
Arg Gln Val Ala Asp Lys Val Lys Arg Phe Phe Ser Lys Tyr Ser Met	
260 265 270	
aac aga cac aag atg acc acg ctc aca ccc gcg tac cac gcc gag aac	1762
Asn Arg His Lys Met Thr Thr Leu Thr Pro Ala Tyr His Ala Glu Asn	
275 280 285 290	
tac agc cct gag gac aac agg ttt gat ctg cga cca ttt ctg tac aac	1810
Tyr Ser Pro Glu Asp Asn Arg Phe Asp Leu Arg Pro Phe Leu Tyr Asn	
295 300 305	
aca agc tgg cct tgg cag ttt cgg tgc ata gaa aat cag gtg cta cag	1858
Thr Ser Trp Pro Trp Gln Phe Arg Cys Ile Glu Asn Gln Val Leu Gln	
310 315 320	
ctc gag agg gca gag cca cag tcc ctg gac ggc gtg gac tgaggccggt	1907
Leu Glu Arg Ala Glu Pro Gln Ser Leu Asp Gly Val Asp	
325 330 335	
tccttctctgg aggcctctctg tcctcgggga cccagcacc tcatcatcag cattgctgga	1967
gccaagggtta ggagccctac actaggagcc caggatggga cggcgcatca gccgagaggg	2027
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aaaaaaaaa a	2098

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<211> 428

<212> DNA
<213> Homo sapiens

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<222> 85..342

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ctacaattta cagttcctct atcc atg tgc tgg gtt ata aat cat gcc atc 111
Met Cys Trp Val Ile Asn His Ala Ile
1 5
ctc cct aga atg aga atg cac agc aag cgg cag aca atc acc cgg cat 159
Leu Pro Arg Met Arg Met His Ser Lys Arg Gln Thr Ile Thr Arg His
10 15 20 25
tcg gca tct ctt tct ttt cac gcg ctc cct cgc tcc gcc ttt ctc cag 207
Ser Ala Ser Leu Ser Phe His Ala Leu Pro Arg Ser Ala Phe Leu Gln
30 35 40
ctc tgc ctt ctc agg cag ata cat cag ata cct tgt tta tcc atc ttc 255
Leu Cys Leu Leu Arg Gln Ile His Gln Ile Pro Cys Leu Ser Ile Phe
45 50 55
agc tcc act ctg agg gcg cag acg cac gat tcc ggg atc ggg tgc acc 303
Ser Ser Thr Leu Arg Ala Gln Thr His Asp Ser Gly Ile Gly Cys Thr
60 65 70
acg gcg aas cca ggc ggg aga cgg cag gag cag ctc agg taaccagggg 352
Thr Ala Xaa Pro Gly Gly Arg Arg Gln Glu Gln Leu Arg
75 80 85
aagcttgctg gcccacggag atgcagccgt ggagctgtga ggaaagacgg tctggcttca 412
aaaaaaaaa aaaaaa 428

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atattgctgc taacctcaca cagctgagcc ttcc atg aaa att gct ctc tgc caa 175
Met Lys Ile Ala Leu Cys Gln
1 5
aga gaa ctt cct agt cca agg tca tgt cta ctc tcc aga gat gtg act 223
Arg Glu Leu Pro Ser Pro Arg Ser Cys Leu Leu Ser Arg Asp Val Thr
10 15 20
gga gtg att tgc acc cgg atg cct aga ctc gcc atc tgc tca aag act 271
Gly Val Ile Cys Thr Arg Met Pro Arg Leu Ala Ile Cys Ser Lys Thr
25 30 35
gct cag aaa gcc ctc cca tgc att ccc ctg ctg cat acc agc cca ctc 319
Ala Gln Lys Ala Leu Pro Cys Ile Pro Leu Leu His Thr Ser Pro Leu
40 45 50 55
tgc ctg cag ctg ctg tct gca gga ctt cat atc tat gcc aca ctg tgt 367
Cys Leu Gln Leu Leu Ser Ala Gly Leu His Ile Tyr Ala Thr Leu Cys
60 65 70
aaa agc tgt gct tca aga aat cac aaa aac att ttc ctg cac cta cta 415

Lys Ser Cys Ala Ser Arg Asn His Lys Asn Ile Phe Leu His Leu Leu
75 80 85
cac agc ctg agt gcg gca taagttgacc ttgcttgcta agaaatgggg 463
His Ser Leu Ser Ala Ala
90
caagaaatgc ttttttgtat gtgtcatgtc tgtttgtttt tcaattaaga gaggaaagca 523
ttaggcagat ggaatgtaca tgtgaggatg aggagacaga aaacaagtag ccctttccat 583
caagatagag ggttttctgg ggttgctggc tattgaatgt cactcctgat ttctctttcc 643
aaggcactgt accaccagcc tactgagatt gtgtgggagc tttcatgggg gttgtatttc 703
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aaaaaa 769

<210> 212
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<212> DNA
<213> Homo sapiens

<220>
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<222> 63..386

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tc atg gcg gtc cga gct tcg ttc gag aac aac tgt gag atc ggc tgc 107
Met Ala Val Arg Ala Ser Phe Glu Asn Asn Cys Glu Ile Gly Cys
1 5 10 15
ttt gcc aag ctc acc aac acc tac tgt ctg gta gcg atc gga ggc tca 155
Phe Ala Lys Leu Thr Asn Thr Tyr Cys Leu Val Ala Ile Gly Gly Ser
20 25 30
gag aac ttc tac agt gtg ttc gag ggc gag ctc tcc gat acc atc ccc 203
Glu Asn Phe Tyr Ser Val Phe Glu Gly Glu Leu Ser Asp Thr Ile Pro
35 40 45
gtg gtg cac gcg tct atc gcc ggc tgc cgc atc atc ggg cgc atg tgt 251
Val Val His Ala Ser Ile Ala Gly Cys Arg Ile Ile Gly Arg Met Cys
50 55 60
gtg gga gac aga aga aat tct ggc aga tgt gct caa ggt gga agt ctt 299
Val Gly Asp Arg Arg Asn Ser Gly Arg Cys Ala Gln Gly Gly Ser Leu
65 70 75
cag aca gac agt ggc cga cca ggt gct agt agg aag cta ctg tgt ctt 347
Gln Thr Asp Ser Gly Arg Pro Gly Ala Ser Arg Lys Leu Leu Cys Leu
80 85 90 95
cag caa tca ggg agg gct ggt gca tcc caa gac ttc aat tgaagaccag 396
Gln Gln Ser Gly Arg Ala Gly Ala Ser Gln Asp Phe Asn
100 105
gatgagctgt cctctcttct tcaagtcccc cttgtggcgg ggactgtgaa ccgaggcagt 456
gaggtgattg ctgctgggat ggtggtgaat gactggtgtg ccttctgtgg cctggacaca 516
accagcacag agctgtcagt ggtggagagt gtcttcaagc tgaatgaagc ccagcctagc 576
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gttgttccat gggctcctgg ctctggactg tggccaacct tctccacatt ccgccaatc 696
tgtacctgat gctggcaggg aggtggcaga gagctcactg ggactgaggg gctgggcacc 756
caaccctttt ccacctgtgc ttatcgcttg gatctatcat tactgcaaaa acctgctctg 816
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cattaaagtg cagttccctc caaaaaaaaa aaaaaaaaaa 914

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ggcttggatt	tggatattct	caacagaaag	ggttaaaggc	tgatgggtacc	taaagcctgg	180
tacttgaatt	ttgatcaaga	taagctgcct	taagttctct	tcattacaca	aatgatccta	240
gataattgat	agatcctgtg	gttcaactgg	atttctagat	agaagctgga	ttcatgtgat	300
gccagaggag	taaaatttca	agagactgaa	accagatctg	agtttcgctg	ttccagctctg	360
gacctctttg	gtgctgtaaa	tcttgatat	actgtagatg	agtactgcgt	ttttctttta	420
tggactctct	tcagcttctg	gagacctcac	tatcttatt	atg tct ttg tgt gaa		474
				Met Ser Leu Cys Glu		
				1	5	
gac atg ctg ctt tgt aat tat cga aag tgt cgc atc aaa ctc tct ggc						522
Asp Met Leu Leu Cys Asn Tyr Arg Lys Cys Arg Ile Lys Leu Ser Gly						
	10		15		20	
tat gca tgg gtc act gcc tgc tct cac atc ttc tgt gat cag cat ggc						570
Tyr Ala Trp Val Thr Ala Cys Ser His Ile Phe Cys Asp Gln His Gly						
	25		30		35	
agt ggt gag ttt agt cgc tca cca gct atc tgt cct gcc tgc aac agt						618
Ser Gly Glu Phe Ser Arg Ser Pro Ala Ile Cys Pro Ala Cys Asn Ser						
	40		45		50	
acc ctt tct gga aag cta gat att gtc cgc aca gaa ctc agt cca tca						666
Thr Leu Ser Gly Lys Leu Asp Ile Val Arg Thr Glu Leu Ser Pro Ser						
	55		60		65	
gag gaa tat aaa gct atg gta ttg gca gga ctg cga cca gag atc gtg						714
Glu Glu Tyr Lys Ala Met Val Leu Ala Gly Leu Arg Pro Glu Ile Val						
	70		75		80	85
ttg gac att agc tcc cga gcg ctg gcc ttc tgg aca tat cag gta cat						762
Leu Asp Ile Ser Ser Arg Ala Leu Ala Phe Trp Thr Tyr Gln Val His						
	90		95		100	
cag gaa cgt ctc tat caa gaa tac aat ttc agc aag gct gag ggc cat						810
Gln Glu Arg Leu Tyr Gln Glu Tyr Asn Phe Ser Lys Ala Glu Gly His						
	105		110		115	
ctg aaa cag atg gag aag ata tat act cag caa ata caa agc aag gat						858
Leu Lys Gln Met Glu Lys Ile Tyr Thr Gln Gln Ile Gln Ser Lys Asp						
	120		125		130	
gta gaa ttg acc tct atg aaa ggg gag gtt acc tcc atg aag aaa gta						906
Val Glu Leu Thr Ser Met Lys Gly Glu Val Thr Ser Met Lys Lys Val						
	135		140		145	
cta gaa gaa tac aag aaa aag ttc agt gac atc tct gag aaa ctt atg						954
Leu Glu Glu Tyr Lys Lys Lys Phe Ser Asp Ile Ser Glu Lys Leu Met						
	150		155		160	165
gag cgc aat cgt cag tat caa aag ctc caa ggc ctc tat gat agc ctt						1002
Glu Arg Asn Arg Gln Tyr Gln Lys Leu Gln Gly Leu Tyr Asp Ser Leu						
	170		175		180	
agg cta cga aac atc act att gct aac cat gaa ggc acc ctt gaa cca						1050
Arg Leu Arg Asn Ile Thr Ile Ala Asn His Glu Gly Thr Leu Glu Pro						
	185		190		195	
tcc atg att gca cag tct ggt gtt ctt ggc ttc cca tta ggt aac aac						1098
Ser Met Ile Ala Gln Ser Gly Val Leu Gly Phe Pro Leu Gly Asn Asn						
	200		205		210	
tcc aag ttt cct ttg gat aat aca cct gtt cga aat cgg ggc gat gga						1146
Ser Lys Phe Pro Leu Asp Asn Thr Pro Val Arg Asn Arg Gly Asp Gly						
	215		220		225	

gat gga gat ttt cag ttc aga cca ttt ttt gcg ggt tct ccc aca gca	1194
Asp Gly Asp Phe Gln Phe Arg Pro Phe Phe Ala Gly Ser Pro Thr Ala	
230 235 240 245	
cct gaa ccc agc aac agc ttt ttt agt ttt gtc tct cca agt cgt gaa	1242
Pro Glu Pro Ser Asn Ser Phe Phe Ser Phe Val Ser Pro Ser Arg Glu	
250 255 260	
tta gag cag cag caa gtt tct agc agg gcc ttc aaa gta aaa aga att	1290
Leu Glu Gln Gln Gln Val Ser Ser Arg Ala Phe Lys Val Lys Arg Ile	
265 270 275	
tgagccacgc atagtgtcac gcacctgtga tcccagctac ttaggagggtt gaggctggga	1350
ggatcacttg agcccaggag tctgaggctt tagtgatcta agatcatgcc actgcactcc	1410
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tcaaaaaaaaaa aaaaaaaaaa	1489

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<211> 776

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> 21..539

<400> 214

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1 5 10	
ggt tac cta acc ttc tat gga gaa gtt gaa gat gaa tta ctt cat gcc	101
Gly Tyr Leu Thr Phe Tyr Gly Glu Val Glu Asp Glu Leu Leu His Ala	
15 20 25	
tac agc aaa gtg tat aca tta gac atc cct ctt ctc atg gtt cgc ctg	149
Tyr Ser Lys Val Tyr Thr Leu Asp Ile Pro Leu Leu Met Val Arg Leu	
30 35 40	
gca gtc ctt gtg gca gta aca cta act gtg ccc att gtc ctc ttc cca	197
Ala Val Leu Val Ala Val Thr Leu Thr Val Pro Ile Val Leu Phe Pro	
45 50 55	
att cgt aca tca gtg atc aca ctg tta ttt ccc aaa cga ccc ttc agc	245
Ile Arg Thr Ser Val Ile Thr Leu Leu Phe Pro Lys Arg Pro Phe Ser	
60 65 70 75	
tgg ata cga cat ttc ctg att gca gct gtg ctt att gca ctt aat aat	293
Trp Ile Arg His Phe Leu Ile Ala Ala Val Leu Ile Ala Leu Asn Asn	
80 85 90	
gtt ctg gtc atc ctt gtg cca act ata aaa tac atc ttc gga ttc ata	341
Val Leu Val Ile Leu Val Pro Thr Ile Lys Tyr Ile Phe Gly Phe Ile	
95 100 105	
ggg gct tct tct gcc act atg ctg att ttt att ctt cca gca gtt ttt	389
Gly Ala Ser Ser Ala Thr Met Leu Ile Phe Ile Leu Pro Ala Val Phe	
110 115 120	
tat ctt aaa ctt gtc aag aaa gaa act ttt agg tca ccc caa aag gtc	437
Tyr Leu Lys Leu Val Lys Lys Glu Thr Phe Arg Ser Pro Gln Lys Val	
125 130 135	
ggg gct tta att ttc ctt gtg gtt gga ata ttc ttc atg att gga agc	485
Gly Ala Leu Ile Phe Leu Val Val Gly Ile Phe Phe Met Ile Gly Ser	
140 145 150 155	
atg gca ctc att ata att gac tgg att tat gat cct cca aat tcc aag	533
Met Ala Leu Ile Ile Ile Asp Trp Ile Tyr Asp Pro Pro Asn Ser Lys	
160 165 170	
cat cac taacacaagg aaaaatactt tctttttcta ttggaaatgg ttacaagtta	589

His His
tactccaaaa gatatttgaa ttatcttgat tggaatgtta ttcataggaa ataacaggaa 649
gattccaaag acgtttacca gtmatatcac caggcacctg cagaagagga aaatcactgt 709
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aaaaaaa 776

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<213> Homo sapiens

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<222> 34..1143

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Met Ser Ala Ser Ala Ala Thr
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ggg gtc ttc gtg ctg tcc ctc tcg gcc atc ccg gtc acc tat gtc ttc 102
Gly Val Phe Val Leu Ser Leu Ser Ala Ile Pro Val Thr Tyr Val Phe
10 15 20
aac cac ctg gcg gcc cag cat gat tcc tgg act att gta ggg gtt gct 150
Asn His Leu Ala Ala Gln His Asp Ser Trp Thr Ile Val Gly Val Ala
25 30 35
gcc ctc atc ctg ttc ctg gta gca ctg ctg gct cgt gtc ctc gtc aaa 198
Ala Leu Ile Leu Phe Leu Val Ala Leu Leu Ala Arg Val Leu Val Lys
40 45 50 55
aga aaa cca ccc cgg gac cca ctg ttc tat gtg tat gca gtt ttt gga 246
Arg Lys Pro Pro Arg Asp Pro Leu Phe Tyr Val Tyr Ala Val Phe Gly
60 65 70
ttt acc agc gtg gtg aac ctc atc ata gga ctg gag caa gat gga atc 294
Phe Thr Ser Val Val Asn Leu Ile Ile Gly Leu Glu Gln Asp Gly Ile
75 80 85
att gac ggg ttc atg aca cac tac ttg aga gag ggt gaa ccg tat ctg 342
Ile Asp Gly Phe Met Thr His Tyr Leu Arg Glu Gly Glu Pro Tyr Leu
90 95 100
aac acc gca tat ggg cac atg atc tgc tac tgg gat ggc tct gct cat 390
Asn Thr Ala Tyr Gly His Met Ile Cys Tyr Trp Asp Gly Ser Ala His
105 110 115
tat ctg atg tac ctg gtg atg gtg gca gcc ata gca tgg gag gaa act 438
Tyr Leu Met Tyr Leu Val Met Val Ala Ala Ile Ala Trp Glu Glu Thr
120 125 130 135
tat aga acc att ggc cta tat tgg gtt gga tct att att atg agt gtt 486
Tyr Arg Thr Ile Gly Leu Tyr Trp Val Gly Ser Ile Ile Met Ser Val
140 145 150
gtt gtt ttt gtg cca gga aac att gta ggg aag tat gga aca cga att 534
Val Val Phe Val Pro Gly Asn Ile Val Gly Lys Tyr Gly Thr Arg Ile
155 160 165
tgc cct gct ttt ttc tta agc ata cca tat act tgt ctt cct gtc tgg 582
Cys Pro Ala Phe Phe Leu Ser Ile Pro Tyr Thr Cys Leu Pro Val Trp
170 175 180
gct ggt ttc aga atc tat aat cag cca tca gaa aat tat aat tac ccc 630
Ala Gly Phe Arg Ile Tyr Asn Gln Pro Ser Glu Asn Tyr Asn Tyr Pro
185 190 195
tca aag gtt att caa gaa gcc caa gcg aaa gac ctg ctg aga aga cca 678
Ser Lys Val Ile Gln Glu Ala Gln Ala Lys Asp Leu Leu Arg Arg Pro
200 205 210 215

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ttt gat tta atg ttg gtt gtg tgt ctc ctc ctg gca act gga ttt tgc      726
Phe Asp Leu Met Leu Val Val Cys Leu Leu Leu Ala Thr Gly Phe Cys
                220                225                230

ctg ttc aga ggt ttg att gct ttg gat tgc cca tct gag ctc tgc cga      774
Leu Phe Arg Gly Leu Ile Ala Leu Asp Cys Pro Ser Glu Leu Cys Arg
                235                240                245

tta tat acg caa ttt caa gag ccc tat cta aag gat cct gct gct tat      822
Leu Tyr Thr Gln Phe Gln Glu Pro Tyr Leu Lys Asp Pro Ala Ala Tyr
                250                255                260

cct aaa att cag atg ctg gca tat atg ttc tat tct gtt cct tac ttt      870
Pro Lys Ile Gln Met Leu Ala Tyr Met Phe Tyr Ser Val Pro Tyr Phe
                265                270                275

gtg act gca ctg tat ggc tta gtg gtt cct gga tgt tcc tgg atg cct      918
Val Thr Ala Leu Tyr Gly Leu Val Val Pro Gly Cys Ser Trp Met Pro
                280                285                290                295

gac atc aca ttg ata cat gct gga ggt ctg gct cag gct cag ttt tct      966
Asp Ile Thr Leu Ile His Ala Gly Gly Leu Ala Gln Ala Gln Phe Ser
                300                305                310

cac att ggt gca tct ctt cat gct aga act gct tat gtc tac aga gtc     1014
His Ile Gly Ala Ser Leu His Ala Arg Thr Ala Tyr Val Tyr Arg Val
                315                320                325

cct gaa gaa gca aaa atc ctt ttt tta gca tta aac ata gca tat gga     1062
Pro Glu Glu Ala Lys Ile Leu Phe Leu Ala Leu Asn Ile Ala Tyr Gly
                330                335                340

gtt ctt cct cag ctc ttg gcc tat cgt tgt atc tac aaa cca gag ttc     1110
Val Leu Pro Gln Leu Leu Ala Tyr Arg Cys Ile Tyr Lys Pro Glu Phe
                345                350                355

ttc ata aaa aca aag gca gaa gaa aaa gtg gaa taaaaatatt acttcatggt     1163
Phe Ile Lys Thr Lys Ala Glu Glu Lys Val Glu
                360                365                370

cctccttttct aaattactaa cttttgttat actggtactg atattttgtc ccatttcact     1223
ctcttctcat acgtgagtac ttaagaatat gtacattctt gctctgcact gtatgtgtga     1283
gctatatggt attgtgtaaa ttttttttga aggaaaatgg aaattcttga gaaacagttt     1343
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<211> 1773

<212> DNA

<213> Homo sapiens

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<221> CDS

<222> 6..1184

<400> 216

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gag ccc cgg cca gga ttt cat ggt gtc ttg ggt atc aat tcc atc act      98
Glu Pro Arg Pro Gly Phe His Gly Val Leu Gly Ile Asn Ser Ile Thr
                20                25                30

ggg aag gag gag cct ctg tac ccc agc tac aag aga cag ttg cgc att     146
Gly Lys Glu Glu Pro Leu Tyr Pro Ser Tyr Lys Arg Gln Leu Arg Ile
                35                40                45

tac ctg gtc tcc ctg cca ttc gtg tgc ctc tgc ctc tat ttc tca ctg     194
Tyr Leu Val Ser Leu Pro Phe Val Cys Leu Cys Leu Tyr Phe Ser Leu
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Tyr Val Met Met Ile Tyr Phe Asp Met Glu Val Trp Ala Leu Gly Leu	
65 70 75	
cat gag aac agc ggg tct gag tgg acc agt gtc ctg ttg tat gtg ccc	290
His Glu Asn Ser Gly Ser Glu Trp Thr Ser Val Leu Leu Tyr Val Pro	
80 85 90 95	
agc atc atc tat gcc att gtg att gag atc atg aat cgt ctc tat cga	338
Ser Ile Ile Tyr Ala Ile Val Ile Glu Ile Met Asn Arg Leu Tyr Arg	
100 105 110	
tat gct gcc gag ttt tta act tca tgg gag aat cac aga ttg gaa tct	386
Tyr Ala Ala Glu Phe Leu Thr Ser Trp Glu Asn His Arg Leu Glu Ser	
115 120 125	
gcc tat cag aac cat cta att ctg aaa gtt tta gtg ttc aac ttc ctc	434
Ala Tyr Gln Asn His Leu Ile Leu Lys Val Leu Val Phe Asn Phe Leu	
130 135 140	
aat tgc ttt gcc tca ctc ttc tat att gcc ttt gtc ttg aaa gat atg	482
Asn Cys Phe Ala Ser Leu Phe Tyr Ile Ala Phe Val Leu Lys Asp Met	
145 150 155	
aag ctt ttg cgc cag agc ttg gcc act ctc cta att acc tcc cag atc	530
Lys Leu Leu Arg Gln Ser Leu Ala Thr Leu Leu Ile Thr Ser Gln Ile	
160 165 170 175	
ctc aac caa att atg gaa tct ttt ctt cct tat tgg ctc caa agg aag	578
Leu Asn Gln Ile Met Glu Ser Phe Leu Pro Tyr Trp Leu Gln Arg Lys	
180 185 190	
cat ggt gtg cgg gtg aag agg aag gtg cag gct tta aag gca gac att	626
His Gly Val Arg Val Lys Arg Lys Val Gln Ala Leu Lys Ala Asp Ile	
195 200 205	
gat gct aca tta tat gaa caa gtc atc ctg gaa aaa gaa atg gga act	674
Asp Ala Thr Leu Tyr Glu Gln Val Ile Leu Glu Lys Glu Met Gly Thr	
210 215 220	
tat ttg ggc acc ttt gat gat tac ttg gag tta ttc ctg cag ttt ggt	722
Tyr Leu Gly Thr Phe Asp Asp Tyr Leu Glu Leu Phe Leu Gln Phe Gly	
225 230 235	
tat gtg agc ctt ttc tcc tgt gtt tac cca tta gca gct gcc ttt gct	770
Tyr Val Ser Leu Phe Ser Cys Val Tyr Pro Leu Ala Ala Ala Phe Ala	
240 245 250 255	
gtg tta aat aac ttc act gaa gta aat tca gat gcc tta aaa atg tgc	818
Val Leu Asn Asn Phe Thr Glu Val Asn Ser Asp Ala Leu Lys Met Cys	
260 265 270	
agg gtc ttc aaa cgt cca ttc tca gaa cct tca gcc aat att ggt gtg	866
Arg Val Phe Lys Arg Pro Phe Ser Glu Pro Ser Ala Asn Ile Gly Val	
275 280 285	
tgg cag ttg gct ttt gaa acg atg agt gtt ata tct gtg gtc act aac	914
Trp Gln Leu Ala Phe Glu Thr Met Ser Val Ile Ser Val Val Thr Asn	
290 295 300	
tgt gcg ctg att gga atg tca cca caa gtg aat gca gtc ttt cca gaa	962
Cys Ala Leu Ile Gly Met Ser Pro Gln Val Asn Ala Val Phe Pro Glu	
305 310 315	
tca aaa gca gac ctc att ttg att gta gta gca gtg gag cac gca ctc	1010
Ser Lys Ala Asp Leu Ile Leu Ile Val Val Ala Val Glu His Ala Leu	
320 325 330 335	
ctg gct tta aag ttt ata ctt gca ttt gcc ata cct gat aag cca cgg	1058
Leu Ala Leu Lys Phe Ile Leu Ala Phe Ala Ile Pro Asp Lys Pro Arg	
340 345 350	
cat atc cag atg aaa cta gcc aga ctg gaa ttt gag tct ttg gag gca	1106
His Ile Gln Met Lys Leu Ala Arg Leu Glu Phe Glu Ser Leu Glu Ala	
355 360 365	
ctc aag cag cag caa atg aag ctc gtg acc gag aac ctg aag gag gaa	1154

Leu	Lys	Gln	Gln	Gln	Met	Lys	Leu	Val	Thr	Glu	Asn	Leu	Lys	Glu	Glu	
	370						375					380				
cca	atg	gaa	agc	ggg	aag	gag	aag	gca	acc	tgagt	gcccc	gcgt	gcccc			1204
Pro	Met	Glu	Ser	Gly	Lys	Glu	Lys	Ala	Thr							
	385						390									
ctg	ccct	ggt	ggc	agag	gcc	tgt	gtct	gtg	ccac	acct	gca	cac	ggt	ggga	gggggg	gtac
ccg	gggc	cagc	atcg	tggt	ctc	ctga	accc	cag	accca	atgct	tag	ccaa	acg	aagt	ggct	cc
cat	gtgg	caa	gcacc	cttct	cag	tttc	gca	gtgg	cttggc	tcggg	atcct	tgg	cagt	ttcc		1384
ccc	agcccc	ccct	gtct	gtc	tcct	tccc	cag	ttcct	tccc	ggcccc	acac	gct	gtc	ccag		1444
ctg	ccaact	tt	tgct	gcag	ag	ccact	gccgc	cctt	gagcct	ctcacc	atga	gtg	agc	cacc		1504
agc	tctccac	gtt	cccc	tca	tag	cagt	gtc	act	ccca	acc	ccacc	atggc	ccagg	gacc		1564
gtg	gacaggt	tgggg	atggg	gtgt	gtgccc	act	gtgctca	tcac	aggagc	ctcagt	ttgag					1624
agt	gagcggg	gtac	agtaag	gcagt	gtctt	ccac	actgga	cct	cttt	cct	ggtt	ctctt				1684
tgca	atacat	taac	agaccc	tttat	caaca	taa	acaatag	taact	gagct	attaa	aggca					1744
aaaaaaaa	taaaaaaaaa	aaaaaaaa														1773

<210> 217
 <211> 1251
 <212> DNA
 <213> Homo sapiens

<220>
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 <222> 29..376

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							1				5					
gca	gtg	gag	gag	ctg	gtt	tcg	ggg	gtg	cgg	cag	gcg	gcc	gac	ttc	gcg	100
Ala	Val	Glu	Glu	Leu	Val	Ser	Gly	Val	Arg	Gln	Ala	Ala	Asp	Phe	Ala	
	10					15				20						
gag	cag	ttc	cgc	tcc	tac	tca	gag	agc	gag	aag	caa	tgg	aag	gcc	cgc	148
Glu	Gln	Phe	Arg	Ser	Tyr	Ser	Glu	Ser	Glu	Lys	Gln	Trp	Lys	Ala	Arg	
	25				30					35				40		
atg	gaa	ttc	atc	ctg	cgc	cac	ctg	ccc	gac	tac	cgc	gac	ccg	ccc	gac	196
Met	Glu	Phe	Ile	Leu	Arg	His	Leu	Pro	Asp	Tyr	Arg	Asp	Pro	Pro	Asp	
			45					50					55			
ggc	agt	ggc	cgc	ctg	gac	cag	ctg	ctc	tcc	ctc	tcc	atg	gtc	tgg	gcc	244
Gly	Ser	Gly	Arg	Leu	Asp	Gln	Leu	Leu	Ser	Leu	Ser	Met	Val	Trp	Ala	
			60			65						70				
aac	cat	ctc	ttc	cta	ggc	tgc	agt	tac	aat	aaa	gac	ctt	tta	gac	aag	292
Asn	His	Leu	Phe	Leu	Gly	Cys	Ser	Tyr	Asn	Lys	Asp	Leu	Leu	Asp	Lys	
	75					80					85					
gtg	atg	gaa	atg	gcc	gat	ggg	att	gaa	gtg	gaa	gac	ctg	cca	caa	ttt	340
Val	Met	Glu	Met	Ala	Asp	Gly	Ile	Glu	Val	Glu	Asp	Leu	Pro	Gln	Phe	
	90					95					100					
act	acc	aga	agt	gaa	tta	atg	aaa	aag	cat	caa	agc	taag	ccagaa			386
Thr	Thr	Arg	Ser	Glu	Leu	Met	Lys	Lys	His	Gln	Ser					
	105				110					115						
gatt	tat	cat	ca	atttt	cat	ca	gcag	ctac	ag	gatt	agaa	gag	gct	ggga	tga	atgtgac
atag	acc	caca	gcag	ctct	ct	taag	act	ctc	tg	tatt	acca	acata	aa	gag	gcag	gtggaa
tgag	aagg	ac	tct	gt	ctaga	ttgg	ctttt	tt	taac	att	ctc	atttt	ccc	ag	gag	ttatcac
tgta	aaa	agta	tgat	gg	ata	tttat	gtatt	tata	aat	cat	gcact	cta	ag	atg	ag	ttcat
caac	att	gta	aaag	cc	ctct	ttt	ctgttt	cagg	gttttt	tttt	cttt	at	cgaca	agg	gtc	686
tcact	ctg	tc	gcc	agg	cag	aat	caca	aa	gtg	catt	att	ggct	catt	gc	agc	ctcgaac
tcct	ggg	ctc	atatt	ttt	cag	ggt	tttt	gt	tttt	gttt	gttt	tttt	tga	gac	ag	agct
tgct	ctg	ttg	ccc	agg	cagt	agt	gcm	agt	gcg	cat	ata	tttt	cag	ttt	taaac	gtca
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gaatttttgt ttaaaatgcc tttttgggct gggccacagt ggccttatgc ccataataat 926
cccagcactt tgggaggccg aggtgagcag atcacctgag gttaggagtt tgagaccagc 986
ctggccaaca cgatgaaacc ccgtctctac taaaaatata aacaaaatta gctgggcatg 1046
gtggcggaaca tctgtaatcc cagctactca ggaggetgaa gcagaagaac tgcttgaacc 1106
tgggaggtgg aggttgacgt gagccaagat cgcaccattg cactccatcc tgggcgacaa 1166
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<210> 218
<211> 894
<212> DNA
<213> Homo sapiens

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<221> CDS
<222> 78..566

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acaagacagc aagcagg atg gag cac tac cgg aaa gct ggc tct gta gag 110
Met Glu His Tyr Arg Lys Ala Gly Ser Val Glu
1 5 10
ctc cca gcg cct tcc cca atg ccc cag cta cct cct gat acc ctt gag 158
Leu Pro Ala Pro Ser Pro Met Pro Gln Leu Pro Pro Asp Thr Leu Glu
15 20 25
atg cgg gtc cga gat ggc agc aaa att cgc aac ctg ctg ggg ttg gct 206
Met Arg Val Arg Asp Gly Ser Lys Ile Arg Asn Leu Leu Gly Leu Ala
30 35 40
ctg ggt cgg ttg gag ggc ggc agt gct cgg cat gta gtg ttc tca ggt 254
Leu Gly Arg Leu Glu Gly Gly Ser Ala Arg His Val Val Phe Ser Gly
45 50 55
tct ggc agg gct gca gga aag gct gtc agc tgc gct gag att gtc aag 302
Ser Gly Arg Ala Ala Gly Lys Ala Val Ser Cys Ala Glu Ile Val Lys
60 65 70 75
cgg cgg gtc cca ggc ctg cac cag ctc acc aag cta cgt ttc ctt cag 350
Arg Arg Val Pro Gly Leu His Gln Leu Thr Lys Leu Arg Phe Leu Gln
80 85 90
act gag gac agc tgg gtc cca gcc tca cct gac aca ggg cta gac ccc 398
Thr Glu Asp Ser Trp Val Pro Ala Ser Pro Asp Thr Gly Leu Asp Pro
95 100 105
ctc aca gtg cgc cgc cat gtg cct gca gtg tgg gtg ctg ctc agc cgg 446
Leu Thr Val Arg Arg His Val Pro Ala Val Trp Val Leu Leu Ser Arg
110 115 120
gac ccc ctg gac ccc aat gag tgt ggt tac caa ccc cca gga gca ccc 494
Asp Pro Leu Asp Pro Asn Glu Cys Gly Tyr Gln Pro Pro Gly Ala Pro
125 130 135
cct ggc ctg ggt tcc atg ccc agc tcc agc tgt ggc cct cgt tcc cga 542
Pro Gly Leu Gly Ser Met Pro Ser Ser Ser Cys Gly Pro Arg Ser Arg
140 145 150 155
aga agg gct cga gac acc cga tcg tgaagacctg ctgagccagc ctgttctccg 596
Arg Arg Ala Arg Asp Thr Arg Ser
160
ggcctgaatg tctggggtgc ttgtgccttt tctgagaagc gttgtgactg ctcaacatcc 656
ccatcaagggt ttgagtccac aaaagtggac ctccctatca tgcttccctt tccctctagc 716
atgtgggaag ggactgctgt gaagaatgac agatgtgggg cctctgcca gttctgcatt 776
gctaaataag ggcttccctct gccttctacc tacagtgcac ttgaactgcc ttctgaaaga 836
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<210> 219
 <211> 910
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> 16..705

<400> 219
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 Met Val Val Phe Gly Tyr Glu Ala Gly Thr Lys Pro
 agg gat tca ggt gtg gtg ccg gtg gga act gag gaa gcg ccc aag gtt 99
 Arg Asp Ser Gly Val Val Pro Val Gly Thr Glu Glu Ala Pro Lys Val
 15 20 25
 ttc aag atg gca gca tct atg cat ggt cag ccc agt cct tct cta gaa 147
 Phe Lys Met Ala Ala Ser Met His Gly Gln Pro Ser Pro Ser Leu Glu
 30 35 40
 gat gca aaa ctc aga aga cca atg gtc ata gaa atc ata gaa aaa aat 195
 Asp Ala Lys Leu Arg Arg Pro Met Val Ile Glu Ile Ile Glu Lys Asn
 45 50 55 60
 ttt gac tat ctt aga aaa gaa atg aca caa aat ata tat caa atg gcg 243
 Phe Asp Tyr Leu Arg Lys Glu Met Thr Gln Asn Ile Tyr Gln Met Ala
 65 70 75
 aca ttt gga aca aca gct ggt ttc tct gga ata ttc tca aac ttc ctg 291
 Thr Phe Gly Thr Thr Ala Gly Phe Ser Gly Ile Phe Ser Asn Phe Leu
 80 85 90
 ttc aga cgc tgc ttc aag gtt aaa cat gat gct ttg aag aca tat gca 339
 Phe Arg Arg Cys Phe Lys Val Lys His Asp Ala Leu Lys Thr Tyr Ala
 95 100 105
 tca ttg gct aca ctt cca ttt ttg tct act gtt gtt act gac aag ctt 387
 Ser Leu Ala Thr Leu Pro Phe Leu Ser Thr Val Val Thr Asp Lys Leu
 110 115 120
 ttt gta att gat gct ttg tat tca gat aat ata agc aag gaa aac tgt 435
 Phe Val Ile Asp Ala Leu Tyr Ser Asp Asn Ile Ser Lys Glu Asn Cys
 125 130 135 140
 gtt ttc aga agc tca ctg att ggc ata gtt tgt ggt gtt ttc tat ccc 483
 Val Phe Arg Ser Ser Leu Ile Gly Ile Val Cys Gly Val Phe Tyr Pro
 145 150 155
 agt tct ttg gct ttt act aaa aat gga cgc ctg gca acc aag tat cat 531
 Ser Ser Leu Ala Phe Thr Lys Asn Gly Arg Leu Ala Thr Lys Tyr His
 160 165 170
 acc gtt cca ctg cca cca aaa gga agg gtt tta atc cat tgg atg acg 579
 Thr Val Pro Leu Pro Pro Lys Gly Arg Val Leu Ile His Trp Met Thr
 175 180 185
 ctt tgt caa aca caa atg aaa tta atg gcg att cct cta gtc ttt cag 627
 Leu Cys Gln Thr Gln Met Lys Leu Met Ala Ile Pro Leu Val Phe Gln
 190 195 200
 att atg ttt gga ata tta aat ggt cta tac cat tat gca gta ttt gaa 675
 Ile Met Phe Gly Ile Leu Asn Gly Leu Tyr His Tyr Ala Val Phe Glu
 205 210 215 220
 gag aca ctt gag aaa act ata cat gaa gag taacaaaaaa aatgaatggt 725
 Glu Thr Leu Glu Lys Thr Ile His Glu Glu
 225 230
 tgctaactta gcaaaatgaa gtttctataa agaggactca ggcattgctg aaagagttaa 785
 aagtaactgt gaacaaataa tttgttctgt gccttttgcc tggatatatag caaataactca 845
 aaaaatattc aataattcaa tcaataaata taagtttcat cttacaccaa aaaaaaaaaa 905

aaaaaa 910

<210> 220
<211> 519
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> 103..405

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gccagctcc gccgccgagc gcctgtgccg gcacgbhaca cc atg gag cgc ccg 114
Met Glu Arg Pro
1
gat aag gcg gcg ctg aac gca ctg cag cct cct gag ttc aga aat gaa 162
Asp Lys Ala Ala Leu Asn Ala Leu Gln Pro Pro Glu Phe Arg Asn Glu
5 10 15 20
agc tca tta gca tct aca ctg aag acg ctc ctg ttc ttc aca gct tta 210
Ser Ser Leu Ala Ser Thr Leu Lys Thr Leu Leu Phe Phe Thr Ala Leu
25 30 35
atg atc act gtt cct att ggg tta tat ttc aca act aaa tct tac ata 258
Met Ile Thr Val Pro Ile Gly Leu Tyr Phe Thr Thr Lys Ser Tyr Ile
40 45 50
ttt gaa ggc gcc ctt ggg atg tcc aat agg gac agc tat ttt tac gct 306
Phe Glu Gly Ala Leu Gly Met Ser Asn Arg Asp Ser Tyr Phe Tyr Ala
55 60 65
gct att gtt gca gtg gtc gcc gtc cat gtg gtg ctg gcc ctc ttt gtg 354
Ala Ile Val Ala Val Val Ala Val His Val Val Leu Ala Leu Phe Val
70 75 80
tat gtg gcc tgg aat gaa ggc tca cga cag tgc cgt gaa ggc aaa cag 402
Tyr Val Ala Trp Asn Glu Gly Ser Arg Gln Xaa Arg Glu Gly Lys Gln
85 90 95 100
gat taaagtgaac atcacctttt tatagcatta aattcatttt ttaaaatgat 455
Asp
aatgctggag ggggccatct gatttgaata aagttgaaag aacatgtaaa aaaaaaaaaa 515
aaaa 519

<210> 221
<211> 632
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> 72..350

<400> 221
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tgcaggccggc c atg gat tcc ttg cgg aaa atg ctg atc tca gtc gca atg 110
Met Asp Ser Leu Arg Lys Met Leu Ile Ser Val Ala Met
1 5 10
ctg ggc gca ggg gct ggc gtg ggc tac gcg ctc ctc gtt atc gtg acc 158
Leu Gly Ala Gly Ala Gly Val Gly Tyr Ala Leu Leu Val Ile Val Thr
15 20 25
ccg gga gag cgg cgg aag cag gaa atg cta aag gag atg cca ctg cag 206
Pro Gly Glu Arg Arg Lys Gln Glu Met Leu Lys Glu Met Pro Leu Gln

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30          35          40          45
gac cca agg agc aga gag gag gcg gcc agg acc cag cag cta ttg ctg      254
Asp Pro Arg Ser Arg Glu Glu Ala Ala Arg Thr Gln Gln Leu Leu Leu
          50          55          60
gcc act ctg cag gag gca gcg acc acg cag gag aac gtg gcc tgg agg      302
Ala Thr Leu Gln Glu Ala Ala Thr Thr Gln Glu Asn Val Ala Trp Arg
          65          70          75
aag aac tgg atg gtt ggc ggc gaa ggc ggc gcc ggc ggg agg tca ccg      350
Lys Asn Trp Met Val Gly Gly Glu Gly Gly Ala Gly Gly Arg Ser Pro
          80          85          90
tgagaccgga cttgcctccg tgggcgcggg accttggett gggcgcagga atccgaggca      410
gcctttctcc ttcgtggggc cagcggagag tccggaccga gataccatgc caggactctc      470
cggggtcccg tgagctgccg tcgggtgagc acgtttcccc caaacctgg actgactgct      530
ttaaggtccg caaggcgggc cagggccgag acgcgagtcg gatgtggtga actgaaagaa      590
ccaataaaat catgttcctc cacccaaaaa aaaaaaaaaa aa                        632

<210> 222
<211> 652
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> 38..436

<400> 222
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                                Met Gly His Gly Asp Glu
                                1          5
atc gtt ctt gcg gac ttg aac ttc ccg gcc tcc tcc atc tgc cag tgt      103
Ile Val Leu Ala Asp Leu Asn Phe Pro Ala Ser Ser Ile Cys Gln Cys
          10          15          20
ggg ccc atg gag atc cgt gca gac ggc ctg ggc atc ccg cag ctc ctg      151
Gly Pro Met Glu Ile Arg Ala Asp Gly Leu Gly Ile Pro Gln Leu Leu
          25          30          35
gag gcc gtg ctg aag ctg ctg ccc ctg gac acc tat gtg gag agt ccg      199
Glu Ala Val Leu Lys Leu Leu Pro Leu Asp Thr Tyr Val Glu Ser Pro
          40          45          50
gct gca gtc atg gag ctg gtg ccc agc gac aag gag agg ggc ctg cag      247
Ala Ala Val Met Glu Leu Val Pro Ser Asp Lys Glu Arg Gly Leu Gln
          55          60          65          70
acc cca gtg tgg acg gag tac gag tcc atc cta cgc agg gcc ggc tgt      295
Thr Pro Val Trp Thr Glu Tyr Glu Ser Ile Leu Arg Arg Ala Gly Cys
          75          80          85
gtg aga gcc ctg gca aag ata gag agg ttt gag ttt tat gaa cgg gct      343
Val Arg Ala Leu Ala Lys Ile Glu Arg Phe Glu Phe Tyr Glu Arg Ala
          90          95          100
aag aag gct ttt gct gtt gtg gca acg ggg gag acg gcc ctc tac gga      391
Lys Lys Ala Phe Ala Val Val Ala Thr Gly Glu Thr Ala Leu Tyr Gly
          105          110          115
aac ctc atc ctc agg aag ggg gtg ctt gcc ctc aac ccc ctg ctg      436
Asn Leu Ile Leu Arg Lys Gly Val Leu Ala Leu Asn Pro Leu Leu
          120          125          130
taggcctggg gaagaccacc tgggccggaa gaggaactgg gggcaccctg agctccagta      496
ccaccactca caacaggcct cccagtggca gctcccagac ctgggccctg gccagggctc      556
taggggccgg cagtcttggg gtgggccctg ccaattggga cgagtatccc tgatttgtga      616
aatgatgga aaaacgttca aaaaaaaaaa aaaaaa                        652

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				150				155				160					
gag	ctt	gcc	atc	caa	cag	ggt	caa	ctg	gag	aca	act	ctg	aag	gag	ctt		704
Glu	Leu	Ala	Ile	Gln	Gln	Gly	Gln	Leu	Glu	Thr	Thr	Leu	Lys	Glu	Leu		
		165					170					175					
cag	acc	ctg	agg	aac	atg	cag	aag	gaa	gct	att	gct	gct	cac	aag	gaa		752
Gln	Thr	Leu	Arg	Asn	Met	Gln	Lys	Glu	Ala	Ile	Ala	Ala	His	Lys	Glu		
		180					185					190					
aac	aag	cta	cat	ctg	cag	caa	cat	gtg	tcc	atg	gag	ttt	cta	aag	ctg		800
Asn	Lys	Leu	His	Leu	Gln	Gln	His	Val	Ser	Met	Glu	Phe	Leu	Lys	Leu		
		195				200					205				210		
cat	cag	ttc	ctg	cac	agc	aaa	gaa	aag	gac	att	tta	act	gag	ctc	cgg		848
His	Gln	Phe	Leu	His	Ser	Lys	Glu	Lys	Asp	Ile	Leu	Thr	Glu	Leu	Arg		
				215					220					225			
gaa	gag	ggg	aaa	gcc	ttg	aat	gag	gag	atg	gag	ttg	aat	ctg	agc	cag		896
Glu	Glu	Gly	Lys	Ala	Leu	Asn	Glu	Glu	Met	Glu	Leu	Asn	Leu	Ser	Gln		
			230					235					240				
ctt	cag	gag	caa	tgt	ctc	tta	gcc	aag	gat	atg	ttg	gtg	agc	att	cag		944
Leu	Gln	Glu	Gln	Cys	Leu	Leu	Ala	Lys	Asp	Met	Leu	Val	Ser	Ile	Gln		
		245					250					255					
gca	aag	acg	gaa	caa	cag	aac	tcc	ttc	gac	ttt	ctc	aaa	gac	atc	aca		992
Ala	Lys	Thr	Glu	Gln	Gln	Asn	Ser	Phe	Asp	Phe	Leu	Lys	Asp	Ile	Thr		
		260				265					270						
act	ctc	tta	cat	agc	ttg	gag	caa	gga	atg	aag	gtg	ctg	gca	acc	aga		1040
Thr	Leu	Leu	His	Ser	Leu	Glu	Gln	Gly	Met	Lys	Val	Leu	Ala	Thr	Arg		
				280					285						290		
gag	ctt	att	tcc	aga	aag	ctg	aac	ctg	ggc	cag	tac	aaa	ggg	cct	atc		1088
Glu	Leu	Ile	Ser	Arg	Lys	Leu	Asn	Leu	Gly	Gln	Tyr	Lys	Gly	Pro	Ile		
				295				300						305			
cag	tac	atg	gta	tgg	agg	gaa	atg	cag	gac	act	ctc	tgc	cca	ggc	ctg		1136
Gln	Tyr	Met	Val	Trp	Arg	Glu	Met	Gln	Asp	Thr	Leu	Cys	Pro	Gly	Leu		
			310				315						320				
tct	cca	cta	act	ctg	gac	cct	aaa	aca	gct	cac	cca	aat	ctg	gtg	ctc		1184
Ser	Pro	Leu	Thr	Leu	Asp	Pro	Lys	Thr	Ala	His	Pro	Asn	Leu	Val	Leu		
			325			330					335						
tcc	aaa	agc	caa	acc	agc	gtc	tgg	cat	ggg	gac	att	aag	aag	ata	atg		1232
Ser	Lys	Ser	Gln	Thr	Ser	Val	Trp	His	Gly	Asp	Ile	Lys	Lys	Ile	Met		
		340				345					350						
cct	gat	gat	cct	gag	agg	ttt	gac	tca	agt	gtg	gct	gta	ctg	ggc	tca		1280
Pro	Asp	Asp	Pro	Glu	Arg	Phe	Asp	Ser	Ser	Val	Ala	Val	Leu	Gly	Ser		
				360			365							370			
aga	ggc	ttc	acc	tct	gga	aag	tgg	tac	tgg	gaa	gta	gaa	gta	gca	aag		1328
Arg	Gly	Phe	Thr	Ser	Gly	Lys	Trp	Tyr	Trp	Glu	Val	Glu	Val	Ala	Lys		
				375			380							385			
aag	aca	aaa	tgg	aca	gtt	gga	gtt	gtc	aga	gaa	tcc	atc	att	cgg	aag		1376
Lys	Thr	Lys	Trp	Thr	Val	Gly	Val	Val	Arg	Glu	Ser	Ile	Ile	Arg	Lys		
			390				395						400				
ggc	agc	tgt	cct	cta	act	cct	gag	caa	gga	ttc	tgg	ctt	tta	aga	cta		1424
Gly	Ser	Cys	Pro	Leu	Thr	Pro	Glu	Gln	Gly	Phe	Trp	Leu	Leu	Arg	Leu		
		405				410						415					
agg	aac	caa	act	gat	cta	aag	gct	ctg	gat	ttg	cct	tct	ttc	agt	ctg		1472
Arg	Asn	Gln	Thr	Asp	Leu	Lys	Ala	Leu	Asp	Leu	Pro	Ser	Phe	Ser	Leu		
		420				425					430						
aca	ctg	act	aac	aac	ctc	gac	aag	gtg	ggc	ata	tac	ctg	gat	tat	gaa		1520
Thr	Leu	Thr	Asn	Asn	Leu	Asp	Lys	Val	Gly	Ile	Tyr	Leu	Asp	Tyr	Glu		
				440			445								450		
gga	gga	cag	ttg	tcc	ttc	tac	aat	gct	aaa	acc	atg	act	cac	att	tac		1568
Gly	Gly	Gln	Leu	Ser	Phe	Tyr	Asn	Ala	Lys	Thr	Met	Thr	His	Ile	Tyr		
				455			460							465			

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acc ttc agt aac act ttc atg gag aaa ctt tat ccc tac ttc tgc ccc 1616
Thr Phe Ser Asn Thr Phe Met Glu Lys Leu Tyr Pro Tyr Phe Cys Pro
      470                      475                      480
tgc ctt aat gat ggt aga gag aat aaa gaa cca ttg cac atc tta cat 1664
Cys Leu Asn Asp Gly Arg Glu Asn Lys Glu Pro Leu His Ile Leu His
      485                      490                      495
cca cag taatgagtca taatattata caaattcaga gtgttattaa agaggttttg 1720
Pro Gln
      500
aaataaaaaaa aaaaaaaaaa 1739

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<210> 226
<211> 657
<212> DNA
<213> Homo sapiens

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<220>
<221> CDS
<222> 199..618

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<400> 226
aactggatag agtactgccc cttcagccc atggagaaaag gcaaatgcct cttcagagt 60
ctacctaatag ctttctcaga taaataagca tgaagaaaag tcaaagtcca ttctagctct 120
aaaataagga atgaaatgtt ttcttgatat gattttttgt ttccatctga taataatttt 180
atatatcaca gaaacagc atg gtt ctt act aaa cct ctt caa aga aat ggc 231
                Met Val Leu Thr Lys Pro Leu Gln Arg Asn Gly
                1                5                10
agc atg atg agc ttt gaa aat gtg aaa gaa aag agc aga gaa gga ggg 279
Ser Met Met Ser Phe Glu Asn Val Lys Glu Lys Ser Arg Glu Gly Gly
      15                20                25
ccc cat gca cac aca ccc gaa gaa gaa ttg tgt ttc gtg gta aca cac 327
Pro His Ala His Thr Pro Glu Glu Glu Leu Cys Phe Val Val Thr His
      30                35                40
tac cct cag gtt cag acc aca ctc aac ctg ttt ttc cat ata ttc aag 375
Tyr Pro Gln Val Gln Thr Thr Leu Asn Leu Phe Phe His Ile Phe Lys
      45                50                55
gtt ctt act caa cca ctt tcc ctt ctg tgg ggt tgt gat cag aag cct 423
Val Leu Thr Gln Pro Leu Ser Leu Leu Trp Gly Cys Asp Gln Lys Pro
      60                65                70                75
cgt act gtt cct acc ctt gga aac ggc gca tgg gat acc tgc caa caa 471
Arg Thr Val Pro Thr Leu Gly Asn Gly Ala Trp Asp Thr Cys Gln Gln
      80                85                90
cac ata cgc act tca tca tgg aca gca aac aca ctc gtc att caa aac 519
His Ile Arg Thr Ser Ser Trp Thr Ala Asn Thr Leu Val Ile Gln Asn
      95                100                105
cag cat tca cgg gaa agc act gtt tct gtt tgc ctt ttt atg tta atc 567
Gln His Ser Arg Glu Ser Thr Val Ser Val Cys Leu Phe Met Leu Ile
      110                115                120
cgc atg caa cat att ttg aaa aca gat aca ctt caa cag ttc aga ata 615
Arg Met Gln His Ile Leu Lys Thr Asp Thr Leu Gln Phe Arg Ile
      125                130                135
tgc tagtactaat aaaaccaaca tggtaaaaaa aaaaaaaaaa 657
Cys
140

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<210> 227
<211> 888
<212> DNA

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<213> Homo sapiens

<220>

<221> CDS

<222> 182..481

<400> 227

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atattgcctc tcagtgttca agcttgagcc cacgcatcca actcctgaga tcttactggg      60
aagctgctga tcatcagttt caggaagtca gcatggatca gccttacgtt catggcctcc      120
aggccctatt ctccctgctc acagggaccg gccaggatct ctatccttac agcacgttgg      180
a atg tat atg ctc ctc tcc cca cat cgc ctt agg gag cag gca ggt gtc      229
  Met Tyr Met Leu Leu Ser Pro His Arg Leu Arg Glu Gln Ala Gly Val
    1         5         10        15
agg ggc agc ata agg acg gcc aac agg aca gaa gac ggg ttg aag atc      277
Arg Gly Ser Ile Arg Thr Ala Asn Arg Thr Glu Asp Gly Leu Lys Ile
      20        25        30
cga gag gct gag tca ctt cca caa agt aac aca gct gat ttt aaa tgc      325
Arg Glu Ala Glu Ser Leu Pro Gln Ser Asn Thr Ala Asp Phe Lys Cys
      35        40        45
ctg cat tca gca tcc ctg cag cag gct cca ggt gga att cta atg gga      373
Leu His Ser Ala Ser Leu Gln Ala Pro Gly Gly Ile Leu Met Gly
      50        55        60
cca gcc tcc agt ccc tgg acc tta gcc gtg gaa gga gag aag agg aca      421
Pro Ala Ser Ser Pro Trp Thr Leu Ala Val Glu Gly Glu Lys Arg Thr
      65        70        75        80
tct gca cct cct ctc aga gaa agc ctg atg cct act aaa gga ctt ggg      469
Ser Ala Pro Pro Leu Arg Glu Ser Leu Met Pro Thr Lys Gly Leu Gly
      85        90        95
tgg tgg acg cag tgaccctcag tctggagctt gttcactgaa cattggagac      521
Trp Trp Thr Gln
      100
tatcatttgc gcagatgggc ttgggcctct atgagcagca ggctgcaccc cacagtgacc      581
tcctcattct actctgaggg atcttcatga aagcagatgt ccattgaaaa gcacccaagt      641
gcagtctcag ctgatgaact tcagaggcga ttgagacaaa ggctctcggt cccctctgcc      701
cttggaatggg gcctctggta tgcacttggc ctctgtgtct ttatttagac tggtcacttc      761
acaacccatc atgtcacccc acccctaacc gtgccactc tgggtcctcc cctcaactgc      821
ctgacttccc actttgagct cagcaaaggc aatagatgtt ttgtctgctt cgaaaaaaaa      881
aaaaaaaaa      888
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<210> 228

<211> 716

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> 161..517

<400> 228

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acctgtcatt atgcttacta acgttcggga cgtctcccg gctgcttggg cgaggagagg      60
caggggtgtg tgaccccggt gggtactgtg ctgcgtaga gcacctaggg cctgctgaag      120
ccctccctcg ccgcgcctc tccttagtcc ttgagatgag atg gca agt tac agc      175
      Met Ala Ser Tyr Ser
      1         5
ggc ttc tcc ggc ctg ctg gag att cgc tac ggg cca gga cac cgc agc      223
Gly Phe Ser Gly Leu Leu Glu Ile Arg Tyr Gly Pro Gly His Arg Ser
      10        15        20
tgc ctt ccc caa ttc gct ttc ttt ccg cag ccg ccg ctg ccc cga ccc      271
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Cys	Leu	Pro	Gln	Phe	Ala	Phe	Phe	Pro	Gln	Pro	Pro	Leu	Pro	Arg	Pro		
			25					30					35				
cgg	atc	tgc	atg	tgg	gtg	ctg	gct	gag	ctg	ctg	gag	cta	ggg	tgt	cct		319
Arg	Ile	Cys	Met	Trp	Val	Leu	Ala	Glu	Leu	Leu	Glu	Leu	Gly	Cys	Pro		
		40					45					50					
gag	cag	agc	ctg	agg	gac	gcc	atc	acc	ctg	gac	ctc	ttc	tgc	cac	gcg		367
Glu	Gln	Ser	Leu	Arg	Asp	Ala	Ile	Thr	Leu	Asp	Leu	Phe	Cys	His	Ala		
		55				60					65						
ctc	att	ttc	tgc	cgc	cag	cag	ggc	ttc	tca	ctg	gag	cag	acg	tca	gcg		415
Leu	Ile	Phe	Cys	Arg	Gln	Gln	Gly	Phe	Ser	Leu	Glu	Gln	Thr	Ser	Ala		
		70			75				80					85			
gct	tgt	gcc	ctg	ctc	cag	gat	ctt	cac	aag	gct	tgt	att	ggg	gag	agg		463
Ala	Cys	Ala	Leu	Leu	Gln	Asp	Leu	His	Lys	Ala	Cys	Ile	Gly	Glu	Arg		
			90					95					100				
ggg	cag	cta	cca	ggg	ttg	agc	ccc	agg	gag	aag	agg	aac	cgg	gcc	tgg		511
Gly	Gln	Leu	Pro	Gly	Leu	Ser	Pro	Arg	Glu	Lys	Arg	Asn	Arg	Ala	Trp		
		105					110					115					
cac	aag	tgaccatggg	aagcagaagc	aggggatttc	tgccctggaat	atgtcattat											567
His	Lys																
tagtagcatc	atcatacaca	agccatcagc	tttccaatcc	actgcttcct	tatctagaaa												627
ttaaggatac	agcacacatt	ttacaggact	gttctgagaa	ataatatatg	caaatatatg												687
catagtgcac	aataaaaaaaaa	aaaaaaaaaa															716
<210>	229																
<211>	654																
<212>	DNA																
<213>	Homo sapiens																
<220>																	
<221>	CDS																
<222>	86..505																
<400>	229																
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ccggtgaatc	ctgccgctgg	cgtgg	atg	aga	agt	gaa	tgc	gtg	ctc	gga	gct						112
			Met	Arg	Ser	Glu	Cys	Val	Leu	Gly	Ala						
			1				5										
gcg	agt	gac	agc	ggg	cag	gag	gcg	ccc	agg	gac	act	tgg	ttt	ctc	cag		160
Ala	Ser	Asp	Ser	Gly	Gln	Glu	Ala	Pro	Arg	Asp	Thr	Trp	Phe	Leu	Gln		
					15				20					25			
ggc	tgg	aag	gct	tct	aga	agg	ttc	ctc	atc	aag	gga	agt	gtg	gct	ggg		208
Gly	Trp	Lys	Ala	Ser	Arg	Arg	Phe	Leu	Ile	Lys	Gly	Ser	Val	Ala	Gly		
			30				35						40				
ggc	gcc	gtc	tac	ctg	gtg	tac	gac	cag	gag	ctg	ctg	ggg	ccc	agc	gac		256
Gly	Ala	Val	Tyr	Leu	Val	Tyr	Asp	Gln	Glu	Leu	Leu	Gly	Pro	Ser	Asp		
			45				50					55					
aag	agc	cag	gca	gcc	cta	cag	aag	gct	ggg	gag	gtg	gtc	ccc	ccc	gcc		304
Lys	Ser	Gln	Ala	Ala	Leu	Gln	Lys	Ala	Gly	Glu	Val	Val	Pro	Pro	Ala		
		60				65					70						
atg	tac	cag	ttc	agc	cag	tac	gtg	tgt	cag	cag	aca	ggc	ctg	cag	ata		352
Met	Tyr	Gln	Phe	Ser	Gln	Tyr	Val	Cys	Gln	Gln	Thr	Gly	Leu	Gln	Ile		
		75				80					85						
ccc	cag	ctc	cca	gcc	cct	cca	aag	att	tac	ttt	ccc	atc	cgt	gac	tcc		400
Pro	Gln	Leu	Pro	Ala	Pro	Pro	Lys	Ile	Tyr	Phe	Pro	Ile	Arg	Asp	Ser		
				95					100					105			
tgg	aat	gca	ggc	atc	atg	acg	gtg	atg	tca	gct	ctg	tcg	gtg	gcc	ccc		448
Trp	Asn	Ala	Gly	Ile	Met	Thr	Val	Met	Ser	Ala	Leu	Ser	Val	Ala	Pro		
			110						115					120			

tcc aag gcc cgc gag tac tcc aag gag ggc tgg gag tat gtg aag gcg	496
Ser Lys Ala Arg Glu Tyr Ser Lys Glu Gly Trp Glu Tyr Val Lys Ala	
125 130 135	
cgc acc aag tagcgagtca gcagggggccg cctgcccccg ccagaacggg	545
Arg Thr Lys	
140	
cagggctgcc actgacctga agactccgga ctgggacccc actccgaggg cagctcccg	605
ccttgccggc ccaataaagg acttcagaag tcaaaaaaaaa aaaaaaaaa	654

<210> 230
 <211> 635
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> 56..382

<400> 230	
aattcgggtg gagctgagcc ggagacaggc agttgtgaaa aacttcagga caaaa atg	58
	Met
	1
ttt cat tta agg act tgt gct gct aag ttg agg cca ttg acg gct tcc	106
Phe His Leu Arg Thr Cys Ala Ala Lys Leu Arg Pro Leu Thr Ala Ser	
5 10 15	
cag act gtt aag aca ttt tca caa aac aga cca gca gca gct agg aca	154
Gln Thr Val Lys Thr Phe Ser Gln Asn Arg Pro Ala Ala Ala Arg Thr	
20 25 30	
ttt caa cag att cgg tgc tat tct gca cct gtt gct gct gag ccc ttt	202
Phe Gln Gln Ile Arg Cys Tyr Ser Ala Pro Val Ala Ala Glu Pro Phe	
35 40 45	
ctc agt ggg act agt tgc aac tat gtg gag gag atg tac tgt gct tgg	250
Leu Ser Gly Thr Ser Ser Asn Tyr Val Glu Glu Met Tyr Cys Ala Trp	
50 55 60 65	
ctg gaa aac ccc aaa agt gta cat aag aca ggg tcc cac tgt tgt cca	298
Leu Glu Asn Pro Lys Ser Val His Lys Thr Gly Ser His Cys Cys Pro	
70 75 80	
ggc tgg agt gca gtg gcg gga tct cgg ctt gct gca acc tcc gac tcc	346
Gly Trp Ser Ala Val Ala Gly Ser Arg Leu Ala Ala Thr Ser Asp Ser	
85 90 95	
tgg gtt caa gtg att ctt atg cct cag cct ccc gag taactgggac	392
Trp Val Gln Val Ile Leu Met Pro Gln Pro Pro Glu	
100 105	
tacaggtgca cgtcaccacg cctgactagt ttttgtatatt ttagtagaga tgggatttta	452
ctttgttggc caggttggtc ttgaaccctt ggcctcaagt gatccaccca ccttggcctc	512
ccaaagtgtc gggattacag gtatgatcaa ccacgcctgg ccatgtcatg ccttgtgaca	572
gaattccttt attctgtttt gagccaataa atatttatag gtttcgaaaa aaaaaaaaaa	632
aaa	635

<210> 231
 <211> 634
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> 56..355

<400> 231

aattcgggtg gagctgagcc ggagacaggc agttgtgaaa aacttcagga caaaa atg 58
Met

1
ttt cat tta agg act tgt gct gct aag ttg agg cca ttg acg gct tcc 106
Phe His Leu Arg Thr Cys Ala Ala Lys Leu Arg Pro Leu Thr Ala Ser

5 10 15
cag act gtt aag aca ttt tca caa aac aga cca gca gca gct agg aca 154
Gln Thr Val Lys Thr Phe Ser Gln Asn Arg Pro Ala Ala Ala Arg Thr

20 25 30
ttt caa cag att cgt gct att ctg cac ctg ttg ctg ctg agc cct ttc 202
Phe Gln Gln Ile Arg Ala Ile Leu His Leu Leu Leu Leu Ser Pro Phe

35 40 45
tca gtg gga cta gtt cga act atg tgg agg aga tgt act gtg ctt ggc 250
Ser Val Gly Leu Val Arg Thr Met Trp Arg Arg Cys Thr Val Leu Gly

50 55 60 65
tgg aaa acc cca aaa gtg tac ata aga cag ggt ccc act gtt gtc cag 298
Trp Lys Thr Pro Lys Val Tyr Ile Arg Gln Gly Pro Thr Val Val Gln

70 75 80
gct gga gtg cag tgg cgg gat ctc ggc ttg ctg caa cct ccg act cct 346
Ala Gly Val Gln Trp Arg Asp Leu Gly Leu Leu Gln Pro Pro Thr Pro

85 90 95
ggg ttc aag tgattcttat gcctcagcct cccgagtaac tgggactaca 395
Gly Phe Lys

100
ggtgcacgtc accacgcctg actagttttt gtatttttag tagagatggg attttacttt 455

ggtggccagg ctggtcttga acccctggcc tcaagtgatc caccacactt ggccctcccaa 515

agtgctggga ttacaggtat gatcaaccac gcctggccat gtcatgcctt gtgacagaat 575

tcctttattc tgttttgagc caataaatat ttatagggtt cgaaaaaaaa aaaaaaaaaa 634

<210> 232

<211> 583

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> 76..498

<400> 232

aatatagcca gccgcgggtg cccttgcgct tcccagagctg gcgggggtccg tgggtgcggga 60

tcgagattgc gggct atg gcg ccg aag gtt ttt cgt cag tac tgg gat atc 111

Met Ala Pro Lys Val Phe Arg Gln Tyr Trp Asp Ile

1 5 10

ccc gat ggc acc gat tgc cac cgc aaa gcc tac agc acc acc agt att 159

Pro Asp Gly Thr Asp Cys His Arg Lys Ala Tyr Ser Thr Thr Ser Ile

15 20 25

gcc agc gtc gct ggc ctg acc gcc gct gcc tac aga gtc aca ctc aat 207

Ala Ser Val Ala Gly Leu Thr Ala Ala Ala Tyr Arg Val Thr Leu Asn

30 35 40

cct ccg ggc acc ttc ctt gaa gga gtg gct aag gtt gga caa tac acg 255

Pro Pro Gly Thr Phe Leu Glu Gly Val Ala Lys Val Gly Gln Tyr Thr

45 50 55 60

ttc act gca gct gct gtc ggg gcc gtg ttt ggc ctc acc acc tgc atc 303

Phe Thr Ala Ala Ala Val Gly Ala Val Phe Gly Leu Thr Thr Cys Ile

65 70 75

agc gcc cat gtc cgc gag aag ccc gac gac ccc ctg aac tac ttc ctc 351

Ser Ala His Val Arg Glu Lys Pro Asp Asp Pro Leu Asn Tyr Phe Leu

	80	85	90	
ggt ggc tgc gcc gga ggc ctg act ctg gga gca cgc acg cac aac tac				399
Gly Gly Cys Ala Gly Gly Leu Thr Leu Gly Ala Arg Thr His Asn Tyr				
	95	100	105	
ggg att ggc gcc gcc gcc tgc gtg tac ttt ggc ata gcg gcc tcc ctg				447
Gly Ile Gly Ala Ala Ala Cys Val Tyr Phe Gly Ile Ala Ala Ser Leu				
	110	115	120	
gtc aag atg ggc cgg ctg gag ggc tgg gag gtg ttt gca aaa ccc aag				495
Val Lys Met Gly Arg Leu Glu Gly Trp Glu Val Phe Ala Lys Pro Lys				
	125	130	135	140
gtg tgagccctgt gcctgccggg acctccagcc tgcagaatgc gtccagaaat				548
Val				
aaattctgtg tctgtgtgaa aaaaaaaaaa aaaaa				583

<210> 233

<211> 753

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> 199..600

<400> 233

atttttccga tgccaggcac cctcaaggca cagaggctgg ggctcatgtt gggggcactt	60
ggcctctcca ggcctcgaag gcttctcttg gctgatgcga gctggggaac gggagggacg	120
gacgtgggag cgagaacgtc aactggagg cagctggtgg cagcatgggg gacagagtga	180
aagagccttc gtgtcacc atg gcc aca cac ccc gat ggc ttc cgg ctt gag	231
Met Ala Thr His Pro Asp Gly Phe Arg Leu Glu	
	1 5 10
gga ccc ctg gct gca gcc cac agc cct ggg cct tgc act gtg ctc tac	279
Gly Pro Leu Ala Ala Ala His Ser Pro Gly Pro Cys Thr Val Leu Tyr	
	15 20 25
gaa ggc cct gtc cgt ggg ctc tgc ccy ttt gcc ccg cga aat tcc aac	327
Glu Gly Pro Val Arg Gly Leu Cys Pro Phe Ala Pro Arg Asn Ser Asn	
	30 35 40
acc atg gcg gcg gct gcc ctg gct gcc ccc agc ctg ggc ttc gat ggg	375
Thr Met Ala Ala Ala Ala Leu Ala Ala Pro Ser Leu Gly Phe Asp Gly	
	45 50 55
gtg att ggg gtg ctc gtg gct gat acc agc ctc acg gac atg cac gtg	423
Val Ile Gly Val Leu Val Ala Asp Thr Ser Leu Thr Asp Met His Val	
	60 65 70 75
gtg gat gta gag ctg agc gga ccc cgg ggc ccc act ggc cga agc ttt	471
Val Asp Val Glu Leu Ser Gly Pro Arg Gly Pro Thr Gly Arg Ser Phe	
	80 85 90
gct gtg cac acc cgc aga gag aac cct gcc gag cca ggc gcg gtc acc	519
Ala Val His Thr Arg Arg Glu Asn Pro Ala Glu Pro Gly Ala Val Thr	
	95 100 105
ggc tcc gcc acc gtc acg gcc ttc tgg cgg agc ctc ctg gcc tgc tgc	567
Gly Ser Ala Thr Val Thr Ala Phe Trp Arg Ser Leu Leu Ala Cys Cys	
	110 115 120
cag ctc ccc tcc agg ccg ggg atc cat ctc tgc tgagaagcct cctccctccc	620
Gln Leu Pro Ser Arg Pro Gly Ile His Leu Cys	
	125 130
gagacaagat catctgcctg gcctctcacc accaccatcc caccctgcc ctgccccact	680
ccccagggt ctccttctg actcagtaaa gatcaccgct gcctcccccc gcaaataaaa	740
aaaaaaaaa aaa	753

<210> 234
 <211> 762
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> 211..612

<400> 234
 atttccgatg ccaggcaccc tcaaggcaca gaggctgggg ctcatgttgg gggcacttgg 60
 cctctccagg cctcgaaggc ttctcctggg ctgatgagag ctggggaacg ggagggacgg 120
 acgtgggagc gagaacgtca cactggaggc agctggtggc acgatggggg acagagtgaa 180
 aggtagcaag tcaagagcct tcgtgtcacc atg gcc aca cac ccc gat ggc ttc 234
 Met Ala Thr His Pro Asp Gly Phe
 1 5
 cgg ctt gag gga ccc ctg gct gca gcg cac agc cct ggg cct tgc act 282
 Arg Leu Glu Gly Pro Leu Ala Ala Ala His Ser Pro Gly Pro Cys Thr
 10 15 20
 gtg ctc tac gaa ggc cct gtc cgt ggg ctc tgc ccc ttt gcc ccg cga 330
 Val Leu Tyr Glu Gly Pro Val Arg Gly Leu Cys Pro Phe Ala Pro Arg
 25 30 35 40
 aat tcc aac acc atg tgc gcg gct gcc ctg gct gcc ccc agc ctg ggc 378
 Asn Ser Asn Thr Met Ser Ala Ala Ala Leu Ala Ala Pro Ser Leu Gly
 45 50 55
 ttc gat ggg gtg att ggg gtg ctc gtg gct gat acc agc ctc acg gac 426
 Phe Asp Gly Val Ile Gly Val Leu Val Ala Asp Thr Ser Leu Thr Asp
 60 65 70
 atg cac gtg gtg gat gta gag ctg agc gga ccc cgg ggc ccc acg tgc 474
 Met His Val Val Asp Val Glu Leu Ser Gly Pro Arg Gly Pro Thr Cys
 75 80 85
 cga agc ttt gct gtg cac acc cgc aga gag aac cct gcc gag cca ggc 522
 Arg Ser Phe Ala Val His Thr Arg Arg Glu Asn Pro Ala Glu Pro Gly
 90 95 100
 gcg gtc acc ggc tcc gcc acc gtc acg gcc ttc tgg cgg agc ctc ctg 570
 Ala Val Thr Gly Ser Ala Thr Val Thr Ala Phe Trp Arg Ser Leu Leu
 105 110 115 120
 gcc tgc tgc cag ctc ccc tcc agg ccg ggg atc cat ctc tgc 612
 Ala Cys Cys Gln Leu Pro Ser Arg Pro Gly Ile His Leu Cys
 125 130
 tgagaagcct cctccctccc gagacaagat catctgcctg gcctctcacc accaccatcc 672
 caccctgcc ctgccccact tccccagggt ctcccttctg actcagtaaa gatcaccgct 732
 gcctcccccc gccaaaaaaaa aaaaaaaaaa 762

<210> 235
 <211> 537
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> 5..259

<400> 235
 aaaa atg cta aag gta gaa gca act ggt agt ccc gag gaa ggg tgg gcg 49
 Met Leu Lys Val Glu Ala Thr Gly Ser Pro Glu Glu Gly Trp Ala
 1 5 10 15
 ggt gga gag ccc cgg act gga gct cct gcg aac tcc cct tcc tgc cct 97

Gly	Gly	Glu	Pro	Arg	Thr	Gly	Ala	Pro	Ala	Asn	Ser	Pro	Ser	Cys	Pro		
			20						25					30			
cag	gag	atg	cca	ctg	cag	gac	cca	agg	agc	agg	gag	gag	gag	gcc	agg	145	
Gln	Glu	Met	Pro	Leu	Gln	Asp	Pro	Arg	Ser	Arg	Glu	Glu	Ala	Ala	Arg		
			35					40					45				
acc	cag	cag	cta	ttg	ctg	gcc	act	ctg	cag	gag	gca	gag	acc	acc	cag	193	
Thr	Gln	Gln	Leu	Leu	Leu	Ala	Thr	Leu	Gln	Glu	Ala	Ala	Thr	Thr	Gln		
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Glu	Asn	Val	Ala	Trp	Arg	Lys	Asn	Trp	Met	Val	Gly	Gly	Glu	Gly	Gly		
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gcc	agc	ggg	agg	tca	ccg	tgagaccgga	cttgccctccg	tgggcgccgg								289	
Ala	Ser	Gly	Arg	Ser	Pro												
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				15				20				25					
ctg	gtg	tct	tct	ctc	ttc	ttt	cat	gtc	cct	gct	gga	tta	ctg	gcc	ctc	148	
Leu	Val	Ser	Ser	Leu	Phe	Phe	His	Val	Pro	Ala	Gly	Leu	Leu	Ala	Leu		
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ttc	acc	ctc	aga	cat	cac	aaa	tat	ggg	agg	ttc	atg	tct	gta	agc	atc	196	
Phe	Thr	Leu	Arg	His	His	Lys	Tyr	Gly	Arg	Phe	Met	Ser	Val	Ser	Ile		
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Leu	Leu	Met	Gly	Ile	Val	Gly	Pro	Ile	Thr	Ala	Gly	Ile	Leu	Thr	Ser		
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Ala	Ala	Ile	Ala	Gly	Val	Tyr	Arg	Ala	Ala	Gly	Lys	Glu	Met	Ile	Pro		
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ttt	gaa	gcc	ctc	aca	ctg	ggc	act	gga	cag	aca	ttt	tgc	gtc	ttg	gtg	340	
Phe	Glu	Ala	Leu	Thr	Leu	Gly	Thr	Gly	Gln	Thr	Phe	Cys	Val	Leu	Val		
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gtc	tcc	ttt	tta	cgg	att	tta	gct	act	cta	tagcatacat	ccttatgctg					390	
Val	Ser	Phe	Leu	Arg	Ile	Leu	Ala	Thr	Leu								
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agttttgaaa	acaaatttgg	tgaaataaag	caggaaaaaa	aatttaagta	taactcaagt	930
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ggc aag ata	ttt gtc tct	gtc atg gtt	aaa ttg	caa aaa	aat aaa	ctt									103
Gly Lys Ile	Phe Val Ser	Val Met Val	Lys Leu Gln	Lys Asn	Lys Leu										
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acc tcc ttc	ccc agg cag	cca ttg tta	aca ttt ttt	gaa tat	cta gaa										151
Thr Ser Phe	Pro Arg Gln	Pro Leu Thr	Phe Phe Glu	Tyr Leu	Glu										
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aaa gtc ctt	tgt tca gga	tta ttt tcc	cac tct gcc	aag agt	cac cat										199
Lys Val Leu	Cys Ser Gly	Leu Phe Ser	His Ser Ala	Lys Ser	His His										
	40		45		50										
gac ctg ctc	aca cgc cac	cct tat gaa	act gcc gcg	cca ctt	ctc agc										247
Asp Leu Leu	Thr Arg His	Pro Tyr Glu	Thr Ala Ala	Pro Leu	Leu Ser										
	55		60		65										
tcc cat ttg	att ctc aca	gaa gct cta	cga aat ggg	ttg ggc	aaa tgt										295
Ser His Leu	Ile Leu Thr	Glu Ala Leu	Arg Asn Gly	Leu Gly	Lys Cys										
	70		75		80										
cat gat cct	cat ttc aca	ggg gaa gaa	act gag gcc	cag agg	ggg aaa										343
His Asp Pro	His Phe Thr	Gly Glu Glu	Thr Glu Ala	Gln Arg	Gly Lys										
	90		95		100										
ctg act acc	taaaattgcc	atgtaggccg	gcgcggtggc	tcacgcctgt											392
Leu Thr Thr															
aatcccagca	ctgtgggagg	ccaaggcggg	tggatcgcca	ggtcaggaga	tcgagaccat										452
cctggctggc	acttgaagcc	ccgtctctac	tagggataca	aataattggc	cgggtgtggt										512
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Leu	Trp	Gly	Gly	Val	Val	Lys	Ser	Cys	Phe	Glu	Gly	Lys	Gly	Pro	Gln	
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Arg	Glu	Ala	Gln	Pro	Ala	Ser	Pro	Gln	Ala	Ala	Pro	Pro	Gly	Pro	Thr	
				35				40					45			
aat	gag	gca	cag	atg	gca	gcc	gct	gcc	gcc	cta	gcc	cgg	ctg	gag	cag	191
Asn	Glu	Ala	Gln	Met	Ala	Ala	Ala	Ala	Ala	Leu	Ala	Arg	Leu	Glu	Gln	
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Lys	Gln	Ser	Arg	Ala	Trp	Gly	Pro	Thr	Ser	Gln	Asp	Thr	Ile	Arg	Asn	
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cag	gtg	aga	aag	gaa	ctt	caa	gcc	gaa	gcc	acc	gtc	agc	ggg	agc	ccc	287
Gln	Val	Arg	Lys	Glu	Leu	Gln	Ala	Glu	Ala	Thr	Val	Ser	Gly	Ser	Pro	
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gag	gcc	cca	ggg	acc	gtg	gta	tct	gag	ccc	aga	gag	gaa	ggc	tct		335
Glu	Ala	Pro	Gly	Thr	Asn	Val	Val	Ser	Glu	Pro	Arg	Glu	Glu	Gly	Ser	
				100					105				110			
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Ala	His	Leu	Ala	Val	Pro	Gly	Val	Tyr	Phe	Thr	Cys	Pro	Leu	Thr	Gly	
				115				120					125			
gcc	acc	ctg	agg	aag	gac	cag	cgg	gac	gcc	tgc	atc	aag	gag	gcc	att	431
Ala	Thr	Leu	Arg	Lys	Asp	Gln	Arg	Asp	Ala	Cys	Ile	Lys	Glu	Ala	Ile	
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ctc	ttg	cac	ttc	tcc	acc	gac	cca	gtg	gcc	gcc	tcc	atc	atg	aag	atc	479
Leu	Leu	His	Phe	Ser	Thr	Asp	Pro	Val	Ala	Ala	Ser	Ile	Met	Lys	Ile	
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tac	acg	ttc	aac	aaa	gac	cag	gac	cgg	gtg	aag	ctg	ggg	gtg	gac	acc	527
Tyr	Thr	Phe	Asn	Lys	Asp	Gln	Asp	Arg	Val	Lys	Leu	Gly	Val	Asp	Thr	
160				165				170					175			
att	gcc	aag	tac	ctg	gac	aac	atc	cac	ctg	cac	ccc	gag	gag	gag	aag	575
Ile	Ala	Lys	Tyr	Leu	Asp	Asn	Ile	His	Leu	His	Pro	Glu	Glu	Glu	Lys	
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Tyr	Arg	Lys	Ile	Lys	Leu	Gln	Asn	Lys	Val	Phe	Gln	Glu	Arg	Ile	Asn	
				195			200					205				
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Cys	Leu	Glu	Gly	Thr	His	Glu	Phe	Phe	Glu	Ala	Ile	Gly	Phe	Gln	Lys	
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gtg	ttg	ctt	ccc	gcc	cag	gat	cag	gag	gac	ccc	gag	gag	ttc	tac	gtg	719
Val	Leu	Leu	Pro	Ala	Gln	Asp	Gln	Glu	Asp	Pro	Glu	Glu	Phe	Tyr	Val	
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Leu	Ser	Glu	Thr	Thr	Leu	Ala	Gln	Pro	Gln	Ser	Leu	Glu	Arg	His	Lys	
				240		245				250				255		
gaa	cag	ctg	ctg	gct	gcg	gag	ccc	gtg	cgc	gcc	aag	ctg	gac	agg	cag	815
Glu	Gln	Leu	Leu	Ala	Ala	Glu	Pro	Val	Arg	Ala	Lys	Leu	Asp	Arg	Gln	
				260			265						270			
cgc	cgc	gtc	ttc	cag	ccc	tcg	ccc	ctg	gcc	tcg	cag	ttc	gaa	ctg	cct	863
Arg	Arg	Val	Phe	Gln	Pro	Ser	Pro	Leu	Ala	Ser	Gln	Phe	Glu	Leu	Pro	
				275			280					285				
ggg	gac	ttc	ttc	aac	ctc	aca	gca	gag	gag	atc	aag	cgg	gag	cag	agg	911
Gly	Asp	Phe	Phe	Asn	Leu	Thr	Ala	Glu	Glu	Ile	Lys	Arg	Glu	Gln	Arg	
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ctc	agg	tcc	gag	gcg	gtg	gag	cgg	ctg	agc	gtg	ctg	cgg	acc	aag	gcc	959
Leu	Arg	Ser	Glu	Ala	Val	Glu	Arg	Leu	Ser	Val	Leu	Arg	Thr	Lys	Ala	

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Met Arg Glu Lys Glu Glu Gln Arg Gly Leu Arg Lys Tyr Asn Tyr Thr			
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ctg ctg cgc gtg cgc ctc ccc gat ggc tgc ctc ctg cag ggc act ttc			1055
Leu Leu Arg Val Arg Leu Pro Asp Gly Cys Leu Leu Gln Gly Thr Phe			
340	345	350	
tac gct cgg gag cgg ctg ggg gcg gtg tac ggg ttc gtc cgg gag gcc			1103
Tyr Ala Arg Glu Arg Leu Gly Ala Val Tyr Gly Phe Val Arg Glu Ala			
355	360	365	
ctg cag agc gac tgg ctg cct ttt gag ctg ctg gcc tcg gga ggg cag			1151
Leu Gln Ser Asp Trp Leu Pro Phe Glu Leu Leu Ala Ser Gly Gly Gln			
370	375	380	
aag ctg tcc gag gac gag aac ctg gcc ttg aac gag tgc ggg ctg gtg			1199
Lys Leu Ser Glu Asp Glu Asn Leu Ala Leu Asn Glu Cys Gly Leu Val			
385	390	395	
ccc tct gcc ctc ctg acc ttc tcg tgg gac atg gct gtg ctg gag gac			1247
Pro Ser Ala Leu Leu Thr Phe Ser Trp Asp Met Ala Val Leu Glu Asp			
400	405	410	415
atc aag gcc gcg ggg gcc gag ccg gac tcc atc ctg aaa ccc gag ctc			1295
Ile Lys Ala Ala Glu Ala Glu Pro Asp Ser Ile Leu Lys Pro Glu Leu			
420	425	430	
ctg tca gcc atc gag aag ctc ttg tgaaataaaa gcagggttg cctcagccct			1349
Leu Ser Ala Ile Glu Lys Leu Leu			
435			
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aatggctgat agagtccaca gaacacgctg tcctcatctc agagaggaga actctgaacc	300
cagaggggaa ggatttacct gcagttgtat ggcaagccag aggtaggcgc tgcactggaa	360
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Met Trp Ala Arg Leu Pro His Thr Pro Glu Gln Met Gly His Arg Leu	
1 5 10 15	
ata ggt ccc aag gaa gct tca ctt cat gtg gta ccc agc tgg cca gcc	516
Ile Gly Pro Lys Glu Ala Ser Leu His Val Val Pro Ser Trp Pro Ala	
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agg aag atg gag ggg ctt ctg gct ggc ctc tct tcc tct cct aga aag	564

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Ser	Cys	Trp	Pro	Phe	Trp	Val	His	Gly	Pro	Lys	Val	His	Glu	Gly	Gly	
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tct	gcc	tgt	gag	aca	tca	agc	tcc	tgg	gtt	gaa	gga	ctt	gga	tta	aga	660
Ser	Ala	Cys	Glu	Thr	Ser	Ser	Ser	Trp	Val	Glu	Gly	Leu	Gly	Leu	Arg	
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Arg	Val	Thr	Ser	Val	His	Ser	Leu	Cys	Gln	Gly	Leu	Gly	Ala	Ser	Val	
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Gln	Leu	Leu	Pro	Gly	Pro	Pro	Pro	Thr	Thr	Thr	Ser	Asp	Lys	Asn	Asn	
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Tyr	Thr	Ser	Gly													
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Tyr	Glu	Lys	Phe	Phe	Ser	Ser	Tyr	Leu	Val	Thr	Leu	Thr	Arg	Arg	Ala	
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Thr	Val	Lys	Arg	Tyr	Val	Arg	Lys	Gly	Val	Pro	Leu	Glu	His	Arg	Ala	
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Pro	Gly	Tyr	Tyr	His	Gln	Leu	Leu	Gln	Gly	Glu	Arg	Asn	Pro	Arg	Leu	
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Gly Met Asn Phe Ile Ala Gly Tyr Leu Ile Leu Ile Thr Asn Asn Glu
    160                      165                      170
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gacctggcgc aggccgtata gactcaggtc ctgatgaggg cgttgtggga gctgtacctg     1370
acaggccttc tgaggaagcc aagacgccag gagaggtcca ggccctgggag tcagtagttt     1430
cctaagaggg agtggaggct cggggccact ctgggtgcag catggcaaac gtgggcggta     1490
tttcagcagc tgggccttca tcaaagagaa gaccatgttg gccgggcgcg gtggctcacg     1550
cctgcagtc cagcactttg ggaggccaag gcgtgtggat cacctgaggt caggagtcca     1610
agaccagcct ggccaacacg gtgaaacccc gtctctacta aaaaatacaa aaattagcca     1670
ggtgtggtgg ctcacgctta tgtagtccca gttactcggg aggctgaggc acgagaatca     1730
cttgaacctg ggaggcggag gttgcagtga gccgagatcg cgccactgca ctccagcctg     1790
ggcaacagag tgagactctg tctcaaaaaa aaaaaaaaaa a                      1831

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<210> 241
 <211> 1830
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> 78..608

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<400> 241
aaggacttaa gcgccccgga gccgggaggc gaacttgga cccgctggcc tcgctcggtg      60
cgcgcctccc tccccgc atg cag ccc gcc gag cgc tcg cgg gtc ccc agg      110
                Met Gln Pro Ala Glu Arg Ser Arg Val Pro Arg
                1                      5                      10
atc gac ccg tac gga ttc gag cgg cct gag gac ttc gac gac gcc gcc      158
Ile Asp Pro Tyr Gly Phe Glu Arg Pro Glu Asp Phe Asp Asp Ala Ala
                15                      20                      25
tac gag aag ttt ttc tcc agc tac ctg gtc acg ctc acc cgc agg gcg      206
Tyr Glu Lys Phe Phe Ser Ser Tyr Leu Val Thr Leu Thr Arg Arg Ala
                30                      35                      40
atc aaa tgg tcc cgg ctg ctg cag ggc ggc ggc gtc ccc agg agc cgg      254
Ile Lys Trp Ser Arg Leu Leu Gln Gly Gly Gly Val Pro Arg Ser Arg
                45                      50                      55
aca gtg aag cgc tat gtc cgg aaa ggc gtc ccg ctg gag cac cgt gcc      302
Thr Val Lys Arg Tyr Val Arg Lys Gly Val Pro Leu Glu His Arg Ala
        60                      65                      70                      75
cgc gtc tgg atg gtg ctg agt ggg gcc cag gcg cag atg gac cag aat      350

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Arg	Val	Trp	Met	Val	Leu	Ser	Gly	Ala	Gln	Ala	Gln	Met	Asp	Gln	Asn	
				80					85					90		
ccc	ggc	tac	tac	cac	cag	ctt	ctc	cag	gga	gag	aga	aac	ccc	agg	ctg	398
Pro	Gly	Tyr	Tyr	His	Gln	Leu	Leu	Gln	Gly	Glu	Arg	Asn	Pro	Arg	Leu	
			95					100				105				
gag	gac	gcc	atc	agg	aca	gac	ctg	aac	cgg	acc	ttc	ccc	gac	aac	gtg	446
Glu	Asp	Ala	Ile	Arg	Thr	Asp	Leu	Asn	Arg	Thr	Phe	Pro	Asp	Asn	Val	
		110					115				120					
aag	ttc	cgg	aag	acc	acg	gac	ccc	tgc	tta	cag	agg	acc	ctg	tac	aat	494
Lys	Phe	Arg	Lys	Thr	Thr	Asp	Pro	Cys	Leu	Gln	Arg	Thr	Leu	Tyr	Asn	
	125					130					135					
gtg	ctg	ctg	gca	tat	ggg	cac	cat	aac	cag	gga	gtg	ggc	tac	tgc	cag	542
Val	Leu	Leu	Ala	Tyr	Gly	His	His	Asn	Gln	Gly	Val	Gly	Tyr	Cys	Gln	
	140				145				150						155	
gga	atg	aat	ttt	ata	gca	gga	tat	ctg	att	ctt	ata	aca	aat	aat	gat	590
Gly	Met	Asn	Phe	Ile	Ala	Gly	Tyr	Leu	Ile	Leu	Ile	Thr	Asn	Asn	Asp	
				160				165						170		
aag	aat	ctt	ttt	ggc	tgt	tagatgctct	tgttggaaga	ataclaccag								638
Lys	Asn	Leu	Phe	Gly	Cys											
			175													
attactacag	cccgccatg	ctgggcctga	agaccgacca	ggaggtcctc	ggggagctgg											698
tgcgggcgaa	gctgccggct	gtggggggccc	tgatggagcg	tctcgggtgtg	ctgtggacgc											758
tgctggtgtc	ccgctgggttc	atctgcctgt	ttgtggacat	cttgcccgtg	gagacagtgc											818
ttcggatctg	ggactgtttg	tttaacgaag	gctcgaagat	tatcttccgg	ttggccctga											878
ccttaattaa	gcagcaccag	gagttgattt	tggaagccac	cagcgttcca	gacatttgcg											938
ataagtttaa	gcagataacc	aaagggagtt	tcgtgatgga	gtgtcacacg	tttatgcagg											998
tgtgtggggc	tgacagtggc	tcagtcacct	cccagggggc	cccgcctcac	ctgcagcccc											1058
ggggctgctc	tgaccacccg	gaggatgcac	aggatgggca	ccagtgggca	tagggcacag											1118
gatgagcctc	cagctctgtc	ctgcactctc	cccctgcgcc	tggcctccga	gggctttcct											1178
gtctatggcg	gcctgtctct	cttgggccctg	gcactgcgga	cgtgtctcct	ggtcctaattg											1238
gctgtactca	tctgtctgtg	gtggtgccag	aagtgtggct	ttccgaggcc	cggcctcccc											1298
actgggtcct	ggacctggcg	caggccgtat	agactcaggt	cctgatgagg	gcgttgtggg											1358
agctgtacct	gacaggcctt	ctgaggaagc	caagacgcca	ggagaggctc	aggcctggga											1418
gtcagtagtt	tcctaagagg	gagtggaggc	tcggggccac	tctgggtgca	gcatggcaaa											1478
cgtgggcggg	atttcagcag	ctgggccttc	atcaaagaga	agaccatgtt	ggccggggcg											1538
ggtggctcac	gcctgcagtc	ccagcacttt	gggaggccaa	ggcgtgtgga	tcacctgagg											1598
tcaggagttc	aagaccagcc	tgcccaacac	ggtgaaaccc	cgtctctact	aaaaaataca											1658
aaaattagcc	aggtgtggcg	gtcacgcctt	atgtagtccc	agttactcgg	gaggctgagg											1718
cacgagaatc	acttgaacct	gggaggcgga	ggttgcaagt	agccgagatc	gcgccactgc											1778
actccagcct	gggcaacaga	gtgagactct	gtctcaaaaa	aaaaaaaaaa	aa											1830

<210> 242

<211> 508

<212> PRT

<213> Homo sapiens

<220>

<221> SIGNAL

<222> -27..-1

<400> 242

Met	Asp	Pro	Lys	Leu	Gly	Arg	Met	Ala	Ala	Ser	Leu	Leu	Ala	Val	Leu	
	-25						-20					-15				
Leu	Leu	Leu	Leu	Leu	Glu	Arg	Gly	Met	Phe	Ser	Ser	Pro	Ser	Pro	Pro	
	-10					-5				1					5	
Pro	Ala	Leu	Leu	Glu	Lys	Val	Phe	Gln	Tyr	Ile	Asp	Leu	His	Gln	Asp	
				10				15						20		
Glu	Phe	Val	Gln	Thr	Leu	Lys	Glu	Trp	Val	Ala	Ile	Glu	Ser	Asp	Ser	

<210> 243
 <211> 331
 <212> PRT
 <213> Homo sapiens

<220>
 <221> SIGNAL
 <222> -31...-1

<400> 243
 Met Trp Leu Trp Glu Asp Gln Gly Gly Leu Leu Gly Pro Phe Ser Phe
 -30 -25 -20
 Leu Leu Leu Val Leu Leu Leu Val Thr Arg Ser Pro Val Asn Ala Cys
 -15 -10 -5 1
 Leu Leu Thr Gly Ser Leu Phe Val Leu Leu Arg Val Phe Ser Phe Glu
 5 10 15
 Pro Val Pro Ser Cys Arg Ala Leu Gln Val Leu Lys Pro Arg Asp Arg
 20 25 30
 Ile Ser Ala Ile Ala His Arg Gly Gly Ser His Asp Ala Pro Glu Asn
 35 40 45
 Thr Leu Ala Ala Ile Arg Gln Ala Ala Lys Asn Gly Ala Thr Gly Val
 50 55 60 65
 Glu Leu Asp Ile Glu Phe Thr Ser Asp Gly Ile Pro Val Leu Met His
 70 75 80
 Asp Asn Thr Val Asp Arg Thr Thr Asp Gly Thr Gly Arg Leu Cys Asp
 85 90 95
 Leu Thr Phe Glu Gln Ile Arg Lys Leu Asn Pro Ala Ala Asn His Arg
 100 105 110
 Leu Arg Asn Asp Phe Pro Asp Glu Lys Ile Pro Thr Leu Met Glu Ala
 115 120 125
 Val Ala Glu Cys Leu Asn His Asn Leu Thr Ile Phe Phe Asp Val Lys
 130 135 140 145
 Gly His Ala His Lys Ala Thr Glu Ala Leu Lys Lys Met Tyr Met Glu
 150 155 160
 Phe Pro Gln Leu Tyr Asn Asn Ser Val Val Cys Ser Phe Leu Pro Glu
 165 170 175
 Val Ile Tyr Lys Met Arg Gln Thr Asp Arg Asp Val Ile Thr Ala Leu
 180 185 190
 Thr His Arg Pro Trp Ser Leu Ser His Thr Gly Asp Gly Lys Pro Arg
 195 200 205
 Tyr Asp Thr Phe Trp Lys His Phe Ile Phe Val Met Met Asp Ile Leu
 210 215 220 225
 Leu Asp Trp Ser Met His Asn Ile Leu Trp Tyr Leu Cys Gly Ile Ser
 230 235 240
 Ala Phe Leu Met Gln Lys Asp Phe Val Ser Pro Ala Tyr Leu Lys Lys
 245 250 255
 Trp Ser Ala Lys Gly Ile Gln Val Val Gly Trp Thr Val Asn Thr Phe
 260 265 270
 Asp Glu Lys Ser Tyr Tyr Glu Ser His Leu Gly Ser Ser Tyr Ile Thr
 275 280 285
 Asp Ser Met Val Glu Asp Cys Glu Pro His Phe
 290 295 300

<210> 244
 <211> 274
 <212> PRT
 <213> Homo sapiens

<220>
 <221> SIGNAL
 <222> -17..-1

<400> 244
 Met Asp Arg Pro Gly Phe Val Ala Ala Leu Val Ala Gly Gly Val Ala
 -15 -10 -5
 Gly Val Ser Val Asp Leu Ile Leu Phe Pro Leu Asp Thr Ile Lys Thr
 1 5 10 15
 Arg Leu Gln Ser Pro Gln Gly Phe Ser Lys Ala Gly Gly Phe His Gly
 20 25 30
 Ile Tyr Ala Gly Val Pro Ser Ala Ala Ile Gly Ser Phe Pro Asn Ala
 35 40 45
 Ala Ala Phe Phe Ile Thr Tyr Glu Tyr Val Lys Trp Phe Leu His Ala
 50 55 60
 Asp Ser Ser Ser Tyr Leu Thr Pro Met Lys His Met Leu Ala Ala Ser
 65 70 75
 Ala Gly Glu Val Val Ala Cys Leu Ile Arg Val Pro Ser Glu Val Val
 80 85 90 95
 Lys Gln Arg Ala Gln Val Ser Ala Ser Thr Arg Thr Phe Gln Ile Phe
 100 105 110
 Ser Asn Ile Leu Tyr Glu Glu Gly Ile Gln Gly Leu Tyr Arg Gly Tyr
 115 120 125
 Lys Ser Thr Val Leu Arg Glu Ile Pro Phe Ser Leu Val Gln Phe Pro
 130 135 140
 Leu Trp Glu Ser Leu Lys Ala Leu Trp Ser Trp Arg Gln Asp His Val
 145 150 155
 Val Asp Ser Trp Gln Ser Ala Val Cys Gly Ala Phe Ala Gly Gly Phe
 160 165 170 175
 Ala Ala Ala Val Thr Thr Pro Leu Asp Val Ala Lys Thr Arg Ile Met
 180 185 190
 Leu Ala Lys Ala Gly Ser Ser Thr Ala Asp Gly Asn Val Leu Ser Val
 195 200 205
 Leu His Gly Val Trp Arg Ser Gln Gly Leu Ala Gly Leu Phe Ala Gly
 210 215 220
 Val Phe Pro Arg Met Ala Ala Ile Ser Leu Gly Gly Phe Ile Phe Leu
 225 230 235
 Gly Ala Tyr Asp Arg Thr His Ser Leu Leu Leu Glu Val Gly Arg Lys
 240 245 250 255
 Ser Pro

<210> 245
 <211> 406
 <212> PRT
 <213> Homo sapiens

<220>
 <221> SIGNAL
 <222> -35..-1

<400> 245
 Met Arg Gly Ser Val Glu Cys Thr Trp Gly Trp Gly His Cys Ala Pro
 -35 -30 -25 -20
 Ser Pro Leu Leu Leu Trp Thr Leu Leu Leu Phe Ala Ala Pro Phe Gly
 -15 -10 -5
 Leu Leu Gly Glu Lys Thr Arg Gln Val Ser Leu Glu Val Ile Pro Asn
 1 5 10
 Trp Leu Gly Pro Leu Gln Asn Leu Leu His Ile Arg Ala Val Gly Thr

Pro Ser Ala Ser Val Ile Arg Thr
1 5

<210> 247
<211> 348
<212> PRT
<213> Homo sapiens

<220>
<221> SIGNAL
<222> -29...-1

<400> 247
Met Ala Pro Gln Ser Leu Pro Ser Ser Arg Met Ala Pro Leu Gly Met
-25 -20 -15
Leu Leu Gly Pro Leu Met Ala Ala Cys Phe Thr Phe Cys Leu Ser His
-10 -5 1
Gln Asn Leu Lys Glu Phe Ala Leu Thr Asn Pro Glu Lys Ser Ser Thr
5 10 15
Lys Glu Thr Glu Arg Lys Glu Thr Lys Ala Glu Glu Leu Asp Ala
20 25 30 35
Glu Val Leu Glu Val Phe His Pro Thr His Glu Trp Gln Ala Leu Gln
40 45 50
Pro Gly Gln Ala Val Pro Ala Gly Ser His Val Arg Leu Asn Leu Gln
55 60 65
Thr Gly Glu Arg Glu Ala Lys Leu Gln Tyr Glu Asp Lys Phe Arg Asn
70 75 80
Asn Leu Lys Gly Lys Arg Leu Asp Ile Asn Thr Asn Thr Tyr Thr Ser
85 90 95
Gln Asp Leu Lys Ser Ala Leu Ala Lys Phe Lys Glu Gly Ala Glu Met
100 105 110 115
Glu Ser Ser Lys Glu Asp Lys Ala Arg Gln Ala Glu Val Lys Arg Leu
120 125 130
Phe Arg Pro Ile Glu Glu Leu Lys Lys Asp Phe Asp Glu Leu Asn Val
135 140 145
Val Ile Glu Thr Asp Met Gln Ile Met Val Arg Leu Ile Asn Lys Phe
150 155 160
Asn Ser Ser Ser Ser Ser Leu Glu Glu Lys Ile Ala Ala Leu Phe Asp
165 170 175
Leu Glu Tyr Tyr Val His Gln Met Asp Asn Ala Gln Asp Leu Leu Ser
180 185 190 195
Phe Gly Gly Leu Gln Val Val Ile Asn Gly Leu Asn Ser Thr Glu Pro
200 205 210
Leu Val Lys Glu Tyr Ala Ala Phe Val Leu Gly Ala Ala Phe Ser Ser
215 220 225
Asn Pro Lys Val Gln Val Glu Ala Ile Glu Gly Gly Ala Leu Gln Lys
230 235 240
Leu Leu Val Ile Leu Ala Thr Glu Gln Pro Leu Thr Ala Lys Lys Lys
245 250 255
Val Leu Phe Ala Leu Cys Ser Leu Leu Arg His Phe Pro Tyr Ala Gln
260 265 270 275
Arg Gln Phe Leu Lys Leu Gly Gly Leu Gln Val Leu Arg Thr Leu Val
280 285 290
Gln Glu Lys Gly Thr Glu Val Leu Ala Val Arg Val Val Thr Leu Leu
295 300 305
Tyr Asp Leu Val Thr Glu Lys Met Phe Ala Glu Glu
310 315

<210> 248
 <211> 397
 <212> PRT
 <213> Homo sapiens

<220>
 <221> SIGNAL
 <222> -36..-1

<400> 248
 Met Glu Glu Leu Gln Glu Pro Leu Arg Gly Gln Leu Arg Leu Cys Phe
 -35 -30 -25
 Thr Gln Ala Ala Arg Thr Ser Leu Leu Leu Leu Arg Leu Asn Asp Ala
 -20 -15 -10 -5
 Ala Leu Arg Ala Leu Gln Glu Cys Gln Arg Gln Gln Val Arg Pro Val
 1 5 10
 Ile Ala Phe Gln Gly His Arg Gly Tyr Leu Arg Leu Pro Gly Pro Gly
 15 20 25
 Trp Ser Cys Leu Phe Ser Phe Ile Val Ser Gln Cys Cys Gln Glu Gly
 30 35 40
 Ala Gly Gly Ser Leu Asp Leu Val Cys Gln Arg Phe Leu Arg Ser Gly
 45 50 55 60
 Pro Asn Ser Leu His Cys Leu Gly Ser Leu Arg Glu Arg Leu Ile Ile
 65 70 75
 Trp Ala Ala Met Asp Ser Ile Pro Ala Pro Ser Ser Val Gln Gly His
 80 85 90
 Asn Leu Thr Glu Asp Ala Arg His Pro Glu Ser Trp Gln Asn Thr Gly
 95 100 105
 Gly Tyr Ser Glu Gly Asp Ala Val Ser Gln Pro Gln Met Ala Leu Glu
 110 115 120
 Glu Val Ser Val Ser Asp Pro Leu Ala Ser Asn Gln Gly Gln Ser Leu
 125 130 135 140
 Pro Gly Ser Ser Arg Glu His Met Ala Gln Trp Glu Val Arg Ser Gln
 145 150 155
 Thr His Val Pro Asn Arg Glu Pro Val Gln Ala Leu Pro Ser Ser Ala
 160 165 170
 Ser Arg Lys Arg Leu Asp Lys Lys Arg Ser Val Pro Val Ala Thr Val
 175 180 185
 Glu Leu Glu Glu Lys Arg Phe Arg Thr Leu Pro Leu Val Pro Ser Pro
 190 195 200
 Leu Gln Gly Leu Thr Asn Gln Asp Leu Gln Glu Gly Glu Asp Trp Glu
 205 210 215 220
 Gln Glu Asp Glu Asp Met Asp Pro Arg Leu Glu His Ser Ser Ser Val
 225 230 235
 Gln Glu Asp Ser Glu Ser Pro Ser Pro Glu Asp Ile Pro Asp Tyr Leu
 240 245 250
 Leu Gln Tyr Arg Ala Ile His Ser Ala Glu Gln Gln His Ala Tyr Glu
 255 260 265
 Gln Asp Phe Glu Thr Asp Tyr Ala Glu Tyr Arg Ile Leu His Ala Arg
 270 275 280
 Val Gly Thr Ala Ser Gln Arg Phe Ile Glu Leu Gly Ala Glu Ile Lys
 285 290 295 300
 Arg Val Arg Arg Gly Thr Pro Glu Tyr Lys Val Leu Glu Asp Lys Ile
 305 310 315
 Ile Gln Glu Tyr Lys Lys Phe Arg Lys Gln Tyr Pro Ser Tyr Arg Glu
 320 325 330
 Glu Lys Arg Arg Cys Glu Tyr Leu His Gln Lys Leu Ser His Ile Lys
 335 340 345

Gly Leu Ile Leu Glu Phe Glu Glu Lys Asn Arg Gly Ser
 350 355 360

<210> 249
 <211> 403
 <212> PRT
 <213> Homo sapiens

<220>
 <221> SIGNAL
 <222> -21...-1

<400> 249

Met	Val	Asn	Asp	Pro	Pro	Val	Pro	Ala	Leu	Leu	Trp	Ala	Gln	Glu	Val
-20						-15					-10				
Gly	Gln	Val	Leu	Ala	Gly	Arg	Ala	Arg	Arg	Leu	Leu	Leu	Gln	Phe	Gly
-5					1			5						10	
Val	Leu	Phe	Cys	Thr	Ile	Leu	Leu	Leu	Leu	Trp	Val	Scr	Val	Phe	Leu
			15					20					25		
Tyr	Gly	Ser	Phe	Tyr	Tyr	Ser	Tyr	Met	Pro	Thr	Val	Ser	His	Leu	Ser
		30					35					40			
Pro	Val	His	Phe	Tyr	Tyr	Arg	Thr	Asp	Cys	Asp	Ser	Ser	Thr	Thr	Ser
		45				50					55				
Leu	Cys	Ser	Phe	Pro	Val	Ala	Asn	Val	Ser	Leu	Thr	Lys	Gly	Gly	Arg
60					65			70							75
Asp	Arg	Val	Leu	Met	Tyr	Gly	Gln	Pro	Tyr	Arg	Val	Thr	Leu	Glu	Leu
				80				85						90	
Glu	Leu	Pro	Glu	Ser	Pro	Val	Asn	Gln	Asp	Leu	Gly	Met	Phe	Leu	Val
			95					100					105		
Thr	Ile	Ser	Cys	Tyr	Thr	Arg	Gly	Gly	Arg	Ile	Ile	Ser	Thr	Ser	Ser
		110					115					120			
Arg	Ser	Val	Met	Leu	His	Tyr	Arg	Ser	Asp	Leu	Leu	Gln	Met	Leu	Asp
		125				130						135			
Thr	Leu	Val	Phe	Ser	Ser	Leu	Leu	Leu	Phe	Gly	Phe	Ala	Glu	Gln	Lys
140					145					150					155
Gln	Leu	Leu	Glu	Val	Glu	Leu	Tyr	Ala	Asp	Tyr	Arg	Glu	Asn	Ser	Val
				160					165						170
Ser	Glu	Tyr	Val	Pro	Thr	Thr	Gly	Ala	Ile	Ile	Glu	Ile	His	Ser	Lys
			175				180						185		
Arg	Ile	Gln	Leu	Tyr	Gly	Ala	Tyr	Leu	Arg	Ile	His	Ala	His	Phe	Thr
		190					195					200			
Gly	Leu	Arg	Tyr	Leu	Leu	Tyr	Asn	Phe	Pro	Met	Thr	Cys	Ala	Phe	Ile
		205				210					215				
Gly	Val	Ala	Ser	Asn	Phe	Thr	Phe	Leu	Ser	Val	Ile	Val	Leu	Phe	Ser
220					225					230					235
Tyr	Met	Gln	Trp	Val	Trp	Gly	Gly	Ile	Trp	Pro	Arg	His	Arg	Phe	Ser
				240					245					250	
Leu	Gln	Val	Asn	Ile	Arg	Lys	Arg	Asp	Asn	Ser	Arg	Lys	Glu	Val	Gln
			255					260					265		
Arg	Arg	Ile	Ser	Ala	His	Gln	Pro	Gly	Ala	Gly	Pro	Glu	Gly	Gln	Glu
		270					275					280			
Glu	Ser	Thr	Pro	Gln	Ser	Asp	Val	Thr	Glu	Asp	Gly	Glu	Ser	Pro	Glu
		285				290					295				
Asp	Pro	Ser	Gly	Thr	Glu	Gly	Gln	Leu	Ser	Glu	Glu	Glu	Lys	Pro	Asp
300					305					310					315
Gln	Gln	Pro	Leu	Ser	Gly	Glu	Glu	Glu	Leu	Glu	Pro	Glu	Ala	Ser	Asp
				320					325				330		
Gly	Ser	Gly	Ser	Trp	Glu	Asp	Ala	Ala	Leu	Leu	Thr	Glu	Ala	Asn	Leu

335 340 345
 Pro Ala Pro Ala Pro Ala Ser Ala Ser Ala Pro Val Leu Glu Thr Leu
 350 355 360
 Gly Ser Ser Glu Pro Ala Gly Gly Ala Leu Arg Gln Arg Pro Thr Cys
 365 370 375
 Ser Ser Ser
 380

<210> 250
 <211> 111
 <212> PRT
 <213> Homo sapiens

<220>
 <221> SIGNAL
 <222> -26...-1

<400> 250
 Met Pro His Leu Met Glu Arg Met Val Gly Ser Gly Leu Leu Trp Leu
 -25 -20 -15
 Ala Leu Val Ser Cys Ile Leu Thr Gln Ala Ser Ala Val Gln Arg Gly
 -10 -5 1 5
 Tyr Gly Asn Pro Ile Glu Ala Ser Ser Tyr Gly Leu Asp Leu Asp Cys
 10 15 20
 Gly Ala Pro Gly Thr Pro Glu Ala His Val Cys Phe Asp Pro Cys Gln
 25 30 35
 Asn Tyr Thr Leu Leu Asp Leu Gly Pro Ile Thr Arg Arg Gly Ala Gln
 40 45 50
 Ser Pro Gly Val Met Asn Gly Thr Pro Ser Thr Ala Gly Phe Leu Val
 55 60 65 70
 Ala Trp Pro Met Val Leu Leu Thr Val Leu Leu Ala Trp Leu Phe
 75 80 85

<210> 251
 <211> 72
 <212> PRT
 <213> Homo sapiens

<220>
 <221> SIGNAL
 <222> -17...-1

<400> 251
 Met Asp Arg Pro Gly Phe Val Ala Ala Leu Val Ala Gly Gly Val Ala
 -15 -10 -5
 Gly Val Ser Val Asp Leu Ile Leu Phe Pro Leu Asp Thr Ile Lys Thr
 1 5 10 15
 Arg Leu Gln Ser Pro Gln Gly Phe Asn Lys Ala Gly Gly Phe His Gly
 20 25 30
 Ile Tyr Ala Gly Val Pro Ser Ala Ala Ile Gly Ser Phe Pro Asn Gly
 35 40 45
 Cys Leu Pro Asp Ser Ser Ser Ile
 50 55

<210> 252
 <211> 138
 <212> PRT
 <213> Homo sapiens

<220>
 <221> SIGNAL
 <222> -15..-1

<400> 252

Met	Lys	Phe	Thr	Thr	Leu	Leu	Phe	Leu	Ala	Ala	Val	Ala	Gly	Ala	Leu
-15					-10				-5						1
Val	Tyr	Ala	Glu	Asp	Ala	Ser	Ser	Asp	Ser	Thr	Gly	Ala	Asp	Pro	Ala
		5					10					15			
Gln	Glu	Ala	Gly	Thr	Ser	Lys	Pro	Asn	Glu	Glu	Ile	Ser	Gly	Pro	Ala
	20						25					30			
Glu	Pro	Ala	Ser	Pro	Pro	Glu	Thr	Thr	Thr	Thr	Ala	Gln	Glu	Thr	Ser
	35					40					45				
Ala	Ala	Ala	Val	Gln	Gly	Thr	Ala	Lys	Val	Thr	Ser	Ser	Arg	Gln	Glu
50				55					60						65
Leu	Asn	Pro	Leu	Lys	Ser	Ile	Val	Glu	Lys	Ser	Ile	Leu	Leu	Thr	Glu
			70					75						80	
Gln	Ala	Leu	Ala	Lys	Ala	Gly	Lys	Gly	Met	His	Gly	Gly	Val	Pro	Gly
		85					90					95			
Gly	Lys	Gln	Phe	Ile	Glu	Asn	Gly	Ser	Glu	Phe	Ala	Gln	Lys	Leu	Leu
	100						105					110			
Lys	Lys	Phe	Ser	Leu	Leu	Lys	Pro	Trp	Ala						
	115					120									

<210> 253
 <211> 108
 <212> PRT
 <213> Homo sapiens

<220>
 <221> SIGNAL
 <222> -31..-1

<220>
 <221> UNSURE
 <222> 45
 <223> Xaa = Glu,Gln

<220>
 <221> UNSURE
 <222> 44
 <223> Xaa = Lys,Asn

<400> 253

Met	Trp	Leu	Trp	Glu	Asp	Gln	Gly	Gly	Leu	Leu	Gly	Pro	Phe	Ser	Phe
-30						-25					-20				
Leu	Leu	Leu	Val	Leu	Leu	Val	Thr	Arg	Ser	Pro	Val	Asn	Ala	Cys	
-15				-10				-5						1	
Leu	Leu	Thr	Gly	Ser	Leu	Phe	Val	Leu	Leu	Arg	Val	Phe	Ser	Phe	Glu
		5					10				15				
Pro	Val	Pro	Ser	Cys	Arg	Ala	Leu	Gln	Val	Leu	Lys	Pro	Arg	Asp	Arg
	20					25					30				
Ile	Ser	Ala	Ile	Ala	His	Arg	Gly	Gly	Ser	Xaa	Xaa	Ala	Pro	Glu	Asn
	35				40					45					
Thr	Leu	Ala	Ala	Ile	Arg	Gln	Leu	Arg	Met	Glu	Gln	Gln	Ala	Trp	Ser
50				55					60						65
Trp	Thr	Leu	Ser	Leu	Leu	Leu	Thr	Gly	Phe	Leu	Ser				

<210> 254
 <211> 147
 <212> PRT
 <213> Homo sapiens

<220>
 <221> SIGNAL
 <222> -24...-1

<400> 254
 Met Val Met Gly Leu Gly Val Leu Leu Leu Val Phe Val Leu Gly Leu
 -20 -15 -10
 Gly Leu Thr Pro Pro Thr Leu Ala Gln Asp Asn Ser Arg Tyr Thr His
 -5 1 5
 Phe Leu Thr Gln His Tyr Asp Ala Lys Pro Gln Gly Arg Asp Asp Arg
 10 15 20
 Tyr Cys Glu Ser Ile Met Arg Arg Arg Gly Leu Thr Ser Pro Cys Lys
 25 30 35 40
 Asp Ile Asn Thr Phe Ile His Gly Asn Lys Arg Thr Ile Lys Ala Ile
 45 50 55
 Cys Glu Asn Lys Asn Gly Asn Pro His Arg Glu Asn Leu Arg Ile Ser
 60 65 70
 Lys Ser Ser Phe Gln Val Thr Thr Cys Lys Leu His Gly Gly Ser Pro
 75 80 85
 Trp Pro Pro Cys Gln Tyr Arg Ala Thr Ala Gly Phe Arg Asn Val Val
 90 95 100
 Val Ala Cys Glu Asn Gly Leu Pro Val His Leu Asp Gln Ser Ile Phe
 105 110 115 120
 Arg Arg Pro

<210> 255
 <211> 381
 <212> PRT
 <213> Homo sapiens

<220>
 <221> SIGNAL
 <222> -33...-1

<400> 255
 Met Ser Trp Thr Val Pro Val Val Arg Ala Ser Gln Arg Val Ser Ser
 -30 -25 -20
 Val Gly Ala Asn Phe Leu Cys Leu Gly Met Ala Leu Cys Pro Arg Gln
 -15 -10 -5
 Ala Thr Arg Ile Pro Leu Asn Gly Thr Trp Leu Phe Thr Pro Val Ser
 1 5 10 15
 Lys Met Ala Thr Val Lys Ser Glu Leu Ile Glu Arg Phe Thr Ser Glu
 20 25 30
 Lys Pro Val His Ser Lys Val Ser Ile Ile Gly Thr Gly Ser Val
 35 40 45
 Gly Met Ala Cys Ala Ile Ser Ile Leu Leu Lys Gly Leu Ser Asp Glu
 50 55 60
 Leu Ala Leu Val Asp Leu Asp Glu Asp Lys Leu Lys Gly Glu Thr Met
 65 70 75
 Asp Leu Gln His Gly Ser Pro Phe Thr Lys Met Pro Asn Ile Val Cys
 80 85 90 95

Ser	Lys	Asp	Tyr	Phe	Val	Thr	Ala	Asn	Ser	Asn	Leu	Val	Ile	Ile	Thr
				100					105					110	
Ala	Gly	Ala	Arg	Gln	Glu	Lys	Gly	Glu	Thr	Arg	Leu	Asn	Leu	Val	Gln
			115					120					125		
Arg	Asn	Val	Ala	Ile	Phe	Lys	Leu	Met	Ile	Ser	Ser	Ile	Val	Gln	Tyr
		130					135					140			
Ser	Pro	His	Cys	Lys	Leu	Ile	Ile	Val	Ser	Asn	Pro	Val	Asp	Ile	Leu
	145					150					155				
Thr	Tyr	Val	Ala	Trp	Lys	Leu	Ser	Ala	Phe	Pro	Lys	Asn	Arg	Ile	Ile
160					165				170					175	
Gly	Ser	Gly	Cys	Asn	Leu	Asp	Thr	Ala	Arg	Phe	Arg	Phe	Leu	Ile	Gly
				180					185					190	
Gln	Lys	Leu	Gly	Ile	His	Ser	Glu	Ser	Cys	His	Gly	Trp	Ile	Leu	Gly
			195				200						205		
Glu	His	Gly	Asp	Ser	Ser	Val	Pro	Val	Trp	Ser	Gly	Val	Asn	Ile	Ala
	210						215					220			
Gly	Val	Pro	Leu	Lys	Asp	Leu	Asn	Ser	Asp	Ile	Gly	Thr	Asp	Lys	Asp
	225					230					235				
Pro	Glu	Gln	Trp	Lys	Asn	Val	His	Lys	Glu	Val	Thr	Ala	Thr	Ala	Tyr
240					245					250				255	
Glu	Ile	Ile	Lys	Met	Lys	Gly	Tyr	Thr	Ser	Trp	Ala	Ile	Gly	Leu	Ser
				260					265					270	
Val	Ala	Asp	Leu	Thr	Glu	Ser	Ile	Leu	Lys	Asn	Leu	Arg	Arg	Ile	His
		275						280					285		
Pro	Val	Ser	Thr	Ile	Ile	Lys	Gly	Leu	Tyr	Gly	Ile	Asp	Glu	Glu	Val
	290						295					300			
Phe	Leu	Ser	Ile	Pro	Cys	Ile	Leu	Gly	Glu	Asn	Gly	Ile	Thr	Asn	Leu
	305					310					315				
Ile	Lys	Ile	Lys	Leu	Thr	Pro	Glu	Glu	Glu	Ala	His	Leu	Lys	Lys	Ser
320					325					330					335
Ala	Lys	Thr	Leu	Trp	Glu	Ile	Gln	Asn	Lys	Leu	Lys	Leu			
				340					345						

<210> 256
 <211> 139
 <212> PRT
 <213> Homo sapiens

<220>
 <221> SIGNAL
 <222> -33..-1

<400> 256

Met	Ser	Trp	Thr	Val	Pro	Val	Val	Arg	Ala	Ser	Gln	Arg	Met	Ser	Ser
			-30					-25					-20		
Val	Gly	Ala	Asn	Phe	Leu	Cys	Leu	Gly	Met	Ala	Leu	Cys	Leu	Arg	Gln
		-15					-10					-5			
Ala	Thr	Arg	Ile	Pro	Leu	Asn	Gly	Thr	Trp	Leu	Phe	Thr	Pro	Val	Ser
1				5					10					15	
Lys	Met	Ala	Thr	Val	Lys	Ser	Glu	Leu	Ile	Glu	Arg	Phe	Thr	Ser	Glu
				20				25						30	
Lys	Pro	Val	His	Ser	Lys	Val	Ser	Ile	Ile	Gly	Thr	Gly	Ser	Val	
			35				40					45			
Gly	Met	Ala	Cys	Ala	Ile	Ser	Ile	Leu	Leu	Lys	Gly	Leu	Ser	Asp	Glu
		50					55					60			
Leu	Ala	Leu	Val	Asp	Leu	Asp	Glu	Asp	Lys	Leu	Lys	Gly	Glu	Thr	Met
	65					70					75				
Asp	Leu	Gln	His	Gly	Ser	Pro	Phe	Thr	Lys	Met	Pro	Ile	Leu	Phe	Val

80		85		90		95				
Ala	Lys	Ile	Thr	Leu	Ser	Gln	Gln	Thr	Pro	Thr
				100					105	

<210> 257
 <211> 265
 <212> PRT
 <213> Homo sapiens

<220>
 <221> SIGNAL
 <222> -14...-1

<400> 257	Met	Asn	Phe	Ile	Leu	Phe	Ile	Phe	Ile	Pro	Gly	Val	Phe	Ser	Leu	Lys	
					-10					-5					1		
	Ser	Ser	Thr	Leu	Lys	Pro	Thr	Ile	Glu	Ala	Leu	Pro	Asn	Val	Leu	Pro	
			5					10					15				
	Leu	Asn	Glu	Asp	Val	Asn	Lys	Gln	Glu	Glu	Lys	Asn	Glu	Asp	His	Thr	
		20				25						30					
	Pro	Asn	Tyr	Ala	Pro	Ala	Asn	Glu	Lys	Asn	Gly	Asn	Tyr	Tyr	Lys	Asp	
	35					40				45					50		
	Ile	Lys	Gln	Tyr	Val	Phe	Thr	Thr	Gln	Asn	Pro	Asn	Gly	Thr	Glu	Ser	
					55					60					65		
	Glu	Ile	Ser	Val	Arg	Ala	Thr	Thr	Asp	Leu	Asn	Phe	Ala	Leu	Lys	Asn	
				70					75					80			
	Gly	Ser	Thr	Pro	Asn	Val	Pro	Ala	Phe	Trp	Thr	Met	Leu	Ala	Lys	Ala	
			85					90					95				
	Ile	Asn	Gly	Thr	Ala	Val	Val	Met	Asp	Asp	Lys	Asp	Gln	Leu	Phe	His	
		100					105					110					
	Pro	Ile	Pro	Glu	Ser	Asp	Val	Asn	Ala	Thr	Gln	Gly	Glu	Asn	Gln	Pro	
	115					120					125					130	
	Asp	Leu	Glu	Asp	Leu	Lys	Ile	Lys	Ile	Met	Leu	Gly	Ile	Ser	Leu	Met	
					135					140					145		
	Thr	Leu	Leu	Leu	Phe	Val	Val	Leu	Leu	Ala	Phe	Cys	Ser	Ala	Thr	Leu	
				150					155					160			
	Tyr	Lys	Leu	Arg	His	Leu	Ser	Tyr	Lys	Ser	Cys	Glu	Ser	Gln	Tyr	Ser	
				165				170					175				
	Val	Asn	Pro	Glu	Leu	Ala	Thr	Met	Ser	Tyr	Phe	His	Pro	Ser	Glu	Gly	
		180				185						190					
	Val	Ser	Asp	Thr	Ser	Phe	Ser	Lys	Ser	Ala	Glu	Ser	Ser	Thr	Phe	Leu	
	195					200					205					210	
	Gly	Thr	Thr	Ser	Ser	Asp	Met	Arg	Arg	Ser	Gly	Thr	Arg	Thr	Ser	Glu	
				215						220					225		
	Ser	Lys	Ile	Met	Thr	Asp	Ile	Ile	Ser	Ile	Gly	Ser	Asp	Asn	Glu	Met	
				230					235					240			
	His	Glu	Asn	Asp	Glu	Ser	Val	Thr	Arg								
				245				250									

<210> 258
 <211> 200
 <212> PRT
 <213> Homo sapiens

<220>
 <221> SIGNAL
 <222> -20...-1

<400> 258
 Met Asp Ser Ser Thr Ala His Ser Pro Val Phe Leu Val Phe Pro Pro
 -20 -15 -10 -5
 Glu Ile Thr Ala Ser Glu Tyr Glu Ser Thr Glu Leu Ser Ala Thr Thr
 1 5 10
 Phe Ser Thr Gln Ser Pro Leu Gln Lys Leu Phe Ala Arg Lys Met Lys
 15 20 25
 Ile Leu Gly Thr Ile Gln Ile Leu Phe Gly Ile Met Thr Phe Ser Phe
 30 35 40
 Gly Val Ile Phe Leu Phe Thr Leu Leu Lys Pro Tyr Pro Arg Phe Pro
 45 50 55 60
 Phe Ile Phe Leu Ser Gly Tyr Pro Phe Trp Gly Ser Val Leu Phe Ile
 65 70 75
 Asn Ser Gly Ala Phe Leu Ile Ala Val Lys Arg Lys Thr Thr Glu Thr
 80 85 90
 Leu Ile Ile Leu Ser Arg Ile Met Asn Phe Leu Ser Ala Leu Gly Ala
 95 100 105
 Ile Ala Gly Ile Ile Leu Leu Thr Phe Gly Phe Ile Leu Asp Gln Asn
 110 115 120
 Tyr Ile Cys Gly Tyr Ser His Gln Asn Ser Gln Cys Lys Ala Val Thr
 125 130 135 140
 Val Leu Phe Leu Gly Ile Leu Ile Thr Leu Met Thr Phe Ser Ile Ile
 145 150 155
 Glu Leu Phe Ile Ser Leu Pro Phe Ser Ile Leu Gly Cys His Ser Glu
 160 165 170
 Asp Cys Asp Cys Glu Gln Cys Cys
 175 180

<210> 259
 <211> 394
 <212> PRT
 <213> Homo sapiens

<220>
 <221> SIGNAL
 <222> -39...-1

<400> 259
 Met Ala Thr Ala Gln Leu Gln Arg Thr Pro Met Ser Ala Leu Val Phe
 -35 -30 -25
 Pro Asn Lys Ile Ser Thr Glu His Gln Ser Leu Val Leu Val Lys Arg
 -20 -15 -10
 Leu Leu Ala Val Ser Val Ser Cys Ile Thr Tyr Leu Arg Gly Ile Phe
 -5 1 5
 Pro Glu Cys Ala Tyr Gly Thr Arg Tyr Leu Asp Asp Leu Cys Val Lys
 10 15 20 25
 Ile Leu Arg Glu Asp Lys Asn Cys Pro Gly Ser Thr Gln Leu Val Lys
 30 35 40
 Trp Ile Leu Gly Cys Tyr Asp Ala Leu Gln Lys Lys Tyr Leu Arg Met
 45 50 55
 Val Val Leu Ala Val Tyr Thr Asn Pro Glu Asp Pro Gln Thr Ile Ser
 60 65 70
 Glu Cys Tyr Gln Phe Lys Phe Lys Tyr Thr Asn Asn Gly Pro Leu Met
 75 80 85
 Asp Phe Ile Ser Lys Asn Gln Ser Asn Glu Ser Met Leu Ser Thr
 90 95 100 105
 Asp Thr Lys Lys Ala Ser Ile Leu Leu Ile Arg Lys Ile Tyr Ile Leu
 110 115 120

Met	Gln	Asn	Leu	Gly	Pro	Leu	Pro	Asn	Asp	Val	Cys	Leu	Thr	Met	Lys
			125					130					135		
Leu	Phe	Tyr	Tyr	Asp	Glu	Val	Thr	Pro	Pro	Asp	Tyr	Gln	Pro	Pro	Gly
			140					145				150			
Phe	Lys	Asp	Gly	Asp	Cys	Glu	Gly	Val	Ile	Phe	Glu	Gly	Glu	Pro	Met
			155				160				165				
Tyr	Leu	Asn	Val	Gly	Glu	Val	Ser	Thr	Pro	Phe	His	Ile	Phe	Lys	Val
170						175				180					185
Lys	Val	Thr	Thr	Glu	Arg	Glu	Arg	Met	Glu	Asn	Ile	Asp	Ser	Thr	Ile
				190					195					200	
Leu	Ser	Pro	Lys	Gln	Ile	Lys	Thr	Pro	Phe	Gln	Lys	Ile	Leu	Arg	Asp
			205					210					215		
Lys	Asp	Val	Glu	Asp	Glu	Gln	Glu	His	Tyr	Thr	Ser	Asp	Asp	Leu	Asp
			220				225					230			
Ile	Glu	Thr	Lys	Met	Glu	Glu	Gln	Glu	Lys	Asn	Pro	Ala	Ser	Ser	Glu
			235			240					245				
Leu	Glu	Glu	Pro	Ser	Leu	Val	Cys	Glu	Glu	Asp	Glu	Ile	Met	Arg	Ser
250					255					260					265
Lys	Glu	Ser	Pro	Asp	Leu	Ser	Ile	Ser	His	Ser	Gln	Val	Glu	Gln	Leu
				270					275					280	
Val	Asn	Lys	Thr	Ser	Glu	Leu	Asp	Met	Ser	Glu	Ser	Lys	Thr	Arg	Ser
			285					290					295		
Gly	Lys	Val	Phe	Gln	Asn	Lys	Met	Ala	Asn	Gly	Asn	Gln	Pro	Val	Lys
			300				305					310			
Ser	Ser	Lys	Glu	Asn	Arg	Lys	Arg	Ser	Gln	His	Glu	Ser	Gly	Arg	Ile
			315			320					325				
Val	Leu	His	His	Phe	Asp	Ser	Ser	Ser	Gln	Glu	Ser	Val	Pro	Lys	Arg
330					335					340					345
Arg	Lys	Phe	Ser	Glu	Pro	Lys	Glu	His	Ile						
				350					355						

<210> 260

<211> 158

<212> PRT

<213> Homo sapiens

<220>

<221> SIGNAL

<222> -17..-1

<400> 260

Met	Ala	Leu	Glu	Val	Leu	Met	Leu	Leu	Ala	Val	Leu	Ile	Trp	Thr	Gly
		-15					-10					-5			
Ala	Glu	Asn	Leu	His	Val	Lys	Ile	Ser	Cys	Ser	Leu	Asp	Trp	Leu	Met
					5					10					15
Val	Ser	Val	Ile	Pro	Val	Ala	Glu	Ser	Arg	Asn	Leu	Tyr	Ile	Phe	Ala
				20					25					30	
Asp	Glu	Leu	His	Leu	Gly	Met	Gly	Cys	Pro	Ala	Asn	Arg	Ile	His	Thr
			35				40					45			
Tyr	Val	Tyr	Glu	Phe	Ile	Tyr	Leu	Val	Arg	Asp	Cys	Gly	Ile	Arg	Thr
		50				55					60				
Arg	Val	Val	Ser	Glu	Glu	Thr	Leu	Leu	Phe	Gln	Thr	Glu	Leu	Tyr	Phe
					70						75				
Thr	Pro	Arg	Asn	Ile	Asp	His	Asp	Pro	Gln	Glu	Ile	His	Leu	Glu	Cys
80					85					90					95
Ser	Thr	Ser	Arg	Lys	Ser	Val	Trp	Leu	Thr	Pro	Val	Ser	Thr	Glu	Asn
				100					105					110	
Glu	Ile	Lys	Leu	Asp	Pro	Ser	Pro	Phe	Ile	Ala	Asp	Phe	Gln	Thr	Thr

			115					120				125			
Ala	Glu	Glu	Leu	Gly	Leu	Leu	Ser	Ser	Ser	Pro	Asn	Leu	Leu		
		130					135					140			

<210> 261
 <211> 233
 <212> PRT
 <213> Homo sapiens

<220>
 <221> SIGNAL
 <222> -32...-1

<400> 261
 Met Ala Thr Pro Pro Phe Arg Leu Ile Arg Lys Met Phe Ser Phe Lys
 -30 -25 -20
 Val Ser Arg Trp Met Gly Leu Ala Cys Phe Arg Ser Leu Ala Ala Ser
 -15 -10 -5
 Ser Pro Ser Ile Arg Gln Lys Lys Leu Met His Lys Leu Gln Glu Glu
 1 5 10 15
 Lys Ala Phe Arg Glu Glu Met Lys Ile Phe Arg Glu Lys Ile Glu Asp
 20 25 30
 Phe Arg Glu Glu Met Trp Thr Phe Arg Gly Lys Ile His Ala Phe Arg
 35 40 45
 Gly Gln Ile Leu Gly Phe Trp Glu Glu Glu Arg Pro Phe Trp Glu Glu
 50 55 60
 Glu Lys Thr Phe Trp Lys Glu Glu Lys Ser Phe Trp Glu Met Glu Lys
 65 70 75 80
 Ser Phe Arg Glu Glu Lys Thr Phe Trp Lys Lys Tyr Arg Thr Phe
 85 90 95
 Trp Lys Glu Asp Lys Ala Phe Trp Lys Glu Asp Asn Ala Leu Trp Glu
 100 105 110
 Arg Asp Arg Asn Leu Leu Gln Glu Asp Lys Ala Leu Trp Glu Glu Glu
 115 120 125
 Lys Ala Leu Trp Val Glu Glu Arg Ala Leu Leu Glu Gly Glu Lys Ala
 130 135 140
 Leu Trp Glu Asp Lys Thr Ser Leu Trp Glu Glu Asn Ala Leu Trp
 145 150 155 160
 Glu Glu Glu Arg Ala Phe Trp Met Glu Asn Asn Gly His Ile Ala Gly
 165 170 175
 Glu Gln Met Leu Glu Asp Gly Pro His Asn Ala Asn Arg Gly Gln Arg
 180 185 190
 Leu Leu Ala Phe Ser Arg Gly Arg Ala
 195 200

<210> 262
 <211> 67
 <212> PRT
 <213> Homo sapiens

<220>
 <221> SIGNAL
 <222> -20...-1

<400> 262
 Met Asp Ser Ser Thr Ala His Ser Pro Val Phe Leu Val Phe Pro Pro
 -20 -15 -10 -5
 Glu Ile Thr Ala Ser Glu Tyr Glu Ser Thr Glu Leu Ser Ala Thr Thr

1 5 10
 Phe Ser Thr Gln Ser Pro Leu Gln Lys Leu Phe Ala Arg Lys Met Lys
 15 20 25
 Ile Leu Gly Asp Ile His Ser Gly Ala Leu Phe Cys Ser Leu Ile Leu
 30 35 40
 Glu Pro Ser
 45

<210> 263
 <211> 94
 <212> PRT
 <213> Homo sapiens

<220>
 <221> SIGNAL
 <222> -25..-1

<400> 263
 Met Cys Phe Leu Val Ser Phe Asn Leu Pro Ile His Ile Ser Leu Ser
 -25 -20 -15 -10
 His Leu Phe Leu Asp Leu Ser Arg Ser Leu Trp Phe Leu Ala Cys Pro
 -5 1 5
 Gly Leu Asn Leu Val Tyr Leu Ala Leu Asp Ser Phe Ser Asp Leu Arg
 10 15 20
 Pro Ser Leu Asn Leu Leu Phe Tyr Phe Val Pro Gly Phe Gly Val Ser
 25 30 35
 Lys Tyr Leu Thr Ser Ala Gln Pro Val Leu Gly Phe Leu Leu Leu Pro
 40 45 50 55
 Asp Ile Asp Asn Pro Ala Leu Leu Gly Thr Glu Arg Trp Ser
 60 65

<210> 264
 <211> 174
 <212> PRT
 <213> Homo sapiens

<220>
 <221> SIGNAL
 <222> -19..-1

<400> 264
 Met Phe Leu Thr Val Lys Leu Leu Leu Gly Gln Arg Cys Ser Leu Lys
 -15 -10 -5
 Val Ser Gly Gln Glu Ser Val Ala Thr Leu Lys Arg Leu Val Ser Arg
 1 5 10
 Arg Leu Lys Val Pro Glu Glu Gln Gln His Leu Leu Phe Arg Gly Gln
 15 20 25
 Leu Leu Glu Asp Asp Lys His Leu Ser Asp Tyr Cys Ile Gly Pro Asn
 30 35 40 45
 Ala Ser Ile Asn Val Ile Met Gln Pro Leu Glu Lys Met Ala Leu Lys
 50 55 60
 Glu Ala His Gln Pro Gln Thr Gln Pro Leu Trp His Gln Leu Gly Leu
 65 70 75
 Val Leu Ala Lys His Phe Glu Pro Gln Asp Ala Lys Ala Val Leu Gln
 80 85 90
 Leu Leu Arg Gln Glu His Glu Glu Arg Leu Gln Lys Ile Ser Leu Glu
 95 100 105
 His Leu Glu Gln Leu Ala Gln Tyr Leu Leu Ala Glu Glu Pro His Val

110 115 120 125
 Glu Pro Ala Gly Glu Arg Glu Leu Glu Ala Lys Ala Arg Pro Gln Ser
 130 135 140
 Ser Cys Asp Met Glu Glu Lys Glu Glu Ala Ala Ala Asp Gln
 145 150 155

<210> 265
 <211> 106
 <212> PRT
 <213> Homo sapiens

<220>
 <221> SIGNAL
 <222> -17...-1

<400> 265
 Met Ala Leu Glu Val Leu Met Leu Leu Ala Val Leu Ile Trp Thr Gly
 -15 -10 -5
 Ala Glu Asn Leu His Val Lys Ile Ser Cys Ser Leu Asp Trp Leu Met
 1 5 10 15
 Val Ser Val Ile Pro Val Ala Glu Ser Arg Asn Leu Tyr Ile Phe Ala
 20 25 30
 Asp Glu Leu His Leu Gly Met Gly Cys Pro Ala Asn Arg Ile His Thr
 35 40 45
 Tyr Val Tyr Glu Phe Ile Tyr Leu Val Arg Asp Cys Gly Ile Arg Thr
 50 55 60
 Arg Val Arg Thr Val Ile Val Cys Lys Lys Tyr Cys Met Phe Cys Gln
 65 70 75
 Thr Phe Met Pro Ser Ile Lys Ile Val Phe
 80 85

<210> 266
 <211> 124
 <212> PRT
 <213> Homo sapiens

<220>
 <221> SIGNAL
 <222> -18...-1

<400> 266
 Met Val Leu Cys Trp Leu Leu Leu Leu Val Met Ala Leu Pro Pro Gly
 -15 -10 -5
 Thr Thr Gly Val Lys Asp Cys Val Phe Cys Glu Leu Thr Asp Ser Met
 1 5 10
 Gln Cys Pro Gly Thr Tyr Met His Cys Gly Asp Asp Glu Asp Cys Phe
 15 20 25 30
 Thr Gly His Gly Val Ala Pro Gly Thr Gly Pro Val Ile Asn Lys Gly
 35 40 45
 Cys Leu Arg Ala Thr Ser Cys Gly Leu Glu Glu Pro Val Ser Tyr Arg
 50 55 60
 Gly Val Thr Tyr Ser Leu Thr Thr Asn Cys Cys Thr Gly Arg Leu Cys
 65 70 75
 Asn Arg Ala Pro Ser Ser Gln Thr Val Gly Ala Thr Thr Ser Leu Ala
 80 85 90
 Leu Gly Leu Gly Met Leu Leu Pro Pro Arg Leu Leu
 95 100 105

<210> 267
 <211> 261
 <212> PRT
 <213> Homo sapiens

<220>
 <221> SIGNAL
 <222> -16...-1

<400> 267
 Met Glu Asn Phe Ser Leu Leu Ser Ile Ser Gly Pro Pro Ile Ser Ser
 -15 -10 -5
 Ser Ala Leu Ser Ala Phe Pro Asp Ile Met Phe Ser Arg Ala Thr Ser
 1 5 10 15
 Leu Pro Asp Ile Ala Lys Thr Ala Val Pro Thr Glu Ala Ser Ser Pro
 20 25 30
 Ala Gln Ala Leu Pro Pro Gln Tyr Gln Ser Ile Ile Val Arg Gln Gly
 35 40 45
 Ile Gln Asn Thr Val Leu Ser Pro Asp Cys Ser Leu Gly Asp Thr Gln
 50 55 60
 His Gly Glu Lys Leu Arg Arg Asn Cys Thr Ile Tyr Arg Pro Trp Phe
 65 70 75 80
 Ser Pro Tyr Ser Tyr Phe Val Cys Ala Asp Lys Glu Ser Gln Leu Glu
 85 90 95
 Ala Tyr Asp Phe Pro Glu Val Gln Gln Asp Glu Gly Lys Trp Asp Asn
 100 105 110
 Cys Leu Ser Glu Asp Met Ala Glu Asn Ile Cys Ser Ser Ser Ser
 115 120 125
 Pro Glu Asn Thr Cys Pro Arg Glu Ala Thr Lys Lys Ser Arg His Gly
 130 135 140
 Leu Asp Ser Ile Thr Ser Gln Asp Ile Leu Met Ala Ser Arg Trp His
 145 150 155 160
 Pro Ala Gln Gln Asn Gly Tyr Lys Cys Val Ala Cys Cys Arg Met Tyr
 165 170 175
 Pro Thr Leu Asp Phe Leu Lys Ser His Ile Lys Arg Gly Phe Arg Glu
 180 185 190
 Gly Phe Ser Cys Lys Val Tyr Tyr Arg Lys Leu Lys Ala Leu Trp Ser
 195 200 205
 Lys Glu Gln Lys Ala Arg Leu Gly Asp Arg Leu Ser Ser Gly Ser Cys
 210 215 220
 Gln Ala Phe Asn Ser Pro Ala Glu His Leu Arg Gln Ile Gly Gly Glu
 225 230 235 240
 Ala Tyr Leu Cys Leu
 245

<210> 268
 <211> 76
 <212> PRT
 <213> Homo sapiens

<220>
 <221> SIGNAL
 <222> -25...-1

<400> 268
 Met Cys Met Ser Leu Ser Met Lys Val Pro Cys Cys Leu Cys Ala Leu
 -25 -20 -15 -10
 Leu Ser Asn Phe Cys Pro Ser Thr Thr Val Lys Gly Asp Val Val Thr

				-5					1				5				
Ser	Phe	Phe	Arg	Ala	Asp	Tyr	Asp	Leu	Ala	Ser	Arg	Ser	Ala	Asp	Gln		
		10					15					20					
Ser	Ser	Gln	Lys	Val	Lys	Leu	Arg	Met	Phe	Thr	Gly	Arg	Leu	Pro	Ile		
	25					30					35						
Gly	Pro	Phe	Ala	Ser	Val	Gly	Asn	Ala	Ala	Glu	Leu						
40					45					50							

<210> 269
 <211> 199
 <212> PRT
 <213> Homo sapiens

<220>
 <221> SIGNAL
 <222> -16...-1

Met	Glu	Thr	Phe	Pro	Leu	Leu	Leu	Leu	Ser	Leu	Gly	Leu	Val	Leu	Ala		
	-15				-10						-5						
Glu	Ala	Ser	Glu	Ser	Thr	Met	Lys	Ile	Ile	Lys	Glu	Glu	Phe	Thr	Asp		
1				5					10					15			
Glu	Glu	Met	Gln	Tyr	Asp	Met	Ala	Lys	Ser	Gly	Gln	Glu	Lys	Gln	Thr		
			20					25					30				
Ile	Glu	Ile	Leu	Met	Asn	Pro	Ile	Leu	Leu	Val	Lys	Asn	Thr	Ser	Leu		
	35					40					45						
Ser	Met	Ser	Lys	Asp	Asp	Met	Ser	Ser	Thr	Leu	Leu	Thr	Phe	Arg	Ser		
	50				55						60						
Leu	His	Tyr	Asn	Asp	Pro	Lys	Gly	Asn	Ser	Ser	Gly	Asn	Asp	Lys	Glu		
65					70				75						80		
Cys	Cys	Asn	Asp	Met	Thr	Val	Trp	Arg	Lys	Val	Ser	Glu	Ala	Asn	Gly		
			85						90					95			
Ser	Cys	Lys	Trp	Ser	Asn	Asn	Phe	Ile	Arg	Ser	Ser	Thr	Glu	Val	Met		
			100					105					110				
Arg	Arg	Val	His	Arg	Ala	Pro	Ser	Cys	Lys	Phe	Val	Gln	Asn	Pro	Gly		
		115				120						125					
Ile	Ser	Cys	Cys	Glu	Ser	Leu	Glu	Leu	Glu	Asn	Thr	Val	Cys	Gln	Phe		
	130					135					140						
Thr	Thr	Gly	Lys	Gln	Phe	Pro	Arg	Cys	Gln	Tyr	His	Ser	Val	Thr	Ser		
145					150				155						160		
Leu	Glu	Lys	Ile	Leu	Thr	Val	Leu	Thr	Gly	His	Ser	Leu	Met	Ser	Trp		
			165					170						175			
Leu	Val	Cys	Gly	Ser	Lys	Leu											
			180														

<210> 270
 <211> 88
 <212> PRT
 <213> Homo sapiens

<220>
 <221> SIGNAL
 <222> -36...-1

Met	Ala	Ser	Val	Val	Pro	Val	Lys	Asp	Lys	Lys	Leu	Leu	Glu	Val	Lys		
	-35					-30					-25						
Leu	Gly	Glu	Leu	Pro	Ser	Trp	Ile	Leu	Met	Arg	Asp	Phe	Ser	Pro	Ser		

-20					-15					-10					-5
Gly	Ile	Phe	Gly	Ala	Phe	Gln	Arg	Gly	Tyr	Tyr	Arg	Tyr	Tyr	Asn	Lys
				1				5					10		
Tyr	Ile	Asn	Val	Lys	Lys	Gly	Ser	Ile	Ser	Gly	Ile	Thr	Met	Val	Leu
		15					20					25			
Ala	Cys	Tyr	Val	Leu	Phe	Ser	Tyr	Ser	Phe	Ser	Tyr	Lys	His	Leu	Lys
	30					35					40				
His	Glu	Arg	Leu	Arg	Lys	Tyr	His								
45					50										

<210> 271
 <211> 481
 <212> PRT
 <213> Homo sapiens

<220>
 <221> SIGNAL
 <222> -25..-1

<400> 271

Met	Gly	Ala	Leu	Ala	Arg	Ala	Leu	Pro	Ser	Ile	Leu	Leu	Ala	Leu	Leu
-25					-20					-15					-10
Leu	Thr	Ser	Thr	Pro	Glu	Ala	Leu	Gly	Ala	Asn	Pro	Gly	Leu	Val	Ala
				-5					1				5		
Arg	Ile	Thr	Asp	Lys	Gly	Leu	Gln	Tyr	Ala	Ala	Gln	Glu	Gly	Leu	Leu
		10					15					20			
Ala	Leu	Gln	Ser	Glu	Leu	Leu	Arg	Ile	Thr	Leu	Pro	Asp	Phe	Thr	Gly
	25				30						35				
Asp	Leu	Arg	Ile	Pro	His	Val	Gly	Arg	Gly	Arg	Tyr	Glu	Phe	His	Ser
40					45					50					55
Leu	Asn	Ile	His	Ser	Cys	Glu	Leu	Leu	His	Ser	Ala	Leu	Arg	Pro	Val
				60					65					70	
Pro	Gly	Gln	Gly	Leu	Ser	Leu	Ser	Ile	Ser	Asp	Ser	Ser	Ile	Arg	Val
		75					80						85		
Gln	Gly	Arg	Trp	Lys	Val	Arg	Lys	Ser	Phe	Phe	Lys	Leu	Gln	Gly	Ser
	90					95						100			
Phe	Asp	Val	Ser	Val	Lys	Gly	Ile	Ser	Ile	Ser	Val	Asn	Leu	Leu	Leu
	105					110					115				
Gly	Ser	Asp	Ser	Ser	Gly	Arg	Pro	Thr	Val	Thr	Ala	Ser	Ser	Cys	Ser
120					125					130					135
Ser	Asp	Ile	Ala	Asp	Val	Glu	Val	Asp	Met	Ser	Gly	Asp	Leu	Gly	Trp
				140					145					150	
Leu	Leu	Asn	Leu	Phe	His	Asn	Gln	Ile	Glu	Ser	Lys	Phe	Gln	Lys	Val
		155					160						165		
Leu	Glu	Ser	Arg	Ile	Cys	Glu	Met	Ile	Gln	Lys	Ser	Val	Ser	Ser	Asp
	170					175						180			
Leu	Gln	Pro	Tyr	Leu	Gln	Thr	Leu	Thr	Val	Thr	Thr	Glu	Ile	Asp	Ser
	185					190					195				
Phe	Ala	Asp	Ile	Asp	Tyr	Ser	Leu	Val	Glu	Ala	Pro	Arg	Ala	Thr	Ala
200					205					210					215
Gln	Met	Leu	Glu	Val	Met	Phe	Lys	Gly	Glu	Ile	Phe	His	Arg	Asn	His
				220					225					230	
Arg	Ser	Pro	Val	Thr	Leu	Leu	Ala	Ala	Val	Met	Ser	Leu	Pro	Glu	Glu
		235					240						245		
His	Asn	Lys	Met	Val	Tyr	Phe	Ala	Ile	Ser	Asp	Tyr	Val	Phe	Asn	Thr
	250					255						260			
Ala	Ser	Leu	Val	Tyr	His	Glu	Glu	Gly	Tyr	Leu	Asn	Phe	Ser	Ile	Thr
	265					270					275				

Asp Asp Met Ile Pro Pro Asp Ser Asn Ile Arg Leu Thr Thr Lys Ser
 280 285 290 295
 Phe Arg Pro Phe Val Pro Arg Leu Ala Arg Leu Tyr Pro Asn Met Asn
 300 305 310
 Leu Glu Leu Gln Gly Ser Val Pro Ser Ala Pro Leu Leu Asn Phe Ser
 315 320 325
 Pro Gly Asn Leu Ser Val Asp Pro Tyr Met Glu Ile Asp Ala Phe Val
 330 335 340
 Leu Leu Pro Ser Ser Ser Lys Glu Pro Val Phe Arg Leu Ser Val Ala
 345 350 355
 Thr Asn Val Ser Ala Thr Leu Thr Phe Asn Thr Ser Lys Ile Thr Gly
 360 365 370 375
 Phe Leu Lys Pro Gly Lys Val Lys Val Glu Leu Lys Glu Ser Lys Val
 380 385 390
 Gly Leu Phe Asn Ala Glu Leu Leu Glu Ala Leu Leu Asn Tyr Tyr Ile
 395 400 405
 Leu Asn Thr Phe Tyr Pro Lys Phe Asn Asp Lys Leu Ala Glu Gly Phe
 410 415 420
 Pro Leu Pro Leu Leu Lys Arg Val Gln Leu Tyr Asp Leu Gly Leu Gln
 425 430 435
 Ile His Lys Asp Phe Leu Phe Leu Gly Ala Asn Val Gln Tyr Met Arg
 440 445 450 455
 Val

<210> 272
 <211> 143
 <212> PRT
 <213> Homo sapiens

<220>
 <221> SIGNAL
 <222> -43...-1

<400> 272
 Met Ala Lys Tyr Gln Gly Glu Val Gln Ser Leu Lys Leu Asp Asp Asp
 -40 -35 -30
 Ser Val Ile Glu Gly Val Ser Asp Gln Val Leu Val Ala Val Val Val
 -25 -20 -15
 Ser Phe Ala Leu Ile Ala Thr Leu Val Tyr Ala Leu Phe Arg Asn Val
 -10 -5 1 5
 His Gln Asn Ile His Pro Glu Asn Gln Glu Leu Val Arg Val Leu Arg
 10 15 20
 Glu Gln Leu Gln Thr Glu Gln Asp Ala Pro Ala Ala Thr Arg Gln Gln
 25 30 35
 Phe Tyr Thr Asp Met Tyr Cys Pro Ile Cys Leu His Gln Ala Ser Phe
 40 45 50
 Pro Val Glu Thr Asn Cys Gly His Leu Phe Cys Gly Ala Cys Ile Ile
 55 60 65
 Ala Tyr Trp Arg Tyr Gly Ser Trp Leu Gly Ala Ile Ser Cys Pro Ile
 70 75 80 85
 Cys Arg Gln Thr Arg His Gly His Ile Ala Leu Ser Arg Thr Ala
 90 95 100

<210> 273
 <211> 82
 <212> PRT
 <213> Homo sapiens

<400> 273
 Met Ala Lys Tyr Gln Gly Glu Val Gln Ser Leu Lys Leu Asp Asp Asp
 1 5 10 15
 Ser Val Ile Glu Gly Val Ser Asp Gln Val Leu Val Ala Val Val Val
 20 25 30
 Ser Phe Ala Leu Ile Ala Thr Leu Val Tyr Ala Leu Phe Arg Asn Val
 35 40 45
 His Gln Asn Ile His Pro Glu Asn Gln Glu Leu Val Arg Val Leu Arg
 50 55 60
 Glu Gln Leu Gln Thr Glu Gln Asp Ala Pro Ala Asp Ser Thr Ala Val
 65 70 75 80
 Leu His

<210> 274

<211> 373

<212> PRT

<213> Homo sapiens

<220>

<221> SIGNAL

<222> -27...-1

<400> 274
 Met Ala Thr Gln Ala His Ser Leu Ser Tyr Ala Gly Cys Asn Phe Leu
 -25 -20 -15
 Cys Gln Arg Leu Val Leu Ser Thr Leu Ser Gly Arg Pro Val Lys Ile
 -10 -5 1 5
 Arg Lys Ile Arg Ala Arg Asp Asp Asn Pro Gly Leu Arg Asp Phe Glu
 10 15 20
 Ala Ser Phe Ile Arg Leu Leu Asp Lys Ile Thr Asn Gly Ser Arg Ile
 25 30 35
 Glu Ile Asn Gln Thr Gly Thr Thr Leu Tyr Tyr Gln Pro Gly Leu Leu
 40 45 50
 Tyr Gly Gly Ser Val Glu His Asp Cys Ser Val Leu Arg Gly Ile Gly
 55 60 65
 Tyr Tyr Leu Glu Ser Leu Leu Cys Leu Ala Pro Phe Met Lys His Pro
 70 75 80 85
 Leu Lys Ile Val Leu Arg Gly Val Thr Asn Asp Gln Ile Asp Pro Ser
 90 95 100
 Val Asp Val Leu Lys Ala Thr Ala Leu Pro Leu Leu Lys Gln Phe Gly
 105 110 115
 Ile Asp Gly Glu Ser Phe Glu Leu Lys Ile Val Arg Arg Gly Met Pro
 120 125 130
 Pro Gly Gly Gly Glu Val Phe Ser Cys Pro Val Arg Lys Val
 135 140 145
 Leu Lys Pro Ile Gln Leu Thr Asp Pro Gly Lys Ile Lys Arg Ile Arg
 150 155 160 165
 Gly Met Ala Tyr Ser Val Arg Val Ser Pro Gln Met Ala Asn Arg Ile
 170 175 180
 Val Asp Ser Ala Arg Ser Ile Leu Asn Lys Phe Ile Pro Asp Ile Tyr
 185 190 195
 Ile Tyr Thr Asp His Ile Lys Gly Val Asn Ser Gly Lys Ser Pro Gly
 200 205 210
 Phe Gly Leu Ser Leu Val Ala Glu Thr Thr Ser Gly Thr Phe Leu Ser
 215 220 225
 Ala Glu Leu Ala Ser Asn Pro Gln Gly Gln Gly Ala Ala Val Leu Pro
 230 235 240 245
 Glu Asp Leu Gly Arg Asn Cys Ala Arg Leu Leu Leu Glu Glu Ile Tyr

Arg	Gly	Gly	Cys	Val	Asp	Ser	Thr	Asn	Gln	Ser	Leu	Ala	Leu	Leu	Leu
			265					270					275		
Met	Thr	Leu	Gly	Gln	Gln	Asp	Val	Ser	Lys	Val	Leu	Leu	Gly	Pro	Leu
		280					285					290			
Ser	Pro	Tyr	Thr	Ile	Glu	Phe	Leu	Arg	His	Leu	Lys	Ser	Phe	Phe	Gln
	295					300					305				
Ile	Met	Phe	Lys	Ile	Glu	Thr	Lys	Pro	Cys	Gly	Glu	Glu	Leu	Lys	Gly
310					315					320					325
Gly	Asp	Lys	Val	Leu	Met	Thr	Cys	Val	Gly	Ile	Gly	Phe	Ser	Asn	Leu
				330					335					340	
Ser	Arg	Thr	Leu	Lys											
			345												

<210> 275

<211> 94

<212> PRT

<213> Homo sapiens

<220>

<221> SIGNAL

<222> -25...-1

<400> 275

Met	Ala	Ser	Val	Val	Leu	Ala	Leu	Arg	Thr	Arg	Thr	Ala	Val	Thr	Ser
-25					-20					-15					-10
Leu	Leu	Ser	Pro	Thr	Pro	Ala	Thr	Ala	Leu	Ala	Val	Arg	Tyr	Ala	Ser
				-5					1				5		
Lys	Lys	Ser	Gly	Gly	Ser	Ser	Lys	Asn	Leu	Gly	Gly	Lys	Ser	Ser	Gly
		10					15					20			
Arg	Arg	Gln	Gly	Ile	Lys	Lys	Met	Glu	Gly	His	Tyr	Val	His	Ala	Gly
	25					30					35				
Asn	Ile	Ile	Ala	Thr	Gln	Arg	His	Phe	Arg	Trp	His	Pro	Gly	Ala	His
40					45					50					55
Val	Ser	Cys	Ser	Val	Ala	Ala	Pro	Leu	Phe	Pro	Phe	Leu	Gly		
				60					65						

<210> 276

<211> 197

<212> PRT

<213> Homo sapiens

<220>

<221> SIGNAL

<222> -20...-1

<400> 276

Met	Thr	Val	Leu	Glu	Ile	Thr	Leu	Ala	Val	Ile	Leu	Thr	Leu	Leu	Gly
-20					-15					-10					-5
Leu	Ala	Ile	Leu	Ala	Ile	Leu	Leu	Thr	Arg	Trp	Ala	Arg	Arg	Lys	Gln
			1					5					10		
Ser	Glu	Met	Tyr	Ile	Ser	Arg	Tyr	Ser	Ser	Glu	Gln	Ser	Ala	Arg	Leu
	15						20					25			
Leu	Asp	Tyr	Glu	Asp	Gly	Arg	Gly	Ser	Arg	His	Ala	Tyr	Ser	Thr	Gln
	30					35					40				
Ser	Glu	Arg	Ser	Lys	Arg	Asp	Tyr	Thr	Pro	Ser	Thr	Asn	Ser	Leu	Ala
45					50					55					60
Leu	Ser	Arg	Ser	Ser	Ile	Ala	Leu	Pro	Gln	Gly	Ser	Met	Ser	Ser	Ile

				65					70					75			
Lys	Cys	Leu	Gln	Thr	Thr	Glu	Glu	Pro	Pro	Ser	Arg	Thr	Ala	Gly	Ala		
			80					85					90				
Met	Met	Gln	Phe	Thr	Ala	Pro	Ile	Pro	Gly	Ala	Thr	Gly	Pro	Ile	Lys		
		95					100					105					
Leu	Ser	Gln	Lys	Thr	Ile	Val	Gln	Thr	Leu	Gly	Pro	Ile	Val	Gln	Tyr		
	110					115					120						
Pro	Gly	Ser	Asn	Gly	Arg	Ile	Asn	Ile	Ser	Gln	Leu	Thr	Ser	Glu	Asp		
125				130						135					140		
Leu	Thr	Gly	Ala	Lys	Gly	Arg	Val	Thr	Ser	Gly	Pro	Gln	Phe	Pro	Asn		
			145						150					155			
Ser	His	His	Val	Pro	Glu	Asn	Leu	His	Gly	Tyr	Met	Asn	Ser	Leu	Ser		
			160					165					170				
Leu	Phe	Ser	Pro	Ala													
			175														

<210> 277

<211> 344

<212> PRT

<213> Homo sapiens

<220>

<221> SIGNAL

<222> -29..-1

<400> 277

Met	Asp	Phe	Leu	Val	Leu	Phe	Leu	Phe	Tyr	Leu	Ala	Ser	Val	Leu	Met		
				-25					-20					-15			
Gly	Leu	Val	Leu	Ile	Cys	Val	Cys	Ser	Lys	Thr	His	Ser	Leu	Lys	Gly		
			-10					-5					1				
Leu	Ala	Arg	Gly	Gly	Ala	Gln	Ile	Phe	Ser	Cys	Ile	Ile	Pro	Glu	Cys		
	5				10					15							
Leu	Gln	Arg	Ala	Val	His	Gly	Leu	Leu	His	Tyr	Leu	Phe	His	Thr	Arg		
20				25					30					35			
Asn	His	Thr	Phe	Ile	Val	Leu	His	Leu	Val	Leu	Gln	Gly	Met	Val	Tyr		
			40					45						50			
Thr	Glu	Tyr	Thr	Trp	Glu	Val	Phe	Gly	Tyr	Cys	Gln	Glu	Leu	Glu	Leu		
			55					60					65				
Ser	Leu	His	Tyr	Leu	Leu	Leu	Pro	Tyr	Leu	Leu	Leu	Gly	Val	Asn	Leu		
	70						75					80					
Phe	Phe	Phe	Thr	Leu	Thr	Cys	Gly	Thr	Asn	Pro	Gly	Ile	Ile	Thr	Lys		
	85				90					95							
Ala	Asn	Glu	Leu	Leu	Phe	Leu	His	Val	Tyr	Glu	Phe	Asp	Glu	Val	Met		
100				105					110						115		
Phe	Pro	Lys	Asn	Val	Arg	Cys	Ser	Thr	Cys	Asp	Leu	Arg	Lys	Pro	Ala		
			120						125					130			
Arg	Ser	Lys	His	Cys	Ser	Val	Cys	Asn	Trp	Cys	Val	His	Arg	Phe	Asp		
			135					140					145				
His	His	Cys	Val	Trp	Val	Asn	Asn	Cys	Ile	Gly	Ala	Trp	Asn	Ile	Arg		
	150					155					160						
Tyr	Phe	Leu	Ile	Tyr	Val	Leu	Thr	Leu	Thr	Ala	Ser	Ala	Ala	Thr	Val		
	165				170					175							
Ala	Ile	Val	Ser	Thr	Thr	Phe	Leu	Val	His	Leu	Val	Val	Met	Ser	Asp		
180				185					190						195		
Leu	Tyr	Gln	Glu	Thr	Tyr	Ile	Asp	Asp	Leu	Gly	His	Leu	His	Val	Met		
			200					205						210			
Asp	Thr	Val	Phe	Leu	Ile	Gln	Tyr	Leu	Phe	Leu	Thr	Phe	Pro	Arg	Ile		
			215					220					225				

Val	Phe	Met	Leu	Gly	Phe	Val	Val	Val	Leu	Ser	Phe	Leu	Leu	Gly	Gly
		230					235					240			
Tyr	Leu	Leu	Phe	Val	Leu	Tyr	Leu	Ala	Ala	Thr	Asn	Gln	Thr	Thr	Asn
	245					250					255				
Glu	Trp	Tyr	Arg	Gly	Asp	Trp	Ala	Trp	Cys	Gln	Arg	Cys	Pro	Leu	Val
260					265					270					275
Ala	Trp	Pro	Pro	Ser	Ala	Glu	Pro	Gln	Val	His	Arg	Asn	Ile	His	Ser
				280					285					290	
His	Gly	Leu	Arg	Ser	Asn	Leu	Gln	Glu	Ile	Phe	Leu	Pro	Ala	Phe	Pro
			295					300					305		
Cys	His	Glu	Arg	Lys	Lys	Gln	Glu								
		310					315								

<210> 278

<211> 541

<212> PRT

<213> Homo sapiens

<220>

<221> SIGNAL

<222> -28...-1

<400> 278

Met	Gly	Ser	Gln	Glu	Val	Leu	Gly	His	Ala	Ala	Arg	Leu	Ser	Ser	Ser
			-25					-20				-15			
Gly	Leu	Leu	Leu	Gln	Val	Leu	Phe	Arg	Leu	Ile	Thr	Phe	Val	Leu	Asn
	-10						-5					1			
Ala	Phe	Ile	Leu	Arg	Phe	Leu	Ser	Lys	Glu	Ile	Val	Gly	Val	Val	Asn
5					10					15					20
Val	Arg	Leu	Thr	Leu	Leu	Tyr	Ser	Thr	Thr	Leu	Phe	Leu	Ala	Arg	Glu
				25					30					35	
Ala	Phe	Arg	Arg	Ala	Cys	Leu	Ser	Gly	Gly	Thr	Gln	Arg	Asp	Trp	Ser
			40					45				50			
Gln	Thr	Leu	Asn	Leu	Leu	Trp	Leu	Thr	Val	Pro	Leu	Gly	Val	Phe	Trp
	55						60					65			
Ser	Leu	Phe	Leu	Gly	Trp	Ile	Trp	Leu	Gln	Leu	Leu	Glu	Val	Pro	Asp
	70					75					80				
Pro	Asn	Val	Val	Pro	His	Tyr	Ala	Thr	Gly	Val	Val	Leu	Phe	Gly	Leu
85					90					95					100
Ser	Ala	Val	Val	Glu	Leu	Leu	Gly	Glu	Pro	Phe	Trp	Val	Leu	Ala	Gln
				105					110					115	
Ala	His	Met	Phe	Val	Lys	Leu	Lys	Val	Ile	Ala	Glu	Ser	Leu	Ser	Val
			120					125					130		
Ile	Leu	Lys	Thr	Val	Leu	Thr	Ala	Phe	Leu	Val	Leu	Trp	Leu	Pro	His
	135						140					145			
Trp	Gly	Leu	Tyr	Ile	Phe	Ser	Leu	Ala	Gln	Leu	Phe	Tyr	Thr	Thr	Val
	150					155					160				
Leu	Val	Leu	Cys	Tyr	Val	Ile	Tyr	Phe	Thr	Lys	Leu	Leu	Gly	Ser	Pro
165					170					175					180
Glu	Ser	Thr	Lys	Leu	Gln	Thr	Leu	Pro	Val	Ser	Arg	Ile	Thr	Asp	Leu
				185					190					195	
Leu	Pro	Asn	Ile	Thr	Arg	Asn	Gly	Ala	Phe	Ile	Asn	Trp	Lys	Glu	Ala
		200						205					210		
Lys	Leu	Thr	Trp	Ser	Phe	Phe	Lys	Gln	Ser	Phe	Leu	Lys	Gln	Ile	Leu
	215						220					225			
Thr	Glu	Gly	Glu	Arg	Tyr	Val	Met	Thr	Phe	Leu	Asn	Val	Leu	Asn	Phe
	230					235					240				
Gly	Asp	Gln	Gly	Val	Tyr	Asp	Ile	Val	Asn	Asn	Leu	Gly	Ser	Leu	Val

Lys Met Asp Glu Leu Tyr Pro Met Glu Pro Glu Glu Glu Ala Asn Gly
 90 95 100
 Ser Glu Ile Leu Ala Lys Arg Tyr Gly Gly Phe Met Lys Lys Asp Ala
 105 110 115 120
 Glu Glu Asp Asp Ser Leu Ala Asn Ser Ser Asp Leu Leu Lys Glu Leu
 125 130 135
 Leu Glu Thr Gly Asp Asn Arg Glu Arg Ser His His Gln Asp Gly Ser
 140 145 150
 Asp Asn Glu Glu Glu Val Ser Lys Arg Tyr Gly Gly Phe Met Arg Gly
 155 160 165
 Leu Lys Arg Ser Pro Gln Leu Glu Asp Glu Ala Lys Glu Leu Gln Lys
 170 175 180
 Arg Tyr Gly Gly Phe Met Arg Arg Val Gly Arg Pro Glu Trp Trp Met
 185 190 195 200
 Asp Tyr Gln Lys Arg Tyr Gly Gly Phe Leu Lys Arg Phe Ala Glu Ala
 205 210 215
 Leu Pro Ser Asp Glu Glu Gly Glu Ser Tyr Ser Lys Glu Val Pro Glu
 220 225 230
 Met Glu Lys Arg Tyr Gly Gly Phe Met Arg Phe
 235 240

<210> 280
 <211> 362
 <212> PRT
 <213> Homo sapiens

<220>
 <221> SIGNAL
 <222> -40..-1

<400> 280
 Met Pro Phe Ala Tyr Phe Phe Thr Glu Ser Glu Gly Phe Ala Gly Ser
 -40 -35 -30 -25
 Arg Lys Gly Val Leu Gly Arg Val Tyr Glu Thr Val Val Met Leu Met
 -20 -15 -10
 Leu Leu Thr Leu Leu Val Leu Gly Met Val Trp Val Ala Ser Ala Ile
 -5 1 5
 Val Asp Lys Asn Lys Ala Asn Arg Glu Ser Leu Tyr Asp Phe Trp Glu
 10 15 20
 Tyr Tyr Leu Pro Tyr Leu Tyr Ser Cys Ile Ser Phe Leu Gly Val Leu
 25 30 35 40
 Leu Leu Leu Val Cys Thr Pro Leu Gly Leu Ala Arg Met Phe Ser Val
 45 50 55
 Thr Gly Lys Leu Leu Val Lys Pro Arg Leu Leu Glu Asp Leu Glu Glu
 60 65 70
 Gln Leu Tyr Cys Ser Ala Phe Glu Glu Ala Ala Leu Thr Arg Arg Ile
 75 80 85
 Cys Asn Pro Thr Ser Cys Trp Leu Pro Leu Asp Met Glu Leu Leu His
 90 95 100
 Arg Gln Val Leu Ala Leu Gln Thr Gln Arg Val Leu Leu Glu Lys Arg
 105 110 115 120
 Arg Lys Ala Ser Ala Trp Gln Arg Asn Leu Gly Tyr Pro Leu Ala Met
 125 130 135
 Leu Cys Leu Leu Val Leu Thr Gly Leu Ser Val Leu Ile Val Ala Ile
 140 145 150
 His Ile Leu Glu Leu Leu Ile Asp Glu Ala Ala Met Pro Arg Gly Met
 155 160 165
 Gln Gly Thr Ser Leu Gly Gln Val Ser Phe Ser Lys Leu Gly Ser Phe

170		175		180
Gly Ala Val Ile Gln Val Val Leu Ile Phe Tyr Leu Met Val Ser Ser				
185		190		195
Val Val Gly Phe Tyr Ser Ser Pro Leu Phe Arg Ser Leu Arg Pro Arg				200
	205		210	
Trp His Asp Thr Ala Met Thr Gln Ile Ile Gly Asn Cys Val Cys Leu				215
	220		225	
Leu Val Leu Ser Ser Ala Leu Pro Val Phe Ser Arg Thr Leu Gly Leu				230
	235		240	
Thr Arg Phe Asp Leu Leu Gly Asp Phe Gly Arg Phe Asn Trp Leu Gly				245
	250		255	
Asn Phe Tyr Ile Val Phe Leu Tyr Asn Ala Ala Phe Ala Gly Leu Thr				260
265		270		275
Thr Leu Tyr Leu Val Lys Thr Phe Thr Ala Ala Val Arg Ala Glu Leu				280
	285		290	
Ile Arg Ala Phe Gly Leu Asp Arg Leu Pro Leu Pro Val Ser Gly Phe				295
	300		305	
Pro Gln Ala Ser Arg Lys Thr Gln His Gln				310
	315		320	

<210> 281
 <211> 81
 <212> PRT
 <213> Homo sapiens

<220>
 <221> SIGNAL
 <222> -21...-1

<400> 281
Met Ser Arg Ser Ser Lys Val Val Leu Gly Leu Ser Val Leu Leu Thr
-20 -15 -10
Ala Ala Thr Val Ala Gly Val His Val Lys Gln Gln Trp Asp Gln Gln
-5 1 5 10
Arg Leu Arg Asp Gly Val Ile Arg Asp Ile Glu Arg Gln Ile Arg Lys
15 20 25
Lys Glu Asn Ile Arg Leu Leu Gly Glu Gln Ile Ile Leu Thr Glu Gln
30 35 40
Leu Glu Ala Glu Arg Glu Lys Met Leu Leu Ala Lys Gly Ser Gln Lys
45 50 55
Ser
60

<210> 282
 <211> 541
 <212> PRT
 <213> Homo sapiens

<220>
 <221> SIGNAL
 <222> -28...-1

<400> 282
Met Gly Ser Gln Glu Val Leu Gly His Ala Ala Arg Leu Ala Ser Ser
-25 -20 -15
Gly Leu Leu Leu Gln Val Leu Phe Arg Leu Ile Thr Phe Val Leu Asn
-10 -5 1
Ala Phe Ile Leu Arg Phe Leu Ser Lys Glu Ile Val Gly Val Val Asn

470		475		480
Leu Gly Thr Ala Phe	Leu Thr Glu Thr Lys	Leu Ile His Phe	Leu Arg	
485	490	495	500	
Thr Gln Leu Gly Val	Pro Arg Arg Thr Asp	Lys Met Thr		
505	510			

<210> 283
 <211> 468
 <212> PRT
 <213> Homo sapiens

<220>
 <221> SIGNAL
 <222> -21...-1

<400> 283

Met Gly Thr Gln Glu Gly Trp Cys Leu Leu Leu Cys Leu Ala Leu Ser	
-20	-15
Gly Ala Ala Glu Thr Lys Pro His Pro Ala Glu Gly Gln Trp Arg Ala	
-5	1
Val Asp Val Val Leu Asp Cys Phe Leu Val Lys Asp Gly Ala His Arg	
15	20
Gly Ala Leu Ala Ser Ser Glu Asp Arg Ala Arg Ala Ser Leu Val Leu	
30	35
Lys Gln Val Pro Val Leu Asp Asp Gly Ser Leu Glu Asp Phe Thr Asp	
45	50
Phe Gln Gly Gly Thr Leu Ala Gln Asp Asp Pro Pro Ile Ile Phe Glu	
60	65
Ala Ser Val Asp Leu Val Gln Ile Pro Gln Ala Glu Ala Leu Leu His	
80	85
Ala Asp Cys Ser Gly Lys Glu Val Thr Cys Glu Ile Ser Arg Tyr Phe	
95	100
Leu Gln Met Thr Glu Thr Thr Val Lys Thr Ala Ala Trp Phe Met Ala	
110	115
Asn Val Gln Val Ser Gly Gly Gly Pro Ser Ile Ser Leu Val Met Lys	
125	130
Thr Pro Arg Val Ala Lys Asn Glu Val Leu Trp His Pro Thr Leu Asn	
140	145
Leu Pro Leu Ser Pro Gln Gly Thr Val Arg Thr Ala Val Glu Phe Gln	
160	165
Val Met Thr Gln Thr Gln Ser Leu Ser Phe Leu Leu Gly Ser Ser Ala	
175	180
Ser Leu Asp Cys Gly Phe Ser Met Ala Pro Gly Leu Asp Leu Ile Ser	
190	195
Val Glu Trp Arg Leu Gln His Lys Gly Arg Gly Gln Leu Val Tyr Ser	
205	210
Trp Thr Ala Gly Gln Gly Gln Ala Val Arg Lys Gly Ala Thr Leu Glu	
220	225
Pro Ala Gln Leu Gly Met Ala Arg Asp Ala Ser Leu Thr Leu Pro Gly	
240	245
Leu Thr Ile Gln Asp Glu Gly Thr Tyr Ile Cys Gln Ile Thr Thr Ser	
255	260
Leu Tyr Arg Ala Gln Gln Ile Ile Gln Leu Asn Ile Gln Ala Ser Pro	
270	275
Lys Val Arg Leu Ser Leu Ala Asn Glu Ala Leu Leu Pro Thr Leu Ile	
285	290
Cys Asp Ile Ala Gly Tyr Tyr Pro Leu Asp Val Val Val Thr Trp Thr	
300	305
	310
	315

Arg Glu Glu Leu Gly Gly Ser Pro Ala Gln Val Ser Gly Ala Ser Phe
 320 325 330
 Ser Ser Leu Arg Gln Ser Val Ala Gly Thr Tyr Ser Ile Ser Ser Ser
 335 340 345
 Leu Thr Ala Glu Pro Gly Ser Ala Gly Ala Thr Tyr Thr Cys Gln Val
 350 355 360
 Thr His Ile Ser Leu Glu Glu Pro Leu Gly Ala Ser Thr Gln Val Val
 365 370 375
 Pro Pro Glu Arg Arg Thr Ala Leu Gly Val Ile Phe Ala Ser Ser Leu
 380 385 390 395
 Phe Leu Leu Ala Leu Met Phe Leu Gly Leu Gln Arg Arg Gln Ala Pro
 400 405 410
 Thr Gly Leu Gly Leu Leu Gln Ala Glu Arg Trp Glu Thr Thr Ser Cys
 415 420 425
 Ala Asp Thr Gln Ser Ser His Leu His Glu Asp Arg Thr Ala Arg Val
 430 435 440
 Ser Gln Pro Ser
 445

<210> 284

<211> 406

<212> PRT

<213> Homo sapiens

<220>

<221> SIGNAL

<222> -31...-1

<400> 284

Met Val Arg Ile Gln Arg Arg Lys Leu Leu Ala Ser Cys Leu Cys Val
 -30 -25 -20
 Thr Ala Thr Val Phe Leu Leu Val Thr Leu Gln Ala Leu Asp Thr Val
 -15 -10 -5 1
 Glu Asn Leu Met Lys Val Thr Gly Pro Pro Gln Gly Val Thr Asp Ser
 5 10 15
 Met Gln Cys Phe Asn Asp Gln Trp Pro Leu Ser Asn Thr Arg Ser Ser
 20 25 30
 Glu His Ile Lys Glu Val Met Val Glu Leu Gly Lys Phe Glu Arg Lys
 35 40 45
 Glu Phe Lys Ser Ser Ser Leu Gln Asp Gly His Thr Lys Met Glu Glu
 50 55 60 65
 Ala Pro Thr His Leu Asn Ser Phe Leu Lys Lys Glu Gly Leu Thr Phe
 70 75 80
 Asn Arg Lys Arg Lys Trp Glu Leu Asp Ser Tyr Pro Ile Met Leu Trp
 85 90 95
 Trp Ser Pro Leu Thr Gly Glu Thr Gly Arg Leu Gly Gln Cys Gly Ala
 100 105 110
 Asp Ala Cys Phe Phe Thr Ile Asn Arg Thr Tyr Leu His His His Met
 115 120 125
 Thr Lys Ala Phe Leu Phe Tyr Gly Thr Asp Phe Asn Ile Asp Ser Leu
 130 135 140 145
 Pro Leu Pro Arg Lys Ala His His Asp Trp Ala Val Phe His Glu Glu
 150 155 160
 Ser Pro Lys Asn Asn Tyr Lys Leu Phe His Lys Pro Val Ile Thr Leu
 165 170 175
 Phe Asn Tyr Thr Ala Thr Phe Ser Arg His Ser His Leu Pro Leu Thr
 180 185 190
 Thr Gln Tyr Leu Glu Ser Ile Glu Val Leu Lys Ser Leu Arg Tyr Leu

195	200	205
Val Pro Leu Gln Ser Lys	Asn Lys Leu Arg Lys	Arg Leu Ala Pro Leu
210	215	220
Val Tyr Val Gln Ser Tyr	Cys Asp Pro Pro Ser	Asp Arg Asp Ser Tyr
	230	235
Val Arg Glu Leu Met Thr Tyr	Ile Glu Val Asp Ser Tyr	Gly Glu Cys
	245	250
Leu Arg Asn Lys Asp Leu Pro	Gln Gln Leu Lys Asn Pro	Ala Ser Met
	260	265
Asp Ala Asp Gly Phe Tyr Arg	Ile Ile Ala Gln Tyr Lys	Phe Ile Leu
	275	280
Ala Phe Glu Asn Ala Val Cys	Asp Asp Tyr Ile Thr Glu	Lys Phe Trp
290	295	300
Arg Pro Leu Lys Leu Gly Val	Val Val Pro Val Tyr Tyr	Gly Ser Pro Ser
	310	315
Ile Thr Asp Trp Leu Pro Ser	Asn Lys Ser Ala Ile Leu	Val Ser Glu
	325	330
Phe Ser His Pro Arg Glu Leu	Ala Ser Tyr Ile Arg Arg	Leu Asp Ser
	340	345
Asp Asp Arg Leu Tyr Glu Ala	Tyr Val Glu Trp Lys Leu	Lys Gly Arg
	355	360
Ser Leu Thr Ser Asp Phe		
370	375	

<210> 285
 <211> 305
 <212> PRT
 <213> Homo sapiens

<220>
 <221> SIGNAL
 <222> -26..-1

<400> 285
Met Gly Ile Gln Thr Ser Pro Val Leu Leu Ala Ser Leu Gly Val Gly
-25 -20 -15
Leu Val Thr Leu Leu Gly Leu Ala Val Gly Ser Tyr Leu Val Arg Arg
-10 -5 1 5
Ser Arg Arg Pro Gln Val Thr Leu Leu Asp Pro Asn Glu Lys Tyr Leu
10 15 20
Leu Arg Leu Leu Asp Lys Thr Thr Val Ser His Asn Thr Lys Arg Phe
25 30 35
Arg Phe Ala Leu Pro Thr Ala His His Thr Leu Gly Leu Pro Val Gly
40 45 50
Lys His Ile Tyr Leu Ser Thr Arg Ile Asp Gly Ser Leu Val Ile Arg
55 60 65 70
Pro Tyr Thr Pro Val Thr Ser Asp Glu Asp Gln Gly Tyr Val Asp Leu
75 80 85
Val Ile Lys Val Tyr Leu Lys Gly Val His Pro Lys Phe Pro Glu Gly
90 95 100
Gly Lys Met Ser Gln Tyr Leu Asp Ser Leu Lys Val Gly Asp Val Val
105 110 115
Glu Phe Arg Gly Pro Ser Gly Leu Leu Thr Tyr Thr Gly Lys Gly His
120 125 130
Phe Asn Ile Gln Pro Asn Lys Lys Ser Pro Pro Glu Pro Arg Val Ala
135 140 145 150
Lys Lys Leu Gly Met Ile Ala Gly Gly Thr Gly Ile Thr Pro Met Leu
155 160 165

Gln Leu Ile Arg Ala Ile Leu Lys Val Pro Glu Asp Pro Thr Gln Cys
 170 175 180
 Phe Leu Leu Phe Ala Asn Gln Thr Glu Lys Asp Ile Ile Leu Arg Glu
 185 190 195
 Asp Leu Glu Glu Leu Gln Ala Arg Tyr Pro Asn Arg Phe Lys Leu Trp
 200 205 210
 Phe Thr Leu Asp His Pro Pro Lys Asp Trp Ala Tyr Ser Lys Gly Phe
 215 220 225 230
 Val Thr Ala Asp Met Ile Arg Glu His Leu Pro Ala Pro Gly Asp Asp
 235 240 245
 Val Leu Val Leu Leu Cys Gly Pro Pro Pro Met Val Gln Leu Ala Cys
 250 255 260
 His Pro Asn Leu Asp Lys Leu Gly Tyr Ser Gln Lys Met Arg Phe Thr
 265 270 275
 Tyr

<210> 286
 <211> 442
 <212> PRT
 <213> Homo sapiens

<220>
 <221> SIGNAL
 <222> -21..-1

 <220>
 <221> UNSURE
 <222> 132
 <223> Xaa = Pro,Arg

<400> 286
 Met Gly Thr Gln Glu Gly Trp Cys Leu Leu Leu Cys Leu Ala Leu Ser
 -20 -15 -10
 Gly Ala Ala Glu Thr Lys Pro His Pro Ala Glu Gly Gln Leu Arg Ala
 -5 1 5 10
 Val Asp Val Val Leu Asp Cys Phe Leu Ala Lys Asp Gly Ala His Arg
 15 20 25
 Gly Ala Leu Ala Ser Ser Glu Asp Arg Ala Arg Ala Ser Leu Val Leu
 30 35 40
 Lys Gln Val Pro Val Leu Asp Asp Gly Ser Leu Glu Asp Phe Thr Asp
 45 50 55
 Phe Gln Gly Gly Thr Leu Ala Gln Asp Asp Pro Pro Ile Ile Phe Glu
 60 65 70 75
 Ala Ser Val Asp Leu Val Gln Ile Pro Gln Ala Glu Ala Leu Leu His
 80 85 90
 Ala Asp Cys Ser Gly Lys Glu Val Thr Cys Glu Ile Ser Arg Tyr Phe
 95 100 105
 Leu Gln Met Thr Glu Thr Thr Val Lys Thr Ala Ala Trp Phe Met Ala
 110 115 120
 Asn Met Gln Val Ser Gly Gly Gly Xaa Ser Ile Ser Leu Val Met Lys
 125 130 135
 Thr Pro Arg Val Thr Lys Asn Glu Ala Leu Trp His Pro Thr Leu Asn
 140 145 150 155
 Leu Pro Leu Ser Pro Gln Gly Thr Val Arg Thr Ala Val Glu Phe Gln
 160 165 170
 Val Met Thr Gln Thr Gln Ser Leu Ser Phe Leu Leu Gly Ser Ser Ala
 175 180 185
 Ser Leu Asp Cys Gly Phe Ser Met Ala Pro Gly Leu Asp Leu Ile Ser

Gly	Phe	Leu	Gly	Cys	Leu	Val	Asn	Leu	Gln	Ala	Gly	His	Tyr	Leu	Ala
			100					105					110		
Met	Thr	Thr	Leu	Leu	Leu	Glu	Met	Ser	Thr	Pro	Phe	Thr	Cys	Val	Ser
		115					120					125			
Trp	Met	Leu	Leu	Lys	Ala	Gly	Trp	Ser	Glu	Ser	Leu	Phe	Trp	Lys	Leu
	130					135					140				
Asn	Gln	Trp	Leu	Met	Ile	His	Met	Phe	His	Cys	Arg	Met	Val	Leu	Thr
145					150					155					160
Tyr	His	Met	Trp	Trp	Val	Cys	Phe	Trp	His	Trp	Asp	Gly	Leu	Val	Ser
			165						170					175	
Ser	Leu	Tyr	Leu	Pro	His	Leu	Thr	Leu	Phe	Leu	Val	Gly	Leu	Ala	Leu
			180					185					190		
Leu	Thr	Leu	Ile	Ile	Asn	Pro	Tyr	Trp	Thr	His	Lys	Lys	Thr	Gln	Gln
		195					200					205			
Leu	Leu	Asn	Pro	Val	Asp	Trp	Asn	Phe	Ala	Gln	Pro	Glu	Ala	Lys	Ser
	210				215						220				
Arg	Pro	Glu	Gly	Asn	Gly	Gln	Leu	Leu	Arg	Lys	Lys	Arg	Pro		
225					230					235					

<210> 288

<211> 398

<212> PRT

<213> Homo sapiens

<220>

<221> SIGNAL

<222> -21...-1

<400> 288

Met	Val	Asn	Asp	Pro	Pro	Val	Pro	Ala	Leu	Leu	Trp	Ala	Gln	Glu	Val
	-20					-15					-10				
Gly	Gln	Val	Leu	Ala	Gly	Arg	Ala	Arg	Arg	Leu	Leu	Leu	Gln	Phe	Gly
-5					1				5					10	
Val	Leu	Phe	Cys	Thr	Ile	Leu	Leu	Leu	Leu	Trp	Val	Ser	Val	Phe	Leu
			15					20					25		
Tyr	Gly	Ser	Phe	Tyr	Tyr	Ser	Tyr	Met	Pro	Thr	Val	Ser	His	Leu	Ser
	30					35						40			
Pro	Val	His	Phe	Tyr	Tyr	Arg	Thr	Asp	Cys	Asp	Ser	Ser	Thr	Thr	Ser
	45					50					55				
Leu	Cys	Ser	Phe	Pro	Val	Ala	Asn	Val	Ser	Leu	Thr	Lys	Gly	Gly	Arg
60					65					70					75
Asp	Arg	Val	Leu	Met	Tyr	Gly	Gln	Pro	Tyr	Arg	Val	Thr	Leu	Glu	Leu
				80					85					90	
Glu	Leu	Pro	Glu	Ser	Pro	Val	Asn	Gln	Asp	Leu	Gly	Met	Phe	Leu	Val
		95						100					105		
Thr	Ile	Ser	Cys	Tyr	Thr	Arg	Gly	Gly	Arg	Ile	Ile	Ser	Thr	Ser	Ser
	110						115					120			
Arg	Ser	Val	Met	Leu	His	Tyr	Arg	Ser	Asp	Leu	Leu	Gln	Met	Leu	Asp
	125					130					135				
Thr	Leu	Val	Phe	Ser	Ser	Leu	Leu	Leu	Phe	Gly	Phe	Ala	Glu	Gln	Lys
140					145					150					155
Gln	Leu	Leu	Glu	Val	Glu	Leu	Tyr	Ala	Asp	Tyr	Arg	Glu	Asn	Ser	Tyr
				160					165					170	
Val	Pro	Thr	Thr	Gly	Ala	Ile	Ile	Glu	Ile	His	Ser	Lys	Arg	Ile	Gln
		175						180					185		
Leu	Tyr	Gly	Ala	Tyr	Leu	Arg	Ile	His	Ala	His	Phe	Thr	Gly	Leu	Arg
	190						195					200			
Tyr	Leu	Leu	Tyr	Asn	Phe	Pro	Met	Thr	Cys	Ala	Phe	Ile	Gly	Val	Ala

205						210						215			
Ser	Asn	Phe	Thr	Phe	Leu	Ser	Val	Ile	Val	Leu	Phe	Ser	Tyr	Met	Gln
220					225					230					235
Trp	Val	Trp	Gly	Gly	Ile	Trp	Pro	Arg	His	Arg	Phe	Ser	Leu	Gln	Val
				240						245				250	
Asn	Ile	Arg	Lys	Arg	Asp	Asn	Ser	Arg	Lys	Glu	Val	Gln	Arg	Arg	Ile
			255					260					265		
Ser	Ala	His	Gln	Pro	Gly	Pro	Glu	Gly	Gln	Glu	Glu	Ser	Thr	Pro	Gln
		270				275						280			
Ser	Asp	Val	Thr	Glu	Asp	Gly	Glu	Ser	Pro	Glu	Asp	Pro	Ser	Gly	Thr
285					290					295					
Glu	Gly	Gln	Leu	Ser	Glu	Glu	Glu	Lys	Pro	Asp	Gln	Gln	Pro	Leu	Ser
300					305				310						315
Gly	Glu	Glu	Glu	Leu	Glu	Pro	Glu	Ala	Ser	Asp	Gly	Ser	Gly	Ser	Trp
				320					325					330	
Glu	Asp	Ala	Ala	Leu	Leu	Thr	Glu	Ala	Asn	Leu	Pro	Ala	Pro	Ala	Pro
		335					340					345			
Ala	Ser	Ala	Ser	Ala	Pro	Val	Leu	Glu	Thr	Leu	Gly	Ser	Ser	Glu	Pro
	350					355				360					
Ala	Gly	Gly	Ala	Leu	Arg	Gln	Arg	Pro	Thr	Cys	Ser	Ser	Ser		
365					370					375					

<210> 289
 <211> 130
 <212> PRT
 <213> Homo sapiens

<220>
 <221> SIGNAL
 <222> -20..-1

<400> 289															
Met	Arg	Gln	Lys	Ala	Val	Ser	Leu	Phe	Phe	Cys	Tyr	Leu	Leu	Leu	Phe
-20				-15						-10					-5
Thr	Cys	Ser	Gly	Val	Glu	Ala	Gly	Lys	Lys	Lys	Cys	Ser	Glu	Ser	Ser
			1				5					10			
Asp	Ser	Gly	Ser	Gly	Phe	Trp	Lys	Ala	Leu	Thr	Phe	Met	Ala	Val	Gly
	15					20					25				
Gly	Gly	Leu	Ala	Val	Ala	Gly	Leu	Pro	Ala	Leu	Gly	Phe	Thr	Gly	Ala
	30				35					40					
Gly	Ile	Ala	Ala	Asn	Ser	Val	Ala	Ala	Ser	Leu	Met	Ser	Trp	Ser	Ala
45				50					55					60	
Ile	Leu	Asn	Gly	Gly	Gly	Val	Pro	Ala	Gly	Gly	Leu	Val	Ala	Thr	Leu
		65						70					75		
Gln	Ser	Leu	Gly	Ala	Gly	Gly	Ser	Ser	Val	Val	Ile	Gly	Asn	Ile	Gly
		80				85						90			
Ala	Leu	Met	Gly	Tyr	Ala	Thr	His	Lys	Tyr	Leu	Asp	Ser	Glu	Glu	Asp
	95					100					105				
Glu	Glu														
110															

<210> 290
 <211> 86
 <212> PRT
 <213> Homo sapiens

<220>
 <221> SIGNAL

<222> -20...-1

<400> 290

Met Ala Val Gly Gly Gly Leu Ala Val Ala Gly Leu Pro Ala Leu Gly
-20 -15 -10 -5
Phe Thr Gly Ala Gly Ile Ala Ala Asn Ser Val Ala Ala Ser Leu Met
1 5 10
Ser Trp Ser Ala Ile Leu Asn Gly Gly Gly Val Pro Ala Gly Gly Leu
15 20 25
Val Ala Thr Leu Gln Ser Leu Gly Ala Gly Gly Ser Ser Val Val Ile
30 35 40
Gly Asn Ile Gly Ala Leu Met Gly Tyr Ala Thr His Lys Tyr Leu Asp
45 50 55 60
Ser Glu Glu Asp Glu Glu
65

<210> 291

<211> 207

<212> PRT

<213> Homo sapiens

<220>

<221> SIGNAL

<222> -23...-1

<400> 291

Met Ala Pro Phe Glu Pro Leu Ala Ser Gly Ile Leu Leu Leu Leu Trp
-20 -15 -10
Leu Ile Ala Pro Ser Arg Ala Cys Thr Cys Val Pro Pro His Pro Gln
-5 1 5
Thr Ala Phe Cys Asn Ser Asp Leu Val Ile Arg Ala Lys Phe Val Gly
10 15 20 25
Thr Pro Glu Val Asn Gln Thr Thr Leu Tyr Gln Arg Tyr Glu Ile Lys
30 35 40
Met Thr Lys Met Tyr Lys Gly Phe Gln Ala Leu Gly Asp Ala Ala Asp
45 50 55
Ile Arg Phe Val Tyr Thr Pro Ala Met Glu Ser Val Cys Gly Tyr Phe
60 65 70
His Arg Ser His Asn Arg Ser Glu Glu Phe Leu Ile Ala Gly Lys Leu
75 80 85
Gln Asp Gly Leu Leu His Ile Thr Thr Cys Ser Phe Val Ala Pro Trp
90 95 100 105
Asn Ser Leu Ser Leu Ala Gln Arg Arg Gly Phe Thr Lys Thr Tyr Thr
110 115 120
Val Gly Cys Glu Glu Cys Thr Val Phe Pro Cys Leu Ser Phe Pro Cys
125 130 135
Lys Leu Gln Ser Gly Thr His Cys Leu Trp Thr Asp Gln Leu Leu Gln
140 145 150
Gly Ser Glu Lys Gly Phe Gln Ser Arg His Leu Ala Cys Leu Pro Arg
155 160 165
Glu Pro Gly Leu Cys Thr Trp Gln Ser Leu Arg Ser Gln Ile Ala
170 175 180

<210> 292

<211> 111

<212> PRT

<213> Homo sapiens

<220>
 <221> SIGNAL
 <222> -24...-1

<400> 292
 Met Lys Tyr Asp Cys Pro Phe Ser Gly Thr Ser Phe Val Val Phe Ser
 -20 -15 -10
 Leu Phe Leu Ile Cys Ala Met Ala Gly Asp Val Val Tyr Ala Asp Ile
 -5 1 5
 Lys Thr Val Arg Thr Ser Pro Leu Glu Leu Ala Phe Pro Leu Gln Arg
 10 15 20
 Ser Val Ser Phe Asn Phe Ser Thr Val His Lys Ser Cys Pro Ala Lys
 25 30 35 40
 Asp Trp Lys Val His Lys Gly Lys Cys Tyr Trp Ile Ala Glu Thr Lys
 45 50 55
 Lys Ser Trp Asn Lys Ser Gln Asn Asp Cys Ala Ile Asn Asn Ser Tyr
 60 65 70
 Leu Met Val Ile Gln Asp Ile Thr Ala Met Val Arg Phe Asn Ile
 75 80 85

<210> 293
 <211> 139
 <212> PRT
 <213> Homo sapiens

<220>
 <221> SIGNAL
 <222> -15...-1

<400> 293
 Met Glu Ala Val Val Phe Val Phe Ser Leu Leu Asp Cys Cys Ala Leu
 -15 -10 -5 1
 Ile Phe Leu Ser Val Tyr Phe Ile Ile Thr Leu Ser Asp Leu Glu Cys
 5 10 15
 Asp Tyr Ile Asn Ala Arg Ser Cys Cys Ser Lys Leu Asn Lys Trp Val
 20 25 30
 Ile Pro Glu Leu Ile Gly His Thr Ile Val Thr Val Leu Leu Leu Met
 35 40 45
 Ser Leu His Trp Phe Ile Phe Leu Leu Asn Leu Pro Val Ala Thr Trp
 50 55 60 65
 Asn Ile Tyr Arg Tyr Ile Met Val Pro Ser Gly Asn Met Gly Val Phe
 70 75 80
 Asp Pro Thr Glu Ile His Asn Arg Gly Gln Leu Lys Ser His Met Lys
 85 90 95
 Glu Ala Met Ile Lys Leu Gly Phe His Leu Leu Cys Phe Phe Met Tyr
 100 105 110
 Leu Tyr Ser Met Ile Leu Ala Leu Ile Asn Asp
 115 120

<210> 294
 <211> 160
 <212> PRT
 <213> Homo sapiens

<220>
 <221> SIGNAL
 <222> -27...-1

<400> 294
Met Gln Arg Val Ser Gly Leu Leu Ser Trp Thr Leu Ser Arg Val Leu
-25 -20 -15
Trp Leu Ser Gly Leu Ser Glu Pro Gly Ala Ala Arg Gln Pro Arg Ile
-10 -5 1 5
Met Glu Glu Lys Ala Leu Glu Val Tyr Asp Leu Ile Arg Thr Ile Arg
10 15 20
Asp Pro Glu Lys Pro Asn Thr Leu Glu Glu Leu Glu Val Val Ser Glu
25 30 35
Ser Cys Val Glu Val Gln Glu Ile Asn Glu Glu Glu Tyr Leu Val Ile
40 45 50
Ile Arg Phe Thr Pro Thr Val Pro His Cys Ser Leu Ala Thr Leu Ile
55 60 65
Gly Leu Cys Leu Arg Val Lys Leu Gln Arg Cys Leu Pro Phe Lys His
70 75 80 85
Lys Leu Glu Ile Tyr Ile Ser Glu Gly Thr His Ser Thr Glu Glu Asp
90 95 100
Ile Asn Lys Gln Ile Asn Asp Lys Glu Arg Val Ala Ala Ala Met Glu
105 110 115
Asn Pro Asn Leu Arg Glu Ile Val Glu Gln Cys Val Leu Glu Pro Asp
120 125 130

<210> 295
<211> 181
<212> PRT
<213> Homo sapiens

<220>
<221> SIGNAL
<222> -16...-1

<400> 295
Met Pro Pro Phe Leu Leu Leu Thr Cys Leu Phe Ile Thr Gly Thr Ser
-15 -10 -5
Val Ser Pro Val Ala Leu Asp Pro Cys Ser Ala Tyr Ile Ser Leu Asn
1 5 10 15
Glu Pro Trp Arg Asn Thr Asp His Gln Leu Asp Glu Ser Gln Gly Pro
20 25 30
Pro Leu Cys Asp Asn His Val Asn Gly Glu Trp Tyr His Phe Thr Gly
35 40 45
Met Ala Gly Asp Ala Met Pro Thr Phe Cys Ile Pro Glu Asn His Cys
50 55 60
Gly Thr His Ala Pro Val Trp Leu Asn Gly Ser His Pro Leu Glu Gly
65 70 75 80
Asp Gly Ile Val Gln Arg Gln Ala Cys Ala Ser Phe Asn Gly Asn Cys
85 90 95
Cys Leu Trp Asn Thr Thr Val Glu Val Lys Ala Cys Pro Gly Gly Tyr
100 105 110
Tyr Val Tyr Arg Leu Thr Lys Pro Ser Val Cys Phe His Val Tyr Cys
115 120 125
Gly Arg Glu Tyr Leu Pro Cys Ala Leu Phe Leu His Gln Gln Gly His
130 135 140
Arg Trp Ser Pro Lys Val Pro Asn Tyr Arg Ile Cys Ser Tyr Ser Gly
145 150 155 160
Asn Tyr Ile Ser Ile
165

<210> 296

<211> 247
 <212> PRT
 <213> Homo sapiens

<220>
 <221> SIGNAL
 <222> -18...-1

<400> 296
 Met Gly Leu Pro Gly Leu Phe Cys Leu Ala Val Leu Ala Ala Ser Ser
 -15 -10 -5
 Phe Ser Lys Ala Arg Glu Glu Glu Ile Thr Pro Val Val Ser Ile Ala
 1 5 10
 Tyr Lys Val Leu Glu Val Phe Pro Lys Gly Arg Trp Val Leu Ile Thr
 15 20 25 30
 Cys Cys Ala Pro Gln Pro Pro Pro Ile Thr Tyr Ser Leu Cys Gly
 35 40 45
 Thr Lys Asn Ile Lys Val Ala Lys Lys Val Val Lys Thr His Glu Pro
 50 55 60
 Ala Ser Phe Asn Leu Asn Val Thr Leu Lys Ser Ser Pro Asp Leu Leu
 65 70 75
 Thr Tyr Phe Cys Arg Ala Ser Ser Thr Ser Gly Ala His Val Asp Ser
 80 85 90
 Ala Arg Leu Gln Met His Trp Glu Leu Trp Ser Lys Pro Val Ser Glu
 95 100 105 110
 Leu Arg Ala Asn Phe Thr Leu Gln Asp Arg Gly Ala Gly Pro Arg Val
 115 120 125
 Glu Met Ile Cys Gln Ala Ser Ser Gly Ser Pro Pro Ile Thr Asn Ser
 130 135 140
 Leu Ile Gly Lys Asp Gly Gln Val His Leu Gln Gln Arg Pro Cys His
 145 150 155
 Arg Gln Pro Ala Asn Phe Ser Phe Leu Pro Ser Gln Thr Ser Asp Trp
 160 165 170
 Phe Trp Cys Gln Ala Ala Asn Asn Ala Asn Val Gln His Ser Ala Leu
 175 180 185 190
 Thr Val Val Pro Pro Gly Gly Leu Pro Arg Ala Pro Thr Ile Val Leu
 195 200 205
 Val Gly Ser Leu Ala Ser Thr Ala Ala Ile Thr Ser Arg Met Leu Gly
 210 215 220
 Trp Thr Thr Trp Ala Arg Trp
 225

<210> 297
 <211> 132
 <212> PRT
 <213> Homo sapiens

<220>
 <221> SIGNAL
 <222> -41...-1

<400> 297
 Met Glu Gly Gly Ala Tyr Gly Ala Gly Lys Ala Gly Gly Ala Phe Asp
 -40 -35 -30
 Pro Tyr Thr Leu Val Arg Gln Pro His Thr Ile Leu Arg Val Val Ser
 -25 -20 -15 -10
 Trp Leu Phe Ser Ile Val Val Phe Gly Ser Ile Val Asn Glu Gly Tyr
 -5 1 5

Leu Asn Ser Ala Ser Glu Gly Glu Gln Phe Cys Ile Tyr Asn Arg Asn
 10 15 20
 Pro Asn Ala Cys Ser Tyr Gly Val Ala Val Gly Val Leu Ala Phe Leu
 25 30 35
 Thr Cys Leu Leu Tyr Leu Ala Leu Asp Val Tyr Phe Pro Gln Ile Ser
 40 45 50 55
 Ser Val Lys Asp Arg Lys Lys Ala Val Leu Ser Asp Ile Gly Val Ser
 60 65 70
 Gly Glu Pro His Pro Ala Gly Thr Pro Cys Thr Glu Ser Thr Glu Gly
 75 80 85
 Cys Pro Gly Pro
 90

<210> 298
 <211> 251
 <212> PRT
 <213> Homo sapiens

<220>
 <221> SIGNAL
 <222> -24...-1

<400> 298
 Met Leu Gly Ala Arg Leu Arg Leu Trp Val Cys Ala Leu Cys Ser Val
 -20 -15 -10
 Cys Ser Met Ser Val Leu Arg Ala Tyr Pro Asn Ala Ser Pro Leu Leu
 -5 1 5
 Gly Ser Ser Trp Gly Gly Leu Ile His Leu Tyr Thr Ala Thr Ala Arg
 10 15 20
 Asn Ser Tyr His Leu Gln Ile His Lys Asn Gly His Val Asp Gly Ala
 25 30 35 40
 Pro His Gln Thr Ile Tyr Ser Ala Leu Met Ile Arg Ser Glu Asp Ala
 45 50 55
 Gly Phe Val Val Ile Thr Gly Val Met Ser Arg Arg Tyr Leu Cys Met
 60 65 70
 Asp Phe Arg Gly Asn Ile Phe Gly Ser His Tyr Phe Asp Pro Glu Asn
 75 80 85
 Cys Arg Phe Gln His Gln Thr Leu Glu Asn Gly Tyr Asp Val Tyr His
 90 95 100
 Ser Pro Gln Tyr His Phe Leu Val Ser Leu Gly Arg Ala Lys Arg Ala
 105 110 115 120
 Phe Leu Pro Gly Met Asn Pro Pro Pro Tyr Ser Gln Phe Leu Ser Arg
 125 130 135
 Arg Asn Glu Ile Pro Leu Ile His Phe Asn Thr Pro Ile Pro Arg Arg
 140 145 150
 His Thr Arg Ser Ala Glu Asp Asp Ser Glu Arg Asp Pro Leu Asn Val
 155 160 165
 Leu Lys Pro Arg Ala Arg Met Thr Pro Ala Pro Ala Ser Cys Ser Gln
 170 175 180
 Glu Leu Pro Ser Ala Glu Asp Asn Ser Pro Met Ala Ser Asp Pro Leu
 185 190 195 200
 Gly Val Val Arg Gly Gly Arg Val Asn Thr His Ala Gly Gly Thr Gly
 205 210 215
 Pro Glu Gly Cys Arg Pro Phe Ala Lys Phe Ile
 220 225

<210> 299
 <211> 137

<212> PRT
 <213> Homo sapiens

<220>
 <221> SIGNAL
 <222> -22...-1

<400> 299
 Met Leu Ser Gly Arg Leu Val Leu Gly Leu Val Ser Met Ala Gly Arg
 -20 -15 -10
 Val Cys Leu Cys Gln Gly Ser Ala Gly Ser Gly Ala Ile Gly Pro Val
 -5 1 5 10
 Glu Ala Ala Ile Arg Thr Lys Leu Glu Glu Ala Leu Ser Pro Glu Val
 15 20 25
 Leu Glu Leu Arg Asn Glu Ser Gly Gly His Ala Val Pro Pro Gly Ser
 30 35 40
 Glu Thr His Phe Arg Val Ala Val Val Ser Ser Arg Phe Glu Gly Leu
 45 50 55
 Ser Pro Leu Gln Arg His Arg Leu Val His Ala Ala Leu Ala Glu Glu
 60 65 70
 Leu Gly Gly Pro Val His Ala Leu Ala Ile Gln Ala Arg Thr Pro Ala
 75 80 85 90
 Gln Trp Arg Glu Asn Ser Gln Leu Asp Thr Ser Pro Pro Cys Leu Gly
 95 100 105
 Gly Asn Lys Lys Thr Leu Gly Thr Pro
 110 115

<210> 300
 <211> 541
 <212> PRT
 <213> Homo sapiens

<220>
 <221> SIGNAL
 <222> -28...-1

<400> 300
 Met Gly Ser Gln Glu Val Leu Gly His Ala Ala Arg Leu Ala Ser Ser
 -25 -20 -15
 Gly Leu Leu Leu Gln Val Leu Phe Arg Leu Ile Thr Phe Val Leu Asn
 -10 -5 1
 Ala Phe Ile Leu Arg Phe Leu Ser Lys Glu Ile Val Gly Val Val Asn
 5 10 15 20
 Val Arg Leu Thr Leu Leu Tyr Ser Thr Thr Leu Phe Leu Ala Arg Glu
 25 30 35
 Ala Phe Arg Arg Ala Cys Leu Ser Gly Gly Thr Gln Arg Asp Trp Ser
 40 45 50
 Gln Thr Leu Asn Leu Leu Trp Leu Thr Val Pro Leu Gly Val Phe Trp
 55 60 65
 Ser Leu Phe Leu Gly Trp Ile Trp Leu Gln Leu Leu Glu Val Pro Asp
 70 75 80
 Pro Asn Val Val Pro His Tyr Ala Thr Gly Val Val Leu Phe Gly Leu
 85 90 95 100
 Ser Ala Val Val Glu Leu Leu Gly Glu Pro Phe Trp Val Leu Ala Gln
 105 110 115
 Ala His Met Phe Val Lys Leu Lys Val Ile Ala Glu Ser Leu Ser Val
 120 125 130
 Ile Leu Lys Ser Val Leu Thr Ala Phe Leu Val Leu Trp Leu Pro His

				50					55					60			
Ser	Leu	Gln	Gln	Glu	Ala	Arg	Gln	Ala	Pro	Arg	Pro	Asn	Asn	Leu	His		
			65					70					75				
Thr	Leu	Cys	Gly	Ala	Pro	Val	His	Val	Arg	Glu	Arg	Gly	Thr	Gly	Ser		
		80					85					90					
Glu	Thr	Asn	Gln	Glu	Thr	Leu	Arg	Ala	Thr	Ala	Pro	Ala	Leu	Pro	Met		
	95					100					105						
Ala	Pro	Ala	Pro	Pro	Leu	Leu	Ala	Ala	Ala	Leu	Ala	Leu	Ala	Tyr	Leu		
110					115					120					125		
Leu	Arg	Pro	Leu	Ala													
				130													

<210> 303
 <211> 148
 <212> PRT
 <213> Homo sapiens

<220>
 <221> SIGNAL
 <222> -25..-1

<400> 303																	
Met	Ala	Ser	Val	Val	Leu	Ala	Leu	Arg	Thr	Arg	Thr	Ala	Val	Thr	Ser		
-25					-20					-15					-10		
Leu	Leu	Ser	Pro	Thr	Pro	Ala	Thr	Ala	Leu	Ala	Val	Arg	Tyr	Ala	Ser		
			-5					1				5					
Lys	Lys	Ser	Gly	Gly	Ser	Ser	Lys	Asn	Leu	Gly	Gly	Lys	Ser	Ser	Gly		
	10					15					20						
Arg	Arg	Gln	Gly	Ile	Lys	Lys	Met	Glu	Gly	His	Tyr	Val	His	Ala	Gly		
25					30					35							
Asn	Ile	Ile	Ala	Thr	Gln	Arg	His	Phe	Arg	Trp	His	Pro	Gly	Ala	His		
40					45				50						55		
Val	Gly	Val	Gly	Lys	Asn	Lys	Cys	Leu	Tyr	Ala	Leu	Glu	Glu	Gly	Ile		
				60				65					70				
Val	Arg	Tyr	Thr	Lys	Glu	Val	Tyr	Val	Pro	His	Pro	Arg	Asn	Thr	Glu		
		75				80						85					
Ala	Val	Asp	Leu	Ile	Thr	Arg	Leu	Pro	Lys	Gly	Ala	Val	Leu	Tyr	Lys		
	90					95				100							
Thr	Phe	Val	His	Val	Val	Pro	Ala	Lys	Pro	Glu	Gly	Thr	Phe	Lys	Leu		
105					110					115							
Val	Ala	Met	Leu														
120																	

<210> 304
 <211> 291
 <212> PRT
 <213> Homo sapiens

<220>
 <221> SIGNAL
 <222> -34..-1

<400> 304																	
Met	Glu	Ser	Glu	Arg	Ser	Lys	Arg	Met	Gly	Asn	Ala	Cys	Ile	Pro	Leu		
			-30					-25						-20			
Lys	Arg	Ile	Ala	Tyr	Phe	Leu	Cys	Leu	Leu	Ser	Ala	Leu	Leu	Leu	Thr		
		-15					-10						-5				
Glu	Gly	Lys	Lys	Pro	Ala	Lys	Pro	Lys	Cys	Pro	Ala	Val	Cys	Thr	Cys		

<212> PRT
 <213> Homo sapiens

<220>
 <221> SIGNAL
 <222> -30..-1

<400> 306
 Met Ala Ala Thr Ser Gly Thr Asp Glu Pro Val Ser Gly Glu Leu Val
 -30 -25 -20 -15
 Ser Val Ala His Ala Leu Ser Leu Pro Ala Glu Ser Tyr Gly Asn Asp
 -10 -5 1
 Pro Asp Ile Glu Met Ala Trp Ala Met Arg Ala Met Gln His Ala Glu
 5 10 15
 Val Tyr Tyr Lys Leu Ile Ser Ser Val Asp Pro Gln Phe Leu Lys Leu
 20 25 30
 Thr Lys Val Asp Asp Gln Ile Tyr Ser Glu Phe Arg Lys Asn Phe Glu
 35 40 45 50
 Thr Leu Arg Ile Asp Val Leu Asp Pro Glu Glu Leu Lys Ser Glu Ser
 55 60 65
 Ala Lys Glu Lys Trp Arg Pro Phe Cys Leu Lys Phe Asn Gly Ile Val
 70 75 80
 Glu Asp Phe Asn Tyr Gly Thr Leu Leu Arg Leu Asp Cys Ser Gln Gly
 85 90 95
 Tyr Thr Glu Glu Asn Thr Ile Phe Ala Pro Arg Ile Gln Phe Phe Ala
 100 105 110
 Ile Glu Ile Ala Arg Asn Arg Glu Gly Tyr Asn Lys Ala Val Tyr Ile
 115 120 125 130
 Ser Val Gln Asp Lys Glu Gly Glu Lys Gly Val Asn Asn Gly Gly Glu
 135 140 145
 Lys Arg Ala Asp Ser Gly Glu Glu Glu Asn Thr Lys Asn Gly Gly Glu
 150 155 160
 Lys Gly Ala Asp Ser Gly Glu Glu Lys Glu Glu Gly Ile Asn Arg Glu
 165 170 175
 Asp Lys Thr Asp Lys Gly Gly Glu Lys Gly Lys Glu Ala Asp Lys Glu
 180 185 190
 Ile Asn Lys Ser Gly Glu Lys Ala Met
 195 200

<210> 307
 <211> 85
 <212> PRT
 <213> Homo sapiens

<220>
 <221> SIGNAL
 <222> -20..-1

<400> 307
 Met Arg Gln Lys Ala Val Ser Leu Phe Leu Cys Tyr Leu Leu Leu Phe
 -20 -15 -10 -5
 Thr Cys Ser Gly Val Glu Ala Gly Lys Lys Cys Ser Glu Ser Ser
 1 5 10
 Asp Ser Gly Ser Gly Phe Trp Lys Ala Leu Thr Phe Met Ala Val Gly
 15 20 25
 Gly Gly Leu Ala Val Ala Gly Leu Pro Ala Leu Gly Phe Thr Gly Ala
 30 35 40
 Gly Ile Ala Ala Asn Ser Val Ala Ala Ser Leu Met Ser Trp Ser Ala

Year	1990	1991	1992	1993	1994	1995	1996	1997	1998	1999	2000	2001	2002	2003	2004	2005	2006	2007	2008	2009	2010	2011	2012	2013	2014	2015	2016	2017	2018	2019	2020	2021	2022	2023	2024	2025	2026	2027	2028	2029	2030	2031	2032	2033	2034	2035	2036	2037	2038	2039	2040	2041	2042	2043	2044	2045	2046	2047	2048	2049	2050	2051	2052	2053	2054	2055	2056	2057	2058	2059	2060	2061	2062	2063	2064	2065	2066	2067	2068	2069	2070	2071	2072	2073	2074	2075	2076	2077	2078	2079	2080	2081	2082	2083	2084	2085	2086	2087	2088	2089	2090	2091	2092	2093	2094	2095	2096	2097	2098	2099	2100
1990	1991	1992	1993	1994	1995	1996	1997	1998	1999	2000	2001	2002	2003	2004	2005	2006	2007	2008	2009	2010	2011	2012	2013	2014	2015	2016	2017	2018	2019	2020	2021	2022	2023	2024	2025	2026	2027	2028	2029	2030	2031	2032	2033	2034	2035	2036	2037	2038	2039	2040	2041	2042	2043	2044	2045	2046	2047	2048	2049	2050	2051	2052	2053	2054	2055	2056	2057	2058	2059	2060	2061	2062	2063	2064	2065	2066	2067	2068	2069	2070	2071	2072	2073	2074	2075	2076	2077	2078	2079	2080	2081	2082	2083	2084	2085	2086	2087	2088	2089	2090	2091	2092	2093	2094	2095	2096	2097	2098	2099	2100	

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<220>
<221> SIGNAL
<222> -43..-1
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<210> 309
<211> 291
<212> PRT
<213> Homo sapiens
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304

Thr	Arg	Gln	His	Gly	Asp	Asp	Ala	Ser	Glu	Glu	Lys	Ala	Ala	Asn	Gln	
			200					205					210			
Ile	Arg	Lys	Cys	Gln	Gln	Ser	Thr	Ser	Ala	Val	Ile	Gly	Val	Arg	Val	
		215					220					225				
Cys	Gly	Met	Gln	Val	Tyr	Gln	Ala	Gly	Ser	Gly	Gln	Leu	Met	Phe	Met	
	230					235					240					
Asn	Lys	Tyr	His	Gly	Arg	Lys	Leu	Ser	Met	Gln	Gly	Phe	Lys	Glu	Ala	
245					250					255					260	
Leu	Phe	Gln	Phe	Phe	His	Asn	Gly	Arg	Tyr	Leu	Arg	Arg	Glu	Leu	Leu	
			265					270						275		
Gly	Pro	Val	Leu	Lys	Lys	Leu	Thr	Glu	Leu	Lys	Ala	Val	Leu	Glu	Arg	
		280					285						290			
Gln	Glu	Ser	Tyr	Arg	Phe	Tyr	Ser	Ser	Ser	Leu	Leu	Val	Ile	Tyr	Asp	
	295						300					305				
Gly	Lys	Glu	Arg	Pro	Glu	Val	Val	Leu	Asp	Ser	Asp	Ala	Glu	Asp	Leu	
	310				315						320					
Glu	Asp	Leu	Ser	Glu	Glu	Ser	Ala	Asp	Glu	Ser	Ala	Gly	Ala	Tyr	Ala	
325					330					335					340	
Tyr	Lys	Pro	Ile	Gly	Ala	Ser	Ser	Val	Asp	Val	Arg	Met	Ile	Asp	Phe	
			345					350						355		
Ala	His	Thr	Thr	Cys	Arg	Leu	Tyr	Gly	Glu	Asp	Thr	Val	Val	His	Glu	
		360					365						370			
Gly	Gln	Asp	Ala	Gly	Tyr	Ile	Phe	Gly	Leu	Gln	Ser	Leu	Ile	Asp	Ile	
		375				380						385				
Val	Thr	Glu	Ile	Ser	Glu	Glu	Ser	Gly	Glu							
	390					395										

<210> 311
 <211> 466
 <212> PRT
 <213> Homo sapiens

<220>
 <221> SIGNAL
 <222> -16...-1

<400>	311															
Met	Gly	Leu	Tyr	Ala	Ala	Ala	Ala	Gly	Val	Leu	Ala	Gly	Val	Glu	Ser	
	-15					-10					-5					
Arg	Gln	Gly	Ser	Ile	Lys	Gly	Leu	Val	Tyr	Ser	Ser	Asn	Phe	Gln	Asn	
1			5					10						15		
Val	Lys	Gln	Leu	Tyr	Ala	Leu	Val	Cys	Glu	Thr	Gln	Arg	Tyr	Ser	Ala	
		20					25						30			
Val	Leu	Asp	Ala	Val	Ile	Ala	Ser	Ala	Gly	Leu	Leu	Arg	Ala	Glu	Lys	
	35					40					45					
Lys	Leu	Arg	Pro	His	Leu	Ala	Lys	Val	Leu	Val	Tyr	Glu	Leu	Leu	Leu	
	50				55						60					
Gly	Lys	Gly	Phe	Arg	Gly	Gly	Gly	Gly	Arg	Trp	Lys	Ala	Leu	Leu	Gly	
65				70				75						80		
Arg	His	Gln	Ala	Arg	Leu	Lys	Ala	Glu	Leu	Ala	Arg	Leu	Lys	Val	His	
			85					90						95		
Arg	Gly	Val	Ser	Arg	Asn	Glu	Asp	Leu	Leu	Glu	Val	Gly	Ser	Arg	Pro	
		100					105						110			
Gly	Pro	Ala	Ser	Gln	Leu	Pro	Arg	Phe	Val	Arg	Val	Asn	Thr	Leu	Lys	
	115					120						125				
Thr	Cys	Ser	Asp	Asp	Val	Val	Asp	Tyr	Phe	Lys	Arg	Gln	Gly	Phe	Ser	
	130				135						140					
Tyr	Gln	Gly	Arg	Ala	Ser	Ser	Leu	Asp	Asp	Leu	Arg	Ala	Leu	Lys	Gly	

145					150					155					160
Lys	His	Phe	Leu	Leu	Asp	Pro	Leu	Met	Pro	Glu	Leu	Leu	Val	Phe	Pro
				165					170					175	
Ala	Gln	Thr	Asp	Leu	His	Glu	His	Pro	Leu	Tyr	Arg	Ala	Gly	His	Leu
			180					185					190		
Ile	Leu	Gln	Asp	Arg	Ala	Ser	Cys	Leu	Pro	Ala	Met	Leu	Leu	Asp	Pro
		195					200					205			
Pro	Pro	Gly	Ser	His	Val	Ile	Asp	Ala	Cys	Ala	Ala	Pro	Gly	Asn	Lys
	210					215					220				
Thr	Ser	His	Leu	Ala	Ala	Leu	Leu	Lys	Asn	Gln	Gly	Lys	Ile	Phe	Ala
225					230					235				240	
Phe	Asp	Leu	Asp	Ala	Lys	Arg	Leu	Ala	Ser	Met	Ala	Thr	Leu	Leu	Ala
				245				250						255	
Arg	Ala	Gly	Val	Ser	Cys	Cys	Glu	Leu	Ala	Glu	Glu	Asp	Phe	Leu	Ala
			260				265					270			
Val	Ser	Pro	Ser	Asp	Pro	Arg	Tyr	His	Glu	Val	His	Tyr	Ile	Leu	Leu
	275						280					285			
Asp	Pro	Ser	Cys	Ser	Gly	Ser	Gly	Met	Pro	Ser	Arg	Gln	Leu	Glu	Glu
	290					295					300				
Pro	Gly	Ala	Gly	Thr	Pro	Ser	Pro	Val	Arg	Leu	His	Ala	Leu	Ala	Gly
305					310					315				320	
Phe	Gln	Gln	Arg	Ala	Leu	Cys	His	Ala	Leu	Thr	Phe	Pro	Ser	Leu	Gln
				325					330					335	
Arg	Leu	Val	Tyr	Ser	Thr	Cys	Ser	Leu	Cys	Gln	Glu	Glu	Asn	Glu	Asp
		340						345					350		
Val	Val	Arg	Asp	Ala	Leu	Gln	Gln	Asn	Pro	Gly	Ala	Phe	Arg	Leu	Ala
	355						360					365			
Pro	Ala	Leu	Pro	Ala	Trp	Pro	His	Arg	Gly	Leu	Ser	Thr	Phe	Pro	Gly
	370					375					380				
Ala	Glu	His	Cys	Leu	Arg	Ala	Ser	Pro	Glu	Thr	Thr	Leu	Ser	Ser	Gly
385					390					395				400	
Phe	Phe	Val	Ala	Val	Ile	Glu	Arg	Val	Glu	Val	Pro	Ser	Ser	Ala	Ser
				405					410					415	
Gln	Ala	Lys	Ala	Ser	Ala	Pro	Glu	Arg	Thr	Pro	Ser	Pro	Ala	Pro	Lys
			420				425					430			
Arg	Lys	Lys	Arg	Gln	Gln	Arg	Ala	Ala	Ala	Gly	Ala	Cys	Thr	Pro	Pro
		435				440						445			
Cys	Thr														
	450														

<210> 312
 <211> 382
 <212> PRT
 <213> Homo sapiens

<220>
 <221> SIGNAL
 <222> -16..-1

<400> 312															
Met	Gly	Leu	Tyr	Ala	Ala	Ala	Ala	Gly	Val	Leu	Ala	Gly	Val	Glu	Ser
-15						-10					-5				
Arg	Gln	Gly	Ser	Ile	Lys	Gly	Leu	Val	Tyr	Ser	Ser	Asn	Phe	Gln	Asn
1			5					10					15		
Val	Lys	Gln	Leu	Tyr	Ala	Leu	Val	Cys	Glu	Thr	Gln	Arg	Tyr	Ser	Ala
		20					25					30			
Val	Leu	Asp	Ala	Val	Ile	Ala	Ser	Ala	Gly	Leu	Leu	Arg	Ala	Glu	Lys
	35					40						45			

Lys Leu Arg Pro His Leu Ala Lys Val Leu Val Tyr Glu Leu Leu Leu
 50 55 60
 Gly Lys Gly Phe Arg Gly Gly Gly Arg Trp Lys Ala Leu Leu Gly
 65 70 75 80
 Arg His Gln Ala Arg Leu Lys Ala Glu Leu Ala Arg Leu Lys Val His
 85 90 95
 Arg Gly Val Ser Arg Asn Glu Asp Leu Leu Glu Val Gly Ser Arg Pro
 100 105 110
 Gly Pro Ala Ser Gln Leu Pro Arg Phe Val Arg Val Asn Thr Leu Lys
 115 120 125
 Thr Cys Ser Asp Asp Val Val Asp Tyr Phe Lys Arg Gln Gly Phe Ser
 130 135 140
 Tyr Gln Gly Arg Ala Ser Ser Leu Asp Asp Leu Arg Ala Leu Lys Gly
 145 150 155 160
 Lys His Phe Leu Leu Asp Pro Leu Met Pro Glu Leu Leu Val Phe Pro
 165 170 175
 Ala Gln Thr Asp Leu His Glu His Pro Leu Tyr Arg Ala Gly His Leu
 180 185 190
 Ile Leu Gln Asp Arg Ala Ser Cys Leu Pro Ala Met Leu Leu Asp Pro
 195 200 205
 Pro Pro Gly Ser His Val Ile Asp Ala Cys Ala Ala Pro Gly Asn Lys
 210 215 220
 Thr Ser His Leu Ala Ala Leu Leu Lys Asn Gln Gly Lys Ile Phe Ala
 225 230 235 240
 Phe Asp Leu Asp Ala Lys Arg Leu Ala Ser Met Ala Thr Leu Leu Ala
 245 250 255
 Arg Ala Gly Val Ser Cys Cys Glu Leu Ala Glu Glu Asp Phe Leu Ala
 260 265 270
 Val Ser Pro Ser Asp Pro Arg Tyr His Glu Val His Tyr Ile Leu Leu
 275 280 285
 Asp Pro Ser Cys Ser Gly Ser Gly Met Pro Ser Arg Gln Leu Glu Glu
 290 295 300
 Pro Gly Ala Gly Thr Pro Ser Pro Val Arg Leu His Ala Leu Ala Ala
 305 310 315 320
 Ser Ser Ser Glu Pro Cys Ala Thr Arg Ser Leu Ser Leu Pro Cys Ser
 325 330 335
 Gly Ser Ser Thr Pro Arg Ala Pro Ser Ala Arg Arg Arg Met Lys Thr
 340 345 350
 Trp Cys Glu Met Arg Cys Ser Arg Thr Arg Ala Pro Ser Gly
 355 360 365

<210> 313
 <211> 258
 <212> PRT
 <213> Homo sapiens

<220>
 <221> SIGNAL
 <222> -36..-1

<400> 313
 Met Glu Glu Leu Gln Glu Pro Leu Arg Gly Glu Leu Arg Leu Cys Phe
 -35 -30 -25
 Thr Gln Ala Ala Arg Thr Ser Leu Leu Leu Leu Arg Leu Asn Asp Ala
 -20 -15 -10 -5
 Ala Leu Arg Ala Leu Gln Glu Cys Gln Arg Gln Gln Val Arg Pro Val
 1 5 10
 Ile Ala Phe Gln Gly His Arg Gly Tyr Leu Arg Leu Pro Gly Pro Gly

<400> 316
 Met Ala Phe Thr Phe Ala Ala Phe Cys Tyr Met Leu Ser Leu Val Leu
 -15 -10 -5
 Cys Ala Ala Leu Ile Phe Phe Ala Ile Trp His Ile Ile Ala Phe Asp
 1 5 10 15
 Glu Leu Arg Thr Asp Phe Lys Ser Pro Ile Asp Gln Cys Asn Pro Val
 20 25 30
 His Ala Arg Glu Arg Leu Arg Asn Ile Glu Arg Ile Cys Phe Leu Leu
 35 40 45
 Arg Lys Leu Val Leu Pro Glu Tyr Ser Ile His Ser Leu Phe Cys Ile
 50 55 60
 Met Phe Leu Cys Ala Gln Glu Trp Leu Thr Leu Gly Leu Asn Val Pro
 65 70 75
 Leu Leu Phe Tyr His Phe Trp Arg Tyr Phe His Cys Pro Ala Asp Ser
 80 85 90 95
 Ser Glu Leu Ala Tyr Asp Pro Pro Val Val Met Asn Pro Asp Thr Leu
 100 105 110
 Ser Tyr Cys Gln Lys Glu Ala Trp Cys Lys Leu Ala Phe Tyr Leu Leu
 115 120 125
 Ser Phe Phe Tyr Tyr Leu Tyr Cys Met Ile Tyr Thr Leu Val Ser Ser
 130 135 140

<210> 317
 <211> 426
 <212> PRT
 <213> Homo sapiens

<220>
 <221> SIGNAL
 <222> -28..-1

<400> 317
 Met Ser Pro Ala Phe Arg Ala Met Asp Val Glu Pro Arg Ala Lys Gly
 -25 -20 -15
 Val Leu Leu Glu Pro Phe Val His Gln Val Gly Gly His Ser Cys Val
 -10 -5 1
 Leu Arg Phe Asn Glu Thr Thr Leu Cys Lys Pro Leu Val Pro Arg Glu
 5 10 15 20
 His Gln Phe Tyr Glu Thr Leu Pro Ser Glu Met Arg Lys Phe Thr Pro
 25 30 35
 Gln Tyr Lys Gly Val Val Ser Val Arg Phe Glu Glu Asp Glu Asp Arg
 40 45 50
 Asn Leu Cys Leu Ile Ala Tyr Pro Leu Lys Gly Asp His Gly Ile Val
 55 60 65
 Asp Ile Val Asp Asn Ser Asp Cys Glu Pro Lys Ser Lys Leu Leu Arg
 70 75 80
 Trp Thr Thr Asn Lys Lys His His Val Leu Glu Thr Glu Lys Thr Pro
 85 90 95 100
 Lys Asp Trp Val Arg Gln His Arg Lys Glu Glu Lys Met Lys Ser His
 105 110 115
 Lys Leu Glu Glu Glu Phe Glu Trp Leu Lys Lys Ser Glu Val Leu Tyr
 120 125 130
 Tyr Thr Val Glu Lys Lys Gly Asn Ile Ser Ser Gln Leu Lys His Tyr
 135 140 145
 Asn Pro Trp Ser Met Lys Cys His Gln Gln Gln Leu Gln Arg Met Lys
 150 155 160
 Glu Asn Ala Lys His Arg Asn Gln Tyr Lys Phe Ile Leu Leu Glu Asn
 165 170 175 180

Leu Thr Ser Arg Tyr Glu Val Pro Cys Val Leu Asp Leu Lys Met Gly
 185 190 195
 Thr Arg Gln His Gly Asp Asp Ala Ser Glu Glu Lys Ala Ala Asn Gln
 200 205 210
 Ile Arg Lys Cys Gln Gln Ser Thr Ser Ala Val Ile Gly Val Arg Val
 215 220 225
 Cys Gly Met Gln Val Tyr Gln Ala Gly Ser Gly Gln Leu Met Phe Met
 230 235 240
 Asn Lys Tyr His Gly Arg Lys Leu Ser Val Gln Gly Phe Lys Glu Ala
 245 250 255 260
 Leu Phe Gln Phe Phe His Asn Gly Arg Tyr Leu Arg Arg Glu Leu Leu
 265 270 275
 Gly Pro Val Leu Lys Lys Leu Thr Glu Leu Lys Ala Val Leu Glu Arg
 280 285 290
 Gln Glu Ser Tyr Arg Phe Tyr Ser Ser Ser Leu Leu Val Ile Tyr Asp
 295 300 305
 Gly Lys Glu Arg Pro Glu Val Val Leu Asp Ser Asp Ala Glu Asp Leu
 310 315 320
 Glu Asp Leu Ser Glu Glu Ser Ala Asp Glu Ser Ala Gly Ala Tyr Ala
 325 330 335 340
 Tyr Lys Pro Ile Gly Ala Ser Ser Val Asp Val Arg Met Ile Asp Phe
 345 350 355
 Ala His Thr Thr Cys Arg Leu Tyr Gly Glu Asp Thr Val Val His Glu
 360 365 370
 Gly Gln Asp Ala Gly Tyr Ile Phe Gly Leu Gln Ser Leu Ile Asp Ile
 375 380 385
 Val Thr Glu Ile Ser Glu Glu Ser Gly Glu
 390 395

<210> 318
 <211> 301
 <212> PRT
 <213> Homo sapiens

<220>
 <221> SIGNAL
 <222> -20...-1

<400> 318
 Met Ala Arg His Gly Leu Pro Leu Leu Pro Leu Leu Ser Leu Leu Val
 -20 -15 -10 -5
 Gly Ala Trp Leu Lys Leu Gly Asn Gly Gln Ala Thr Ser Met Val Gln
 1 5 10
 Leu Gln Gly Gly Arg Phe Leu Met Gly Thr Asn Ser Pro Asp Ser Arg
 15 20 25
 Asp Gly Glu Gly Pro Val Arg Glu Ala Thr Val Lys Pro Phe Ala Ile
 30 35 40
 Asp Ile Phe Pro Val Thr Asn Lys Asp Phe Arg Asp Phe Val Arg Glu
 45 50 55 60
 Lys Lys Tyr Arg Thr Glu Ala Glu Met Phe Gly Leu Ser Phe Val Phe
 65 70 75
 Glu Asp Phe Val Ser Asp Glu Leu Arg Asn Lys Ala Thr Gln Pro Met
 80 85 90
 Lys Ser Val Leu Trp Trp Leu Pro Val Glu Lys Ala Phe Trp Arg Gln
 95 100 105
 Pro Ala Gly Pro Gly Ser Gly Ile Arg Glu Arg Leu Glu His Pro Val
 110 115 120
 Leu His Val Ser Trp Asn Asp Ala Arg Ala Tyr Cys Ala Trp Arg Gly

125					130					135					140
Lys	Arg	Leu	Pro	Thr	Glu	Glu	Glu	Trp	Glu	Phe	Ala	Ala	Arg	Gly	Gly
				145					150					155	
Leu	Lys	Gly	Gln	Val	Tyr	Pro	Trp	Gly	Asn	Trp	Phe	Gln	Pro	Asn	Arg
			160					165					170		
Thr	Asn	Leu	Trp	Gln	Gly	Lys	Phe	Pro	Lys	Gly	Asp	Lys	Ala	Glu	Asp
		175				180						185			
Gly	Phe	His	Gly	Val	Ser	Pro	Val	Asn	Ala	Phe	Pro	Ala	Gln	Asn	Asn
	190				195					200					
Tyr	Gly	Leu	Tyr	Asp	Leu	Leu	Gly	Asn	Val	Trp	Glu	Trp	Thr	Ala	Ser
205				210					215					220	
Pro	Tyr	Gln	Ala	Ala	Glu	Gln	Asp	Met	Arg	Val	Leu	Arg	Gly	Ala	Ser
			225					230					235		
Trp	Ile	Asp	Thr	Ala	Asp	Gly	Ser	Ala	Asn	His	Arg	Ala	Arg	Val	Thr
		240					245					250			
Thr	Arg	Met	Gly	Asn	Thr	Pro	Asp	Ser	Ala	Ser	Asp	Asn	Leu	Gly	Phe
		255			260						265				
Arg	Cys	Ala	Ala	Asp	Ala	Gly	Arg	Pro	Pro	Gly	Glu	Leu			
	270				275						280				

<210> 319
 <211> 119
 <212> PRT
 <213> Homo sapiens

<220>
 <221> SIGNAL
 <222> -17...-1

<400> 319															
Met	Gly	Ser	Gly	Trp	Leu	Thr	Ala	Val	Ala	Ser	Leu	Leu	Pro	Ser	Pro
	-15						-10				-5				
Gly	Asn	Ser	Glu	Leu	Pro	Val	Gln	Ala	Leu	Gly	Arg	Arg	Gly	Gly	Arg
1				5					10				15		
Asp	Trp	Ala	Arg	Asn	Glu	Ala	Gly	Arg	Asp	Leu	Glu	Lys	Pro	Pro	Arg
			20				25						30		
Leu	His	Cys	Ser	Gly	Arg	Gly	Arg	Leu	Glu	Glu	Pro	Val	Pro	Pro	Asn
		35				40						45			
His	Leu	Pro	Val	Gly	Leu	Ser	Val	Arg	Gly	Ser	Gln	Val	Leu	Ser	Ser
	50					55					60				
Ala	Gly	Pro	Arg	Arg	Cys	Arg	Leu	Thr	Gly	Thr	Arg	Asn	Pro	Val	Arg
	65				70				75						
Gly	Pro	Arg	Arg	Val	Glu	Gln	Ile	Ala	Arg	Gly	Gly	Pro	Glu	Ala	Arg
80				85					90					95	
Arg	Gln	Ala	Gly	Asp	Ser	Cys									
				100											

<210> 320
 <211> 95
 <212> PRT
 <213> Homo sapiens

<220>
 <221> SIGNAL
 <222> -39...-1

<400> 320
 Met Asp Tyr Ser Arg Val Phe Gln Gly Val Phe Phe Thr Phe Lys His

				-35					-30					-25			
Ala	Phe	Ala	Asp	Gly	Ala	Trp	Asp	Leu	Ser	Phe	Leu	Cys	Ala	Leu	Cys		
			-20					-15					-10				
Ser	Phe	Cys	Pro	Ile	Ser	Ala	Ala	Ser	Gly	Arg	Pro	Tyr	Arg	Tyr	Leu		
		-5					1				5						
Glu	Phe	Trp	Arg	Leu	Tyr	Leu	Ser	Pro	Ser	Ser	Met	Glu	Asn	Gly	Val		
10				15					20						25		
Gln	Lys	Phe	His	Glu	Thr	Phe	Phe	Ile	Val	Phe	Leu	Leu	Leu	Phe	Asp		
			30					35						40			
Ile	Glu	Arg	Lys	Gly	Lys	Ser	Ser	Val	Cys	Pro	Phe	Cys	Tyr	Arg			
			45					50					55				

<210> 321
 <211> 191
 <212> PRT
 <213> Homo sapiens

<220>
 <221> SIGNAL
 <222> -39...-1

<400> 321																	
Met	Met	Thr	Ile	Thr	Phe	Leu	Pro	Tyr	Thr	Phe	Ser	Leu	Met	Val	Thr		
			-35					-30					-25				
Phe	Pro	Asp	Val	Pro	Leu	Gly	Ile	Phe	Leu	Phe	Cys	Val	Cys	Val	Ile		
		-20					-15				-10						
Ala	Ile	Gly	Val	Val	Gln	Ala	Leu	Ile	Val	Gly	Tyr	Ala	Phe	His	Phe		
		-5				1				5							
Pro	His	Leu	Leu	Ser	Pro	Gln	Ile	Gln	Arg	Ser	Ala	His	Arg	Ala	Leu		
10				15				20						25			
Tyr	Arg	Arg	His	Val	Leu	Gly	Ile	Val	Leu	Gln	Gly	Pro	Ala	Leu	Cys		
			30				35						40				
Phe	Ala	Ala	Ala	Ile	Phe	Ser	Leu	Phe	Phe	Val	Pro	Leu	Ser	Tyr	Leu		
			45				50					55					
Leu	Met	Val	Thr	Val	Ile	Leu	Leu	Pro	Tyr	Val	Ser	Lys	Val	Thr	Gly		
		60				65					70						
Trp	Cys	Arg	Asp	Arg	Leu	Leu	Gly	His	Arg	Glu	Pro	Ser	Ala	His	Pro		
	75				80				85								
Val	Glu	Val	Phe	Ser	Phe	Asp	Leu	His	Glu	Pro	Leu	Ser	Lys	Glu	Arg		
90				95					100					105			
Val	Glu	Ala	Phe	Ser	Asp	Gly	Val	Tyr	Ala	Ile	Val	Ala	Thr	Leu	Leu		
			110				115						120				
Ile	Leu	Asp	Ile	Cys	Pro	Ser	Cys	Ser	Leu	Trp	Leu	Ala	Val	Ala	Ser		
		125				130						135					
Phe	Gln	Arg	Leu	Leu	Leu	Arg	Gly	Leu	Ile	Cys	Leu	Phe	Val	Cys			
		140				145					150						

<210> 322
 <211> 89
 <212> PRT
 <213> Homo sapiens

<220>
 <221> SIGNAL
 <222> -41...-1

<400> 322
 Met Pro Pro Thr Arg Asp Pro Phe Gln Gln Pro Thr Leu Asp Asn Asp

-40 -35 -30
 Asp Ser Tyr Leu Gly Glu Leu Arg Ala Ser Lys Val Leu Trp Phe Leu
 -25 -20 -15 -10
 Ala Gln Ile Pro Ser Arg Val Ala Gly Ser Leu Leu Ser Val Cys Val
 -5 1 5
 Met Ser Arg Asp Gly Asn Ile Lys Asp Ser Gly Glu Asp Thr Gln Ser
 10 15 20
 Gly Thr Arg Glu Val Cys Phe Leu Pro Ala Ser Leu Ser Pro Tyr Ser
 25 30 35
 Ser Arg Leu Thr Phe Gln Arg Arg Phe
 40 45

<210> 323
 <211> 70
 <212> PRT
 <213> Homo sapiens

<220>
 <221> SIGNAL
 <222> -38...-1

<400> 323
 Met Ser Ser Pro Gln Leu Pro Ala Phe Leu Trp Asp Lys Gly Thr Leu
 -35 -30 -25
 Thr Thr Ala Ile Ser Asn Pro Ala Cys Leu Val Asn Val Leu Phe Phe
 -20 -15 -10
 Phe Thr Pro Leu Met Thr Leu Val Thr Leu Leu Ile Leu Val Trp Lys
 -5 1 5 10
 Val Thr Lys Asp Lys Ser Asn Lys Asn Arg Glu Thr His Pro Arg Lys
 15 20 25
 Glu Ala Thr Trp Leu Pro
 30

<210> 324
 <211> 168
 <212> PRT
 <213> Homo sapiens

<220>
 <221> SIGNAL
 <222> -25...-1

<400> 324
 Met Arg Gly Pro Thr Ala Gly Pro Ser Val Leu Ser Ala Ala His Leu
 -25 -20 -15 -10
 Leu Val Val Ile Leu Pro Ala Asn Ala Ala Leu Lys Leu Leu Ser Trp
 -5 1 5
 Glu Arg Leu Ala Ala Pro Ala Ile Glu Val Glu Val Pro Ser Lys Glu
 10 15 20
 Val Leu Ala Ala Pro Thr Lys Ala Lys Leu Ile Pro Ser Glu Asp Met
 25 30 35
 Leu Ala Ala Pro Ala Met Asp Leu Leu Asp Ser Phe Ser Pro Gly Phe
 40 45 50 55
 Leu Ile Ala Ala Pro Ala Ser Ala Val Ile Thr Trp Pro Gly Pro Ala
 60 65 70
 Asp Leu Val Val Ala Met Leu Ile Ala Pro Val Ala Gly Leu Ile Ala
 75 80 85
 Ala Pro Ala Ile Ala Thr Ser Val Leu Gly Pro Val Ala Val Pro Ala

```

          90          95          100
Thr Ala Met Pro Pro Ala Val Leu Ala Ala Pro Pro Ser Ala Ala Pro
    105          110          115
Gly Val Leu Val Asp Gly Glu Ala Ala Leu Ala Val Pro Trp Glu Ala
    120          125          130          135
Cys Trp Ile Pro Ser Pro Pro Ala
          140

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<210> 325
 <211> 166
 <212> PRT
 <213> Homo sapiens

<220>
 <221> SIGNAL
 <222> -15...-1

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<400> 325
Met Leu Pro Leu Leu Ile Ile Cys Leu Leu Pro Ala Ile Glu Gly Lys
-15          -10          -5          1
Asn Cys Leu Arg Cys Trp Pro Glu Leu Ser Ala Leu Ile Asp Tyr Asp
    5          10          15
Leu Gln Ile Leu Trp Val Thr Pro Gly Pro Pro Thr Glu Leu Ser Gln
    20          25          30
Asn Arg Asp His Leu Glu Glu Glu Thr Ala Lys Phe Phe Thr Gln Val
    35          40          45
His Gln Ala Ile Lys Thr Leu Arg Asp Asp Lys Thr Val Leu Leu Glu
    50          55          60          65
Glu Ile Tyr Thr His Lys Asn Leu Phe Thr Glu Arg Leu Asn Lys Ile
    70          75          80
Ser Asp Gly Leu Lys Glu Lys Asp Ile Gln Ser Thr Leu Lys Val Thr
    85          90          95
Ser Cys Ala Asp Cys Arg Thr His Phe Leu Ser Cys Asn Asp Pro Thr
    100          105          110
Phe Cys Pro Ala Arg Asn Arg Arg Thr Ser Leu Trp Ala Val Ser Leu
    115          120          125
Ser Ser Ala Leu Leu Leu Ala Ile Ala Gly Asp Val Ser Phe Thr Gly
    130          135          140          145
Lys Gly Arg Arg Arg Gln
          150

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<210> 326
 <211> 156
 <212> PRT
 <213> Homo sapiens

<220>
 <221> SIGNAL
 <222> -15...-1

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<400> 326
Met Asn Ile Leu Met Leu Thr Phe Ile Ile Cys Gly Leu Leu Thr Arg
-15          -10          -5          1
Val Thr Lys Gly Ser Phe Glu Pro Gln Lys Cys Trp Lys Asn Asn Val
    5          10          15
Gly His Cys Arg Arg Arg Cys Leu Asp Thr Glu Arg Tyr Ile Leu Leu
    20          25          30
Cys Arg Asn Lys Leu Ser Cys Cys Ile Ser Ile Ile Ser His Glu Tyr

```


35	40	45													
Thr	Arg	Arg	Pro	Ala	Phe	Pro	Val	Ile	His	Leu	Glu	Asp	Ile	Thr	Leu
50					55					60					65
Asp	Tyr	Ser	Asp	Val	Asp	Ser	Phe	Thr	Gly	Ser	Pro	Val	Ser	Met	Leu
				70					75					80	
Asn	Asp	Leu	Ile	Thr	Phe	Asp	Thr	Thr	Lys	Phe	Gly	Glu	Thr	Met	Thr
			85					90					95		
Pro	Glu	Thr	Asn	Thr	Pro	Glu	Thr	Thr	Met	Pro	Pro	Ser	Glu	Ala	Thr
	100						105					110			
Thr	Pro	Glu	Thr	Thr	Met	Pro	Pro	Ser	Glu	Thr	Ala	Thr	Ser	Glu	Thr
	115					120					125				
Met	Pro	Pro	Pro	Ser	Gln	Thr	Ala	Leu	Thr	His	Asn				
130					135					140					

<210> 327
 <211> 105
 <212> PRT
 <213> Homo sapiens

<220>
 <221> SIGNAL
 <222> -32..-1

<400> 327															
Met	Ala	Lys	Met	Phe	Asp	Leu	Arg	Thr	Lys	Ile	Met	Ile	Gly	Ile	Glu
	-30						-25					-20			
Ser	Ser	Leu	Leu	Val	Ala	Ala	Met	Val	Leu	Leu	Ser	Val	Val	Phe	Cys
	-15				-10						-5				
Leu	Tyr	Phe	Lys	Val	Ala	Lys	Ala	Leu	Lys	Ala	Ala	Lys	Asp	Pro	Asp
1			5						10					15	
Ala	Val	Ala	Val	Lys	Asn	His	Asn	Pro	Asp	Lys	Val	Cys	Trp	Ala	Thr
			20					25					30		
Asn	Ser	Gln	Ala	Lys	Ala	Thr	Thr	Met	Glu	Ser	Cys	Pro	Ser	Leu	Gln
		35				40					45				
Cys	Cys	Glu	Gly	Cys	Arg	Met	His	Ala	Ser	Ser	Asp	Ser	Leu	Pro	Pro
	50				55						60				
Cys	Cys	Cys	Asp	Ile	Asn	Glu	Gly	Leu							
65					70										

<210> 328
 <211> 81
 <212> PRT
 <213> Homo sapiens

<220>
 <221> SIGNAL
 <222> -27..-1

<400> 328															
Met	Ser	Asp	Glu	Asp	Glu	Ser	Ser	Asp	Tyr	Leu	Cys	Leu	Ser	Ile	Leu
	-25						-20					-15			
Gly	Leu	Phe	Cys	Cys	Leu	Pro	Leu	Ala	Ile	Pro	Ala	Val	Ile	Phe	Ser
	-10					-5					1			5	
Cys	Leu	Thr	Lys	Asn	Tyr	Asn	Lys	Ser	Ser	Asp	Tyr	Glu	Leu	Ala	Ala
			10					15					20		
Lys	Thr	Ser	Lys	Gln	Ala	Tyr	Tyr	Trp	Ala	Ile	Ala	Ser	Ile	Thr	Val
			25				30					35			
Gly	Ile	Leu	Gly	Thr	Ile	Leu	Tyr	Thr	Tyr	Leu	Ile	Tyr	Leu	Leu	Arg

40 45 50
 Leu
 <210> 329
 <211> 95
 <212> PRT
 <213> Homo sapiens
 <220>
 <221> SIGNAL
 <222> -27..-1
 <400> 329
 Met Thr Asp Gln Asp Arg Ile Ile Asn Leu Val Val Gly Ser Leu Thr
 -25 -20 -15
 Ser Leu Leu Ile Leu Val Thr Leu Ile Ser Ala Phe Val Phe Pro Gln
 -10 -5 1 5
 Leu Pro Pro Lys Pro Leu Asn Ile Phe Phe Ala Val Cys Ile Ser Leu
 10 15 20
 Ser Ser Ile Thr Ala Cys Ile Ile Tyr Trp Tyr Arg Gln Gly Asp Leu
 25 30 35
 Glu Pro Lys Phe Arg Lys Leu Ile Tyr Tyr Ile Ile Phe Ser Ile Ile
 40 45 50
 Met Leu Cys Ile Cys Ala Asn Leu Tyr Phe His Asp Val Gly Arg
 55 60 65
 <210> 330
 <211> 84
 <212> PRT
 <213> Homo sapiens
 <220>
 <221> SIGNAL
 <222> -20..-1
 <400> 330
 Met Ala Ala Ala Val Pro Ser Leu Leu Leu Ser Leu Pro Pro His
 -20 -15 -10 -5
 Gln Gly Leu Thr Phe Ser Asn Lys Ile Gln Pro Phe Gly Ala Gln Gly
 1 5 10
 Val Leu His Pro Glu Pro Gly Leu Arg Asp Trp Leu Leu Pro Thr Cys
 15 20 25
 Ser Arg Gln Leu Arg Val Ala Leu Pro Glu Lys Gly Ser Glu Gly Ser
 30 35 40
 Leu Cys Gln Thr Gln Leu Pro Ala Thr Pro Cys Phe Leu Pro Ser Asn
 45 50 55 60
 Thr Val Arg Thr
 <210> 331
 <211> 124
 <212> PRT
 <213> Homo sapiens
 <220>
 <221> SIGNAL
 <222> -32..-1
 <400> 331

Met Val Val Val Glu Pro Gly Ala Ser Leu Phe Pro Asn Gly Val Pro
-30 -25 -20
Trp Leu Tyr Ala Val Phe Ala Val Leu Phe Val Phe Phe Leu Phe Ala
-15 -10 -5
Met Leu Ser Pro Phe Leu Leu Glu Ile Asp Gln His Ile Lys Lys Phe
1 5 10 15
Leu Ile Arg Cys Arg Tyr Ser Leu His Asn Thr Val His Lys Asp Lys
20 25 30
Lys Asn Ser Glu Ile Lys Met Asp His Leu Glu Arg Pro Gly Cys Pro
35 40 45
Leu Glu Ser Pro Arg Arg Gly Val Leu Gly Gly Lys Lys Asn Gly Met
50 55 60
Gly Asn Asp Pro Leu Leu Phe Val Lys Val Thr Lys Glu Pro Arg Asp
65 70 75 80
Ser Glu Ala Glu Ile Tyr Thr Pro Gly Pro Ser Val
85 90

<210> 332
<211> 62
<212> PRT
<213> Homo sapiens

<220>
<221> SIGNAL
<222> -46...-1

<400> 332
Met Asp Gln Leu Val Phe Lys Glu Thr Ile Trp Asn Asp Ala Phe Trp
-45 -40 -35
Gln Asn Pro Trp Asp Gln Gly Gly Leu Ala Val Ile Ile Leu Phe Ile
-30 -25 -20 -15
Thr Ala Val Leu Leu Leu Ile Leu Phe Ala Ile Val Phe Gly Leu Leu
-10 -5 1
Thr Ser Thr Glu Asn Thr Gln Cys Glu Ala Gly Glu Glu Glu
5 10 15

<210> 333
<211> 150
<212> PRT
<213> Homo sapiens

<220>
<221> SIGNAL
<222> -23...-1

<400> 333
Met Ser Asn Gln Arg Leu Pro Leu Ile Phe Ser Leu Leu Phe Ile Cys
-20 -15 -10
Phe Phe Gly Glu Ser Phe Cys Ile Cys Asp Gly Thr Val Trp Thr Lys
-5 1 5
Val Gly Trp Glu Ile Leu Pro Glu Glu Val His Tyr Trp Lys Gly Cys
10 15 20 25
Leu Tyr Leu Ile Tyr Asn Leu Leu Gln Ala Val Phe Phe Val Leu Phe
30 35 40
Val Leu Ser Val His Tyr Leu Trp Lys Lys Trp Lys Lys His Gln Lys
45 50 55
Lys Leu Lys Lys Gln Ala Ser Leu Glu Lys Pro Gly Asn Asp Leu Glu
60 65 70

Ser Pro Leu Ile Asn Asn Ile Asp Gln Thr Leu His Arg Val Ala Thr
75 80 85
Thr Ala Ser Val Ile Tyr Lys Ile Trp Glu His Arg Ser His His Pro
90 95 100 105
Ser Ser Lys Lys Ile Lys His Cys Lys Leu Lys Lys Lys Ser Lys Glu
110 115 120
Glu Gly Ala Arg Arg Tyr
125

<210> 334
<211> 198
<212> PRT
<213> Homo sapiens

<220>
<221> SIGNAL
<222> -13...-1

<400> 334
Met Leu Leu Gly Arg Leu Thr Ser Gln Leu Leu Arg Ala Val Pro Trp
-10 -5 1
Ala Gly Gly Arg Pro Pro Trp Pro Val Ser Gly Val Leu Gly Ser Arg
5 10 15
Val Cys Gly Pro Leu Tyr Ser Thr Ser Pro Ala Gly Pro Gly Arg Ala
20 25 30 35
Ala Ser Leu Pro Arg Lys Gly Ala Gln Leu Glu Leu Glu Glu Met Val
40 45 50
Pro Arg Lys Met Ser Val Ser Pro Leu Glu Ser Trp Leu Thr Ala Arg
55 60 65
Cys Phe Leu Pro Arg Leu Asp Thr Gly Thr Ala Gly Thr Val Ala Pro
70 75 80
Pro Gln Ser Tyr Gln Cys Pro Pro Ser Gln Ile Gly Glu Gly Ala Glu
85 90 95
Gln Gly Asp Glu Gly Val Ala Asp Ala Pro Gln Ile Gln Cys Lys Asn
100 105 110 115
Val Leu Lys Ile Arg Arg Arg Lys Met Asn His His Lys Tyr Arg Lys
120 125 130
Leu Val Lys Lys Thr Arg Phe Leu Arg Arg Lys Val Gln Glu Gly Arg
135 140 145
Leu Arg Arg Lys Gln Ile Lys Phe Glu Lys Asp Leu Arg Arg Ile Trp
150 155 160
Leu Lys Ala Gly Leu Lys Glu Ala Pro Glu Gly Trp Gln Thr Pro Lys
165 170 175
Ile Tyr Leu Arg Gly Lys
180 185

<210> 335
<211> 88
<212> PRT
<213> Homo sapiens

<220>
<221> SIGNAL
<222> -24...-1

<400> 335
Met Val Pro Leu Pro Lys Gln Ser Leu Lys Phe Phe Cys Ala Leu Glu
-20 -15 -10

Val Val Leu Pro Ser Cys Asp Cys Arg Ser Pro Gly Ile Gly Leu Val
 -5 1 5
 Glu Glu Pro Met Asp Lys Val Glu Glu Gly Pro Leu Ser Phe Leu Met
 10 15 20
 Lys Arg Lys Thr Ala Gln Lys Leu Ala Ile Gln Lys Ala Leu Ser Asp
 25 30 35 40
 Ala Phe Gln Lys Leu Leu Ile Val Val Leu Gly Lys Thr Val Leu Ile
 45 50 55
 Ile Leu Glu Val Leu Gln Phe Gln
 60

<210> 336
 <211> 150
 <212> PRT
 <213> Homo sapiens

<220>
 <221> SIGNAL
 <222> -45...-1

<400> 336
 Met Val Leu Met Trp Thr Ser Gly Asp Ala Phe Lys Thr Ala Tyr Phe
 -45 -40 -35 -30
 Leu Leu Lys Gly Ala Pro Leu Gln Phe Ser Val Cys Gly Leu Leu Gln
 -25 -20 -15
 Val Leu Val Asp Leu Ala Ile Leu Gly Gln Ala Tyr Ala Phe Ala Pro
 -10 -5 1
 Pro Pro Glu Ala Gly Ala Pro Arg Arg Ala Pro His Trp His Gln Gly
 5 10 15
 Pro Leu Thr Val Gly Arg Thr Arg Met Trp Asp Arg Gln Pro Arg Ala
 20 25 30 35
 Leu Val Gly Pro Asp Leu Pro Ala Gly Arg Val Gly Ala Val Ala Pro
 40 45 50
 Ala Gly Val Ala Glu Met Gly His Gly His Trp Gly Leu His Gln Pro
 55 60 65
 Leu Trp Gly Val Ser Gly Trp Ala Val Gly Val Gly Leu Gly Arg Cys
 70 75 80
 Leu Cys Ser Ala Gly Thr Ala Arg Val Asp Leu Ala Pro Arg Val Leu
 85 90 95
 Asp Val Phe Arg Met Thr
 100 105

<210> 337
 <211> 142
 <212> PRT
 <213> Homo sapiens

<220>
 <221> SIGNAL
 <222> -19...-1

<400> 337
 Met Ala Thr Ala Ser Pro Ser Val Phe Leu Leu Met Val Asn Gly Gln
 -15 -10 -5
 Val Glu Ser Ala Gln Phe Pro Glu Tyr Asp Asp Phe Tyr Cys Lys Tyr
 1 5 10
 Cys Phe Val Tyr Gly Gln Asp Trp Ala Pro Thr Ala Gly Leu Glu Glu
 15 20 25

Gly	Ile	Ser	Gln	Ile	Thr	Ser	Lys	Ser	Gln	Asp	Val	Arg	Gln	Ala	Leu
30					35					40					45
Val	Trp	Asn	Phe	Pro	Ile	Asp	Val	Thr	Phe	Lys	Ser	Thr	Asn	Pro	Tyr
				50					55					60	
Gly	Trp	Pro	Gln	Ile	Val	Leu	Ser	Val	Tyr	Gly	Pro	Asp	Val	Phe	Gly
			65					70					75		
Asn	Asp	Val	Val	Arg	Gly	Tyr	Gly	Ala	Val	His	Val	Pro	Phe	Ser	Pro
		80					85					90			
Gly	Arg	His	Lys	Arg	Thr	Ile	Pro	Met	Phe	Val	Pro	Glu	Ser	Thr	Ser
	95					100					105				
Lys	Leu	Gln	Lys	Phe	Thr	Arg	Ser	Ala	Ser	Cys	Ser	Thr	His		
110					115					120					

<210> 338
 <211> 112
 <212> PRT
 <213> Homo sapiens

<220>
 <221> SIGNAL
 <222> -27...-1

<220>
 <221> UNSURE
 <222> 21
 <223> Xaa = Ala,Pro

Thr	Ser	Glu	Glu	Arg	Thr	Ala	Met	Lys	Arg	Glu	Gly	Gly	Ala	Ala	His
		-25					-20					-15			
Leu	Cys	Ser	Asp	Ser	Leu	Pro	Glu	Ser	Gln	Gln	Gln	Asp	Gly	Asn	His
	-10					-5				1				5	
Ala	Pro	Asn	Phe	Ser	Ser	His	Gly	Ser	Cys	Arg	Arg	Arg	Gln	Arg	Xaa
				10					15					20	
Asp	Met	Thr	Arg	Arg	Cys	Met	Pro	Ala	Arg	Pro	Gly	Phe	Pro	Ser	Ser
		25						30				35			
Pro	Ala	Pro	Gly	Ser	Ser	Pro	Pro	Arg	Cys	His	Leu	Arg	Pro	Gly	Ser
		40					45					50			
Thr	Ala	His	Ala	Ala	Ala	Gly	Lys	Arg	Thr	Glu	Ser	Pro	Gly	Asp	Arg
	55					60					65				
Tyr	Arg	Ala	Glu	Gly	Leu	Arg	Arg	Gly	Arg	Val	Ala	Gly	Ala	Arg	Val
70					75					80					85

<210> 339
 <211> 90
 <212> PRT
 <213> Homo sapiens

<220>
 <221> SIGNAL
 <222> -32...-1

Met	Pro	Cys	Leu	Asp	Gln	Gln	Leu	Thr	Val	His	Ala	Leu	Pro	Cys	Pro
		-30					-25					-20			
Ala	Gln	Pro	Ser	Ser	Leu	Ala	Phe	Cys	Gln	Val	Gly	Phe	Leu	Thr	Ala
	-15					-10					-5				
Gln	Pro	Ser	Pro	Pro	Arg	Arg	Arg	Asn	Gly	Lys	Asp	Arg	Tyr	Thr	Leu

1 5 10 15
 Val Leu Gln His Gln Glu Cys Gln Asp Asp Leu Ala Thr Ser Ser Leu
 20 25 30
 Val Tyr Leu Ser Leu Pro Cys Phe Lys Asp Leu Gly Arg Ser Lys His
 35 40 45
 Gln Ser Ile Thr Val Ala Asp Thr Asn Lys
 50 55

<210> 340
 <211> 80
 <212> PRT
 <213> Homo sapiens

<220>
 <221> SIGNAL
 <222> -35...-1

<400> 340
 Met Pro Phe Gln Phe Gly Thr Gln Pro Arg Arg Phe Pro Val Glu Gly
 -35 -30 -25 -20
 Gly Asp Ser Ser Ile Glu Leu Glu Pro Gly Leu Ser Ser Ser Ala Ala
 -15 -10 -5
 Cys Asn Gly Lys Glu Met Ser Pro Thr Arg Gln Leu Arg Arg Cys Pro
 1 5 10
 Gly Ser His Cys Leu Thr Ile Thr Asp Val Pro Val Thr Val Tyr Ala
 15 20 25
 Thr Thr Arg Lys Pro Pro Ala Gln Ser Ser Lys Glu Met His Pro Lys
 30 35 40 45

<210> 341
 <211> 131
 <212> PRT
 <213> Homo sapiens

<220>
 <221> SIGNAL
 <222> -15...-1

<400> 341
 Met Ser Leu Leu Met Phe Thr Gln Leu Leu Leu Cys Gly Phe Leu Tyr
 -15 -10 -5 1
 Val Arg Val Asp Gly Ser Arg Leu Arg Gln Glu Asp Phe Pro Pro Arg
 5 10 15
 Ile Val Glu His Pro Ser Asp Val Ile Val Ser Lys Gly Glu Pro Thr
 20 25 30
 Thr Leu Asn Cys Lys Ala Glu Gly Arg Pro Thr Pro Thr Ile Glu Trp
 35 40 45
 Tyr Lys Asp Gly Glu Arg Val Glu Thr Asp Lys Asp Asp Pro Arg Ser
 50 55 60 65
 His Arg Met Leu Leu Pro Ser Gly Ser Leu Phe Phe Leu Arg Ile Val
 70 75 80
 His Gly Arg Arg Ser Lys Pro Asp Glu Gly Ser Tyr Val Cys Val Ala
 85 90 95
 Arg Asn Tyr Leu Gly Glu Ala Val Ser Arg Asn Ala Ser Leu Glu Val
 100 105 110
 Ala Cys Lys
 115

<210> 342
 <211> 99
 <212> PRT
 <213> Homo sapiens

<220>
 <221> SIGNAL
 <222> -39...-1

<400> 342
 Met Asp Leu Ile Gly Phe Gly Tyr Ala Ala Leu Val Thr Phe Gly Ser
 -35 -30 -25
 Ile Phe Gly Tyr Lys Arg Arg Gly Gly Val Pro Ser Leu Ile Ala Gly
 -20 -15 -10
 Leu Phe Val Gly Cys Leu Ala Gly Tyr Gly Ala Tyr Arg Val Ser Asn
 -5 1 5
 Asp Lys Arg Asp Val Lys Val Ser Leu Phe Thr Ala Phe Phe Leu Ala
 10 15 20 25
 Thr Ile Met Gly Val Arg Phe Lys Arg Ser Lys Lys Ile Met Pro Ala
 30 35 40
 Gly Leu Val Ala Gly Leu Ser Leu Met Met Ile Leu Arg Leu Val Leu
 45 50 55
 Leu Leu Leu
 60

<210> 343
 <211> 98
 <212> PRT
 <213> Homo sapiens

<220>
 <221> SIGNAL
 <222> -43...-1

<400> 343
 Met Cys Glu Thr Leu Leu Thr Ser Lys Trp Ala Ser Val Ser Pro Ile
 -40 -35 -30
 Pro Ala Leu Leu Gln Glu Gly Glu Asn Arg Asp Ser Arg Arg Leu Gly
 -25 -20 -15
 Asp Ala Leu Leu Phe Leu Arg Pro Ala Gly Ser Cys Ala Leu Gln Val
 -10 -5 1 5
 Ser Trp Pro Ala Ala Leu Ala Gly Pro Arg Ser His Thr Gly Gln Leu
 10 15 20
 Thr Gln His Phe Cys His Leu Lys Asn Asp Thr Cys Ile Pro Pro Ser
 25 30 35
 Leu Gly Pro Pro Arg Asn Ser Gly Ser Leu Glu Ser Leu Arg Ser Lys
 40 45 50
 Arg Tyr
 55

<210> 344
 <211> 217
 <212> PRT
 <213> Homo sapiens

<220>
 <221> SIGNAL
 <222> -19...-1

<220>
 <221> UNSURE
 <222> 185
 <223> Xaa = Phe,Val

<400> 344
 Met Val Gly Ile Leu Pro Leu Cys Cys Ser Gly Cys Val Pro Ser Leu
 -15 -10 -5
 Cys Cys Ser Ser Tyr Val Pro Ser Val Ala Pro Thr Ala Ala His Ser
 1 5 10
 Val Arg Val Pro His Ser Ala Gly His Cys Gly Gln Arg Val Leu Ala
 15 20 25
 Cys Ser Leu Pro Gln Val Phe Leu Lys Pro Trp Ile Phe Val Glu His
 30 35 40 45
 Phe Ser Ser Trp Leu Ser Leu Glu Leu Phe Ser Phe Leu Arg Tyr Leu
 50 55 60
 Gly Thr Leu Leu Cys Ala Cys Gly His Arg Leu Arg Glu Gly Arg Leu
 65 70 75
 Leu Pro Cys Leu Leu Gly Val Gly Ser Trp Leu Leu Phe Asn Asn Trp
 80 85 90
 Thr Gly Gly Ser Trp Phe Ser Leu His Leu Gln Gln Val Ser Leu Ser
 95 100 105
 Gln Gly Ser His Val Ala Ala Phe Leu Pro Glu Ala Ile Gly Pro Gly
 110 115 120 125
 Val Pro Val Pro Val Ser Gly Glu Ser Thr Ser Ala Gln Gln Ser His
 130 135 140
 Ala Gly Trp Gln Leu Ser Ala Glu Ala Asp Ala Cys Pro Ser Val Leu
 145 150 155
 Tyr Ser Glu Val Leu Glu Trp Asn Lys Asn Ile Asn Thr Tyr Thr Ser
 160 165 170
 Phe His Asp Phe Cys Leu Ile Leu Gly Ile Phe Xaa Val Leu Phe Cys
 175 180 185
 Phe Gly Gly Asp Arg Leu Thr Leu His
 190 195

<210> 345
 <211> 183
 <212> PRT
 <213> Homo sapiens

<220>
 <221> SIGNAL
 <222> -20..-1

<400> 345
 Met Lys Leu Leu Ser Leu Val Ala Val Val Gly Cys Leu Leu Val Pro
 -20 -15 -10 -5
 Pro Ala Glu Ala Asn Lys Ser Ser Glu Asp Ile Arg Cys Lys Cys Ile
 1 5 10
 Cys Pro Pro Tyr Arg Asn Ile Ser Gly His Ile Tyr Asn Gln Asn Val
 15 20 25
 Ser Gln Lys Asp Cys Asn Cys Leu His Val Val Glu Pro Met Pro Val
 30 35 40
 Pro Gly His Asp Val Glu Ala Tyr Cys Leu Leu Cys Glu Cys Arg Tyr
 45 50 55 60
 Glu Glu Arg Ser Thr Thr Thr Ile Lys Val Ile Ile Val Ile Tyr Leu
 65 70 75

Ser Val Val Gly Ala Leu Leu Leu Tyr Met Ala Phe Leu Met Leu Val
80 85 90
Asp Pro Leu Ile Arg Lys Pro Asp Ala Tyr Thr Glu Gln Leu His Asn
95 100 105
Glu Glu Glu Asn Glu Asp Ala Arg Ser Met Ala Ala Ala Ala Ser
110 115 120
Leu Gly Gly Pro Arg Ala Asn Thr Val Leu Glu Arg Val Glu Gly Ala
125 130 135 140
Gln Gln Arg Trp Lys Leu Gln Val Gln Glu Gln Arg Lys Thr Val Phe
145 150 155
Asp Arg His Lys Met Leu Ser
160

<210> 346
<211> 247
<212> PRT
<213> Homo sapiens

<220>
<221> SIGNAL
<222> -13...-1

<400> 346
Met Leu Val Leu Arg Ser Ala Leu Thr Arg Ala Leu Ala Ser Arg Thr
-10 -5 1
Leu Ala Pro Gln Met Cys Ser Ser Phe Ala Thr Gly Pro Arg Gln Tyr
5 10 15
Asp Gly Ile Phe Tyr Glu Phe Arg Ser Tyr Tyr Leu Lys Pro Ser Lys
20 25 30 35
Met Asn Glu Phe Leu Glu Asn Phe Glu Lys Asn Ala His Leu Arg Thr
40 45 50
Ala His Ser Glu Leu Val Gly Tyr Trp Ser Val Glu Phe Gly Gly Arg
55 60 65
Met Asn Thr Val Phe His Ile Trp Lys Tyr Asp Asn Phe Ala His Arg
70 75 80
Thr Glu Val Gln Lys Ala Leu Ala Lys Asp Lys Glu Trp Gln Glu Gln
85 90 95
Phe Leu Ile Pro Asn Leu Ala Leu Ile Asp Lys Gln Glu Ser Glu Ile
100 105 110 115
Thr Tyr Leu Val Pro Trp Cys Lys Leu Glu Lys Pro Pro Lys Glu Gly
120 125 130
Val Tyr Glu Leu Ala Thr Phe Gln Met Lys Pro Gly Gly Pro Ala Leu
135 140 145
Trp Gly Asp Ala Phe Lys Arg Ala Val His Ala His Val Asn Leu Gly
150 155 160
Tyr Thr Lys Leu Val Gly Val Phe His Thr Glu Tyr Gly Ala Leu Asn
165 170 175
Arg Val His Val Leu Trp Trp Asn Glu Ser Ala Asp Ser Arg Ala Ala
180 185 190 195
Gly Arg His Lys Ser His Glu Asp Pro Arg Val Val Ala Ala Val Arg
200 205 210
Glu Ser Val Asn Tyr Leu Val Ser Gln Gln Asn Met Leu Leu Ile Pro
215 220 225
Thr Ser Phe Ser Pro Leu Lys
230

<210> 347
<211> 104

<212> PRT
 <213> Homo sapiens

<220>
 <221> SIGNAL
 <222> -47...-1

<400> 347
 Met Phe Ser Pro Arg Gln Ala Leu Thr Pro Asp Pro Leu His Ser Pro
 -45 -40 -35
 Ala Tyr Ser Pro Val Leu Gly Gly Trp Ser Arg Phe Arg Ser Val Asp
 -30 -25 -20
 Phe Arg Phe Leu Tyr Leu Thr Leu Asn Gln Ser Cys Ile Phe Ala Asn
 -15 -10 -5 1
 Tyr Lys Glu Ala His Ala Asn Arg Tyr Cys Thr Glu Gly Arg Tyr Thr
 5 10 15
 Arg Glu Ile Gln Arg Leu Thr Ser Pro Ala Ala Trp Pro Thr Arg Asp
 20 25 30
 Lys Asn Arg Met Ile Ser Asn Gly Met Ala Leu Asn Ser Pro Ala Glu
 35 40 45
 Gly Leu Ala Phe Gln Cys Arg Phe
 50 55

<210> 348
 <211> 125
 <212> PRT
 <213> Homo sapiens

<220>
 <221> SIGNAL
 <222> -21...-1

<400> 348
 Met Ala Lys Tyr Leu Ala Gln Ile Ile Val Met Gly Val Gln Val Val
 -20 -15 -10
 Gly Arg Ala Phe Ala Arg Ala Leu Arg Gln Glu Phe Ala Ala Ser Arg
 -5 1 5 10
 Ala Ala Ala Asp Ala Arg Gly Arg Ala Gly His Arg Ser Ala Ala Ala
 15 20 25
 Ser Asn Leu Ser Gly Leu Ser Leu Gln Glu Ala Gln Gln Ile Leu Asn
 30 35 40
 Val Ser Lys Leu Ser Pro Glu Val Gln Lys Asn Tyr Glu His Leu
 45 50 55
 Phe Lys Val Asn Asp Lys Ser Val Gly Gly Ser Phe Tyr Leu Gln Ser
 60 65 70 75
 Lys Val Val Arg Ala Lys Glu Arg Leu Asp Glu Glu Leu Lys Ile Gln
 80 85 90
 Ala Gln Glu Asp Arg Glu Lys Gly Gln Met Pro His Thr
 95 100

<210> 349
 <211> 302
 <212> PRT
 <213> Homo sapiens

<220>
 <221> SIGNAL
 <222> -18...-1

<400> 349

Met	Ala	Pro	Asn	Ser	Ile	Thr	Leu	Leu	Gly	Leu	Ala	Val	Asn	Val	Val
			-15					-10					-5		
Thr	Thr	Leu	Val	Leu	Ile	Ser	Tyr	Cys	Pro	Thr	Ala	Thr	Glu	Glu	Ala
		1				5					10				
Pro	Tyr	Trp	Thr	Tyr	Leu	Leu	Cys	Ala	Leu	Gly	Leu	Phe	Ile	Tyr	Gln
15					20					25					30
Ser	Leu	Asp	Ala	Ile	Asp	Gly	Lys	Gln	Ala	Arg	Arg	Thr	Asn	Ser	Cys
				35					40					45	
Ser	Pro	Leu	Gly	Glu	Leu	Phe	Asp	His	Gly	Cys	Asp	Ser	Leu	Ser	Thr
			50					55					60		
Val	Phe	Met	Ala	Val	Gly	Ala	Ser	Ile	Ala	Ala	Arg	Leu	Gly	Thr	Tyr
		65					70					75			
Pro	Asp	Trp	Phe	Phe	Phe	Cys	Ser	Phe	Ile	Gly	Met	Phe	Val	Phe	Tyr
	80					85					90				
Cys	Ala	His	Trp	Gln	Thr	Tyr	Val	Ser	Gly	Met	Leu	Arg	Phe	Gly	Lys
95					100					105					110
Val	Asp	Val	Thr	Glu	Ile	Gln	Ile	Ala	Leu	Val	Ile	Val	Phe	Val	Leu
				115					120					125	
Ser	Ala	Phe	Gly	Gly	Ala	Thr	Met	Trp	Asp	Tyr	Thr	Gly	Thr	Ser	Val
			130					135					140		
Leu	Ser	Pro	Gly	Leu	His	Ile	Gly	Leu	Ile	Ile	Ile	Leu	Ala	Ile	Met
		145					150					155			
Ile	Tyr	Lys	Lys	Ser	Ala	Thr	Asp	Val	Phe	Glu	Lys	His	Pro	Cys	Leu
	160					165					170				
Tyr	Ile	Leu	Met	Phe	Gly	Cys	Val	Phe	Ala	Lys	Val	Ser	Gln	Lys	Leu
175					180					185					190
Val	Val	Ala	His	Met	Thr	Lys	Ser	Glu	Leu	Tyr	Leu	Gln	Asp	Thr	Val
				195					200					205	
Phe	Leu	Gly	Pro	Gly	Leu	Leu	Phe	Leu	Asp	Gln	Tyr	Phe	Asn	Asn	Phe
			210					215					220		
Ile	Asp	Glu	Tyr	Val	Val	Leu	Trp	Met	Ala	Met	Val	Ile	Ser	Ser	Phe
	225						230					235			
Asp	Met	Val	Ile	Tyr	Phe	Ser	Ala	Leu	Cys	Leu	Gln	Ile	Ser	Arg	His
	240				245					250					
Leu	His	Leu	Asn	Ile	Phe	Lys	Thr	Ala	Cys	His	Gln	Ala	Pro	Glu	Gln
255					260					265					270
Val	Gln	Val	Leu	Ser	Ser	Lys	Ser	His	Gln	Asn	Asn	Met	Asp		
				275					280						

<210> 350

<211> 107

<212> PRT

<213> Homo sapiens

<220>

<221> SIGNAL

<222> -14...-1

<400> 350

Met	Ile	Leu	Val	Thr	Val	Pro	Gly	Val	Cys	Pro	Ala	Gln	Cys	Cys	Trp
				-10					-5					1	
Ala	Glu	Gln	Arg	Gly	Arg	Gly	Ser	Gly	Met	Tyr	Phe	Ile	Asp	Lys	Trp
		5					10					15			
Ala	Arg	Pro	Ser	Trp	Val	Pro	His	Trp	Leu	Asn	Asp	Leu	Phe	Ile	Val
		20				25					30				
Lys	Ser	Gly	Tyr	Leu	Val	Cys	Ile	Arg	Thr	Thr	Val	Ile	Arg	Gln	Gly

35 40 45 50
 Ile Val Arg Ile Gly Arg Asn Lys Ile Ser Glu Ser Gly Arg Ser Ala
 55 60 65
 Leu Tyr Thr Ile Ala Lys Asn Lys Met Val Ile Phe Lys Val Pro Asp
 70 75 80
 Cys Met His Leu Asn Ala Asp Tyr Phe Gly Val
 85 90

<210> 351
 <211> 229
 <212> PRT
 <213> Homo sapiens

<220>
 <221> SIGNAL
 <222> -34...-1

<400> 351
 Met Ser Phe Leu Gln Asp Pro Ser Phe Phe Thr Met Gly Met Trp Ser
 -30 -25 -20
 Ile Gly Ala Gly Ala Leu Gly Ala Ala Ala Leu Ala Leu Leu Ala
 -15 -10 -5
 Asn Thr Asp Val Phe Leu Ser Lys Pro Gln Lys Ala Ala Leu Glu Tyr
 1 5 10
 Leu Glu Asp Ile Asp Leu Lys Thr Leu Glu Lys Glu Pro Arg Thr Phe
 15 20 25 30
 Lys Ala Lys Glu Leu Trp Glu Lys Asn Gly Ala Val Ile Met Ala Val
 35 40 45
 Arg Arg Pro Gly Cys Phe Leu Cys Arg Glu Glu Ala Ala Asp Leu Ser
 50 55 60
 Ser Leu Lys Ser Met Leu Asp Gln Leu Gly Val Pro Leu Tyr Ala Val
 65 70 75
 Val Lys Glu His Ile Arg Thr Glu Val Lys Asp Phe Gln Pro Tyr Phe
 80 85 90
 Lys Gly Glu Ile Phe Leu Asp Glu Lys Lys Lys Phe Tyr Gly Pro Gln
 95 100 105 110
 Arg Arg Lys Met Met Phe Met Gly Phe Ile Arg Leu Gly Val Trp Tyr
 115 120 125
 Asn Phe Phe Arg Ala Trp Asn Gly Gly Phe Ser Gly Asn Leu Glu Gly
 130 135 140
 Glu Gly Phe Ile Leu Gly Gly Val Phe Val Val Gly Ser Gly Lys Gln
 145 150 155
 Gly Ile Leu Leu Glu His Arg Glu Lys Glu Phe Gly Asp Lys Val Asn
 160 165 170
 Leu Leu Ser Val Leu Glu Ala Ala Lys Met Ile Lys Pro Gln Thr Leu
 175 180 185 190
 Ala Ser Glu Lys Lys
 195

<210> 352
 <211> 206
 <212> PRT
 <213> Homo sapiens

<220>
 <221> SIGNAL
 <222> -34...-1

<400> 352

Met Ser Phe Leu Gln Asp Pro Ser Phe Phe Thr Met Gly Met Trp Ser
-30 -25 -20
Ile Gly Ala Gly Ala Leu Gly Ala Ala Ala Leu Ala Leu Leu Ala
-15 -10 -5
Asn Thr Asp Val Phe Leu Ser Lys Pro Gln Lys Ala Ala Leu Glu Tyr
1 5 10
Leu Glu Asp Ile Asp Leu Lys Thr Leu Glu Lys Glu Pro Arg Thr Phe
15 20 25 30
Lys Ala Lys Glu Leu Trp Glu Lys Asn Gly Ala Val Ile Met Ala Val
35 40 45
Arg Arg Pro Gly Cys Phe Leu Cys Arg Glu Glu Ala Ala Asp Leu Ser
50 55 60
Ser Leu Lys Ser Met Leu Asp Gln Leu Gly Val Pro Leu Tyr Ala Val
65 70 75
Val Lys Glu His Ile Arg Thr Glu Val Lys Asp Phe Gln Pro Tyr Phe
80 85 90
Lys Gly Glu Ile Phe Leu Asp Glu Lys Lys Lys Phe Tyr Gly Pro Gln
95 100 105 110
Arg Arg Lys Met Met Phe Met Gly Phe Ile Arg Leu Gly Val Trp Tyr
115 120 125
Asn Phe Phe Arg Ala Trp Asn Gly Gly Phe Ser Gly Asn Leu Glu Gly
130 135 140
Glu Gly Phe Ile Leu Gly Gly Val Phe Val Val Gly Ser Gly Ser Arg
145 150 155
Ala Phe Phe Leu Ser Thr Glu Lys Lys Asn Leu Glu Thr Lys
160 165 170

<210> 353

<211> 88

<212> PRT

<213> Homo sapiens

<220>

<221> SIGNAL

<222> -44..-1

<400> 353

Met Ala Ala Glu Gly Trp Ile Trp Arg Trp Gly Trp Gly Arg Arg Cys
-40 -35 -30
Leu Gly Arg Pro Gly Leu Leu Gly Pro Gly Pro Gly Pro Thr Thr Pro
-25 -20 -15
Leu Phe Leu Leu Leu Leu Gly Ser Val Thr Ala Asp Ile Thr Asp
-10 -5 1
Gly Asn Ile Glu His Leu Lys Arg Glu His Ser Leu Ile Lys Pro Tyr
5 10 15 20
Gln Gly Val Gly Ser Ser Ser Pro Ser Gly Thr Ser Arg Ala Ala Leu
25 30 35
Cys Ser Arg Ala Ser Thr Tyr Val
40

<210> 354

<211> 151

<212> PRT

<213> Homo sapiens

<220>

<221> SIGNAL

<222> -32...-1

<400> 354

Met Asp Ser Ala Ser Asn Pro Thr Asn Leu Val Ser Thr Ser Gln Arg
-30 -25 -20
His Arg Pro Leu Leu Ser Ser Cys Gly Leu Pro Pro Ser Thr Ala Ser
-15 -10 -5
Ala Val Arg Arg Leu Cys Ser Arg Gly Val Leu Lys Gly Ser Asn Glu
1 5 10 15
Arg Arg Asp Met Glu Ser Phe Trp Lys Leu Asn Arg Ser Pro Gly Ser
20 25 30
Asp Arg Tyr Leu Glu Ser Arg Asp Ala Ser Arg Leu Ser Gly Arg Asp
35 40 45
Pro Ser Ser Trp Thr Val Glu Asp Val Met Gln Phe Val Arg Glu Ala
50 55 60
Asp Pro Gln Leu Gly Pro His Ala Asp Leu Phe Arg Lys His Glu Ile
65 70 75 80
Asp Gly Lys Ala Leu Leu Leu Leu Arg Ser Asp Met Met Met Lys Tyr
85 90 95
Met Gly Leu Lys Leu Gly Pro Ala Leu Lys Leu Ser Tyr His Ile Asp
100 105 110
Arg Leu Lys Gln Gly Lys Phe
115

<210> 355

<211> 65

<212> PRT

<213> Homo sapiens

<220>

<221> SIGNAL

<222> -16...-1

<400> 355

Met Ala Glu Leu Ala Cys Val Arg Glu Ser Thr Ser Val Ala Trp Ala
-15 -10 -5
Cys Lys Val Arg Gly Gly Thr Ala Pro Ser Pro Ser Gly Ala Glu Gly
1 5 10 15
His Val Met Leu Asn Lys Ser Arg Glu Val Glu Ser Pro Val Ser Ser
20 25 30
Arg Pro Arg Cys Gly Met Pro Thr Val Pro Pro Gly Ser Leu Lys Thr
35 40 45
Leu

<210> 356

<211> 189

<212> PRT

<213> Homo sapiens

<220>

<221> SIGNAL

<222> -24...-1

<220>

<221> UNSURE

<222> 41

<223> Xaa = Ala,Gly

<400> 356
 Met Glu Glu Gly Gly Asn Leu Gly Gly Leu Ile Lys Met Val His Leu
 -20 -15 -10
 Leu Val Leu Ser Gly Ala Trp Gly Met Gln Met Trp Val Thr Phe Val
 -5 1 5
 Ser Gly Phe Leu Leu Phe Arg Ser Leu Pro Arg His Thr Phe Gly Leu
 10 15 20
 Val Gln Ser Lys Leu Phe Pro Phe Tyr Phe His Ile Ser Met Gly Cys
 25 30 35 40
 Xaa Phe Ile Asn Leu Cys Ile Leu Ala Ser Gln His Ala Trp Ala Gln
 45 50 55
 Leu Thr Phe Trp Glu Ala Ser Gln Leu Tyr Leu Leu Phe Leu Ser Leu
 60 65 70
 Thr Leu Ala Thr Val Asn Ala Arg Trp Leu Glu Pro Arg Thr Thr Ala
 75 80 85
 Ala Met Trp Ala Leu Gln Thr Val Glu Lys Glu Arg Gly Leu Gly Gly
 90 95 100
 Glu Val Pro Gly Ser His Gln Gly Pro Asp Pro Tyr Arg Gln Leu Arg
 105 110 115 120
 Glu Lys Asp Pro Lys Tyr Ser Ala Leu Arg Gln Asn Phe Phe Arg Tyr
 125 130 135
 His Gly Leu Ser Ser Leu Cys Asn Leu Gly Cys Val Leu Ser Asn Gly
 140 145 150
 Leu Cys Leu Ala Gly Leu Ala Leu Glu Ile Arg Ser Leu
 155 160 165

<210> 357
 <211> 183
 <212> PRT
 <213> Homo sapiens

<220>
 <221> SIGNAL
 <222> -47...-1

<400> 357
 Met Thr Glu Cys Thr Ser Leu Gln Phe Val Ser Pro Phe Ala Phe Glu
 -45 -40 -35
 Ala Met Gln Lys Val Asp Val Val Cys Leu Ala Ser Leu Ser Asp Pro
 -30 -25 -20
 Glu Leu Arg Leu Leu Leu Pro Cys Leu Val Arg Met Ala Leu Cys Ala
 -15 -10 -5 1
 Pro Ala Asp Gln Ser Gln Ser Trp Ala Gln Asp Lys Lys Leu Ile Leu
 5 10 15
 Arg Leu Leu Ser Gly Val Glu Ala Val Asn Ser Ile Val Ala Leu Leu
 20 25 30
 Ser Val Asp Phe His Ala Leu Glu Gln Asp Ala Ser Lys Glu Gln Gln
 35 40 45
 Leu Arg Pro Ser Leu Ala Leu Leu Pro Arg Leu Glu Cys Gly Gly Val
 50 55 60 65
 Ile Ser Ala His Cys Asn Leu His Leu Leu Gly Ser Ser Asp Ser Ser
 70 75 80
 Ala Ser Val Ser Arg Val Asp Gly Thr Thr Gly Thr Arg His His Ala
 85 90 95
 Arg Leu Phe Cys Ile Ile Ser Arg Asp Glu Val Ser Pro Tyr Trp Pro
 100 105 110
 Gly Trp Ser Arg Thr Pro Asn Leu Val Ile His Leu Pro Gln Pro Pro
 115 120 125

Lys Val Leu Gly Leu Pro Ala
130 135

<210> 358
<211> 102
<212> PRT
<213> Homo sapiens

<220>
<221> SIGNAL
<222> -14..-1

<400> 358
Met Phe Leu Thr Ala Leu Leu Trp Arg Gly Arg Ile Pro Gly Arg Gln
-10 -5 1
Trp Ile Gly Lys His Arg Arg Pro Arg Phe Val Ser Leu Arg Ala Lys
5 10 15
Gln Asn Met Ile Arg Arg Leu Glu Ile Glu Ala Glu Asn His Tyr Trp
20 25 30
Leu Ser Met Pro Tyr Met Thr Arg Glu Gln Glu Arg Gly His Ala Ala
35 40 45 50
Val Arg Arg Arg Glu Ala Phe Glu Ala Ile Lys Ala Ala Ala Thr Ser
55 60 65
Lys Phe Pro Pro His Arg Phe Ile Ala Asp Gln Leu Asp His Leu Asn
70 75 80
Val Thr Lys Lys Trp Ser
85

<210> 359
<211> 244
<212> PRT
<213> Homo sapiens

<220>
<221> SIGNAL
<222> -29..-1

<400> 359
Met Glu Leu Thr Ile Phe Ile Leu Arg Leu Ala Ile Tyr Ile Leu Thr
-25 -20 -15
Phe Pro Leu Tyr Leu Leu Asn Phe Leu Gly Leu Trp Ser Trp Ile Cys
-10 -5 1
Lys Lys Trp Phe Pro Tyr Phe Leu Val Arg Phe Thr Val Ile Tyr Asn
5 10 15
Glu Gln Met Ala Ser Lys Lys Arg Glu Leu Phe Ser Asn Leu Gln Glu
20 25 30 35
Phe Ala Gly Pro Ser Gly Lys Leu Ser Leu Leu Glu Val Gly Cys Gly
40 45 50
Thr Gly Ala Asn Phe Lys Phe Tyr Pro Pro Gly Cys Arg Val Thr Cys
55 60 65
Ile Asp Pro Asn Pro Asn Phe Glu Lys Phe Leu Ile Lys Ser Ile Ala
70 75 80
Glu Asn Arg His Leu Gln Phe Glu Arg Phe Val Val Ala Ala Gly Glu
85 90 95
Asn Met His Gln Val Ala Asp Gly Ser Val Asp Val Val Val Cys Thr
100 105 110 115
Leu Val Leu Cys Ser Val Lys Asn Gln Glu Arg Ile Leu Arg Glu Val
120 125 130

Cys	Arg	Val	Leu	Arg	Pro	Gly	Gly	Ala	Phe	Tyr	Phe	Met	Glu	His	Val
			135					140					145		
Ala	Ala	Glu	Cys	Ser	Thr	Trp	Asn	Tyr	Phe	Trp	Gln	Gln	Val	Leu	Asp
		150					155					160			
Pro	Ala	Trp	His	Leu	Leu	Phe	Asp	Gly	Cys	Asn	Leu	Thr	Arg	Glu	Ser
		165				170					175				
Trp	Lys	Ala	Leu	Glu	Arg	Ala	Ser	Phe	Ser	Lys	Leu	Lys	Leu	Gln	His
180					185					190					195
Ile	Gln	Ala	Pro	Leu	Ser	Trp	Glu	Leu	Val	Arg	Pro	His	Ile	Tyr	Gly
				200					205					210	
Tyr	Ala	Val	Lys												
			215												

<210> 360
 <211> 177
 <212> PRT
 <213> Homo sapiens

<220>
 <221> SIGNAL
 <222> -23..-1

<400>	360														
Met	Ser	Asn	Gln	Arg	Leu	Pro	Leu	Ile	Phe	Ser	Leu	Leu	Phe	Ile	Cys
			-20					-15					-10		
Phe	Phe	Gly	Glu	Ser	Phe	Cys	Ile	Cys	Asp	Gly	Thr	Val	Trp	Thr	Lys
		-5					1				5				
Val	Gly	Trp	Glu	Ile	Leu	Pro	Glu	Glu	Val	His	Tyr	Trp	Lys	Val	Lys
10					15					20					25
Gly	Ser	Pro	Ser	His	Cys	Leu	Pro	Tyr	Leu	Asp	Lys	Leu	Cys	Cys	
				30					35				40		
Asp	Phe	Ala	Asn	Met	Asp	Ile	Phe	Gln	Gly	Cys	Leu	Tyr	Leu	Ile	Tyr
			45					50					55		
Asn	Leu	Leu	Gln	Ala	Val	Phe	Phe	Val	Leu	Phe	Val	Leu	Ser	Val	His
		60				65					70				
Tyr	Leu	Trp	Lys	Lys	Trp	Lys	Lys	His	Gln	Lys	Lys	Leu	Lys	Lys	Gln
		75			80						85				
Ala	Ser	Leu	Glu	Lys	Pro	Gly	Asn	Asp	Leu	Glu	Ser	Pro	Leu	Ile	Asn
90					95					100					105
Asn	Ile	Asp	Gln	Thr	Leu	His	Arg	Val	Ala	Thr	Thr	Ala	Ser	Val	Ile
				110					115						120
Tyr	Lys	Ile	Trp	Glu	His	Arg	Ser	His	His	Pro	Ser	Ser	Lys	Lys	Ile
			125					130					135		
Lys	His	Cys	Lys	Leu	Lys	Lys	Lys	Ser	Lys	Glu	Glu	Gly	Ala	Arg	Arg
		140					145					150			
Tyr															

<210> 361
 <211> 158
 <212> PRT
 <213> Homo sapiens

<220>
 <221> SIGNAL
 <222> -21..-1

<400> 361
 Met Ala Leu Cys Ala Leu Thr Arg Ala Leu Pro Ser Leu Asn Leu Ala

-20 -15 -10
 Pro Pro Thr Val Ala Ala Pro Ala Pro Ser Leu Phe Pro Ala Ala Gln
 -5 1 5 10
 Met Met Asn Asn Gly Leu Leu Gln Gln Pro Ser Ala Leu Met Leu Leu
 15 20 25
 Pro Cys Arg Pro Val Leu Thr Ser Val Ala Leu Asn Ala Asn Phe Val
 30 35 40
 Ser Trp Lys Ser Arg Thr Lys Tyr Thr Ile Thr Pro Val Lys Met Arg
 45 50 55
 Lys Ser Gly Gly Arg Asp His Thr Gly Ala Gly Asn Val Arg Arg Thr
 60 65 70 75
 Val Gly Arg Val Ser Asn Val Asp His Asn Lys Arg Val Ile Gly Lys
 80 85 90
 Ala Gly Arg Asn Arg Trp Leu Gly Lys Arg Pro Asn Ser Gly Arg Trp
 95 100 105
 His Arg Lys Gly Gly Trp Ala Gly Arg Lys Ile Arg Pro Leu Pro Pro
 110 115 120
 Met Lys Ser Tyr Val Lys Leu Pro Ser Ala Ser Ala Gln Ser
 125 130 135

<210> 362
 <211> 186
 <212> PRT
 <213> Homo sapiens

<220>
 <221> SIGNAL
 <222> -19...-1

<400> 362
 Met Ala Thr Ala Ser Pro Ser Val Phe Leu Leu Met Val Asn Gly Gln
 -15 -10 -5
 Val Glu Ser Ala Gln Phe Pro Glu Tyr Asp Asp Leu Tyr Cys Lys Tyr
 1 5 10
 Cys Phe Val Tyr Gly Gln Asp Trp Ala Pro Thr Ala Gly Leu Glu Glu
 15 20 25
 Gly Ile Ser Gln Ile Thr Ser Lys Ser Gln Asp Val Arg Gln Ala Leu
 30 35 40 45
 Val Trp Asn Phe Pro Ile Asp Val Thr Phe Lys Ser Thr Asn Pro Tyr
 50 55 60
 Gly Trp Pro Gln Ile Val Leu Ser Val Tyr Gly Pro Asp Val Phe Gly
 65 70 75
 Asn Asp Val Val Arg Gly Tyr Gly Ala Val His Val Pro Phe Ser Pro
 80 85 90
 Gly Arg His Lys Arg Thr Ile Pro Met Phe Val Pro Glu Ser Thr Ser
 95 100 105
 Lys Leu Gln Lys Phe Thr Ser Trp Phe Met Gly Arg Arg Pro Glu Tyr
 110 115 120 125
 Thr Asp Pro Lys Val Val Ala Gln Gly Glu Gly Arg Glu Ala Ile Thr
 130 135 140
 Ala Pro Arg Lys Ala Val Phe Ser Val His Gly Leu Thr Ser Pro Arg
 145 150 155
 Ala Leu Ala Leu Val His Ile Lys Gly Thr
 160 165

<210> 363
 <211> 150
 <212> PRT

<213> Homo sapiens

<220>

<221> SIGNAL

<222> -47..-1

<400> 363

Met	Gly	Asp	Arg	Val	Lys	Gly	Ser	Lys	Ser	Arg	Ala	Phe	Val	Ser	Pro	
		-45					-40					-35				
Trp	Pro	His	Thr	Pro	Met	Ala	Ser	Gly	Leu	Arg	Asp	Pro	Trp	Leu	Gln	
		-30				-25					-20					
Pro	Thr	Ala	Leu	Gly	Leu	Ala	Leu	Cys	Ser	Thr	Lys	Ala	Leu	Ser	Val	
		-15			-10					-5					1	
Gly	Ser	Ala	Pro	Leu	Pro	Pro	Arg	Asn	Ser	Asn	Thr	Met	Ala	Ala	Ala	
			5				10						15			
Ala	Leu	Ala	Ala	Pro	Ser	Leu	Gly	Phe	Asp	Gly	Val	Ile	Gly	Val	Leu	
		20					25					30				
Val	Ala	Asp	Thr	Ser	Leu	Thr	Asp	Met	His	Val	Val	Asp	Val	Glu	Leu	
		35				40					45					
Ser	Gly	Pro	Arg	Gly	Pro	Thr	Gly	Arg	Ser	Phe	Ala	Val	His	Thr	Arg	
		50			55					60					65	
Arg	Glu	Asn	Pro	Ala	Glu	Pro	Gly	Ala	Val	Thr	Gly	Ser	Ala	Thr	Val	
			70					75						80		
Thr	Ala	Phe	Trp	Arg	Ser	Leu	Leu	Ala	Cys	Cys	Gln	Leu	Pro	Ser	Arg	
			85					90					95			
Pro	Gly	Ile	His	Leu	Cys											
																100

<210> 364

<211> 95

<212> PRT

<213> Homo sapiens

<220>

<221> SIGNAL

<222> -45..-1

<400> 364

Met	Leu	His	His	Val	Ile	Thr	Ala	Gly	Pro	Val	Leu	Leu	Leu	His	Leu	
					-40					-35					-30	
Pro	Arg	Pro	Asp	Thr	Ser	Thr	Arg	Leu	Leu	Leu	Thr	Ser	Val	Ser	Ala	
			-25							-20				-15		
Phe	Ile	Leu	Leu	Leu	Leu	Ser	Gly	Pro	Ala	Glu	Met	Ser	Ser	Ala	Ser	
			-10				-5					1				
Gln	Glu	Ser	Phe	Pro	Gly	Ser	Leu	Gln	Gln	Glu	Ile	Ala	Ser	Leu	Ile	
	5				10						15					
Thr	Val	Ala	Leu	Gly	Ser	Leu	Ile	Ser	Leu	Ser	Cys	Ser	Thr	Leu	Leu	
	20				25					30					35	
Tyr	Phe	Ser	Cys	Glu	Leu	Lys	Ile	Pro	Cys	Glu	Asp	Val	Asn	Leu		
			40						45					50		

<210> 365

<211> 94

<212> PRT

<213> Homo sapiens

<220>

<221> SIGNAL

<222> -26...-1

<400> 365

Met Ala Ala Ile Glu Ile Glu Val Lys Pro Asn Gln Gly Phe Cys Gly
-25 -20 -15
Ser Ala Cys Leu Leu Ala Val Ile Arg Ala Phe Phe Phe Lys Lys Asn
-10 -5 1 5
Ala Cys Leu Leu Arg Glu Ile Leu Gln Ser Lys Leu Gly Gly Met Gly
10 15 20
Pro Val Val Phe Ser Tyr Arg Gly Leu Pro Leu Trp Leu Phe Ala Trp
25 30 35
Leu Phe Pro Arg Cys Thr Val Pro Leu Thr Phe Gly Phe Glu Asn Met
40 45 50
Arg Gly Leu Gly Val Val Ala Tyr Ala Cys Asn Pro Ser Thr
55 60 65

<210> 366

<211> 140

<212> PRT

<213> Homo sapiens

<220>

<221> SIGNAL

<222> -40...-1

<400> 366

Met Thr Ser Met Thr Gln Ser Leu Arg Glu Val Ile Lys Ala Met Thr
-40 -35 -30 -25
Lys Ala Arg Asn Phe Glu Arg Val Leu Gly Lys Ile Thr Leu Val Ser
-20 -15 -10
Ala Ala Pro Gly Lys Val Ile Cys Glu Met Lys Val Glu Glu His
-5 1 5
Thr Asn Ala Ile Gly Thr Leu His Gly Gly Leu Thr Ala Thr Leu Val
10 15 20
Asp Asn Ile Ser Thr Met Ala Leu Leu Cys Thr Glu Arg Gly Ala Pro
25 30 35 40
Gly Val Ser Val Asp Met Asn Ile Thr Tyr Met Ser Pro Ala Lys Leu
45 50 55
Gly Glu Asp Ile Val Ile Thr Ala His Val Leu Lys Gln Gly Lys Thr
60 65 70
Leu Ala Phe Thr Ser Val Asp Leu Thr Asn Lys Ala Thr Gly Lys Leu
75 80 85
Ile Ala Gln Gly Arg His Thr Lys His Leu Gly Asn
90 95 100

<210> 367

<211> 39

<212> PRT

<213> Homo sapiens

<220>

<221> SIGNAL

<222> -35...-1

<400> 367

Met Asp Pro Gly Trp Pro His Phe Lys Leu Thr His Ser Arg Cys Met
-35 -30 -25 -20
Ala Val Leu Phe Leu Gly Thr Leu Pro Leu Cys Pro Val Thr Ser Pro

Val Trp Gly Trp Ser Pro Gly
 1

<210> 368
 <211> 78
 <212> PRT
 <213> Homo sapiens

<220>
 <221> SIGNAL
 <222> -41..-1

<400> 368
 Met Ser Ala Ser Val Val Ser Val Ile Ser Arg Phe Leu Glu Glu Tyr
 -40 -35 -30
 Leu Ser Ser Thr Pro Gln Arg Leu Lys Leu Leu Asp Ala Tyr Leu Leu
 -25 -20 -15 -10
 Tyr Ile Leu Leu Thr Gly Ala Leu Gln Phe Gly Tyr Cys Leu Leu Val
 -5 1 5
 Gly Thr Phe Pro Phe Asn Ser Phe Leu Ser Gly Phe Ile Ser Cys Val
 10 15 20
 Gly Ser Phe Ile Leu Ala Gly Ser Leu Phe Glu Phe Pro Gly
 25 30 35

<210> 369
 <211> 83
 <212> PRT
 <213> Homo sapiens

<220>
 <221> SIGNAL
 <222> -40..-1

<400> 369
 Met Gly Leu Thr Ser Thr Trp Arg Tyr Gly Arg Gly Pro Gly Ile Gly
 -40 -35 -30 -25
 Thr Val Thr Met Val Ser Trp Gly Arg Phe Ile Cys Leu Val Val Val
 -20 -15 -10
 Thr Met Ala Thr Leu Ser Leu Ala Arg Pro Ser Phe Ser Leu Val Glu
 -5 1 5
 Asp Thr Thr Leu Glu Pro Glu Asp Ala Ile Ser Ser Gly Asp Asp Glu
 10 15 20
 Asp Asp Thr Asp Gly Ala Glu Asp Phe Val Ser Glu Asn Ser Asn Asn
 25 30 35 40
 Lys Ser Lys

<210> 370
 <211> 92
 <212> PRT
 <213> Homo sapiens

<220>
 <221> SIGNAL
 <222> -15..-1

<400> 370
 Met Ala Val Leu Ala Gly Ser Leu Leu Gly Pro Thr Ser Arg Ser Ala

-15					-10					-5				1
Ala	Leu	Leu	Gly	Gly	Arg	Trp	Leu	Gln	Pro	Arg	Ala	Trp	Leu	Gly
		5						10					15	Phe
Pro	Asp	Ala	Trp	Gly	Leu	Pro	Thr	Pro	Gln	Gln	Ala	Arg	Gly	Lys
		20					25					30		Ala
Arg	Gly	Asn	Glu	Tyr	Gln	Pro	Ser	Asn	Ile	Lys	Arg	Lys	Asn	Lys
		35				40					45			His
Gly	Trp	Val	Arg	Arg	Leu	Ser	Thr	Pro	Ala	Gly	Val	Gln	Val	Ile
50					55					60				65
Arg	Arg	Met	Leu	Lys	Gly	Arg	Lys	Ser	Leu	Ser	His			
			70						75					

<210> 371
 <211> 279
 <212> PRT
 <213> Homo sapiens

<220>
 <221> SIGNAL
 <222> -42...-1

<400> 371

Met	Ala	Ala	Pro	Val	Arg	Arg	Thr	Leu	Leu	Gly	Val	Ala	Gly	Gly	Trp
		-40					-35					-30			
Arg	Arg	Phe	Glu	Arg	Leu	Trp	Ala	Gly	Ser	Leu	Ser	Ser	Arg	Ser	Leu
		-25				-20					-15				
Ala	Leu	Ala	Ala	Ala	Pro	Ser	Ser	Asn	Gly	Ser	Pro	Trp	Arg	Leu	Leu
-10					-5					1				5	
Gly	Ala	Leu	Cys	Leu	Gln	Arg	Pro	Pro	Val	Val	Ser	Lys	Pro	Leu	Thr
		10					15					20			
Pro	Leu	Gln	Glu	Glu	Met	Ala	Ser	Leu	Leu	Gln	Gln	Ile	Glu	Ile	Glu
		25				30					35				
Arg	Ser	Leu	Tyr	Ser	Asp	His	Glu	Leu	Arg	Ala	Leu	Asp	Glu	Asn	Gln
		40				45					50				
Arg	Leu	Ala	Lys	Lys	Lys	Ala	Asp	Leu	His	Asp	Glu	Glu	Asp	Glu	Gln
				60						65					70
Asp	Ile	Leu	Leu	Ala	Gln	Asp	Leu	Glu	Asp	Met	Trp	Glu	Gln	Lys	Phe
			75					80						85	
Leu	Gln	Phe	Lys	Leu	Gly	Ala	Arg	Ile	Thr	Glu	Ala	Asp	Glu	Lys	Asn
		90					95					100			
Asp	Arg	Thr	Ser	Leu	Asn	Arg	Asn	Leu	Asp	Arg	Asn	Leu	Val	Leu	Leu
		105					110					115			
Val	Arg	Glu	Lys	Phe	Gly	Asp	Gln	Asp	Val	Trp	Ile	Leu	Pro	Gln	Ala
		120				125					130				
Glu	Trp	Gln	Pro	Gly	Glu	Thr	Leu	Arg	Gly	Thr	Ala	Glu	Arg	Thr	Leu
				140					145						150
Ala	Thr	Leu	Ser	Glu	Asn	Asn	Met	Glu	Ala	Lys	Phe	Leu	Gly	Asn	Ala
				155					160					165	
Pro	Cys	Gly	His	Tyr	Thr	Phe	Lys	Phe	Pro	Gln	Ala	Met	Arg	Thr	Glu
			170				175					180			
Ser	Asn	Leu	Gly	Ala	Lys	Val	Phe	Phe	Phe	Lys	Ala	Leu	Leu	Leu	Thr
		185				190					195				
Gly	Asp	Phe	Ser	Gln	Ala	Gly	Asn	Lys	Gly	His	His	Val	Trp	Val	Ile
	200					205					210				
Lys	Asp	Glu	Leu	Gly	Asp	Tyr	Leu	Lys	Pro	Lys	Tyr	Leu	Ala	Gln	Val
				220						225					230
Arg	Arg	Phe	Val	Ser	Asp	Leu									
					235										

<210> 372
 <211> 184
 <212> PRT
 <213> Homo sapiens

<220>
 <221> SIGNAL
 <222> -31..-1

<400> 372
 Met Ala Cys Thr Thr Thr Ala Pro Ala Gln Glu His Met Leu Leu Thr
 -30 -25 -20
 Pro Leu Thr Ala Leu Met Val Gly Ala Ala Ser Leu Leu Glu Gly Arg
 -15 -10 -5 1
 Pro Gln Ile Ser Ala Pro Tyr Ser Arg Ala Ala Cys Cys Ser Pro Gly
 5 10 15
 Ala Leu Gly Cys Pro Ala Ala Arg Val Gly Ile Leu Asp Leu Met Tyr
 20 25 30
 Ser Trp Val Ala Arg Lys Val Leu Arg Cys Ser Asn Thr Gly Leu Gln
 35 40 45
 Gly Leu His Cys Ala Pro Ala Tyr Ala Ala Gln Leu Gly Met Asp Pro
 50 55 60 65
 Gly Arg Gly Gln Arg Ala Gly Gly Pro Val Glu Gln Thr Tyr Phe Ser
 70 75 80
 Pro Met Gly Lys Leu Pro Thr Leu Ser Trp Leu Glu Gly Cys Thr Ala
 85 90 95
 Val Met Thr Leu Ala Ser Ala Trp Leu Leu Gly Ser Pro Arg Glu Thr
 100 105 110
 Tyr Asn His Glu Lys Val Lys Glu Lys Gln Cys Pro Phe Ser Ser Met
 115 120 125
 Val Leu Gly Glu Tyr Gly Phe Leu Pro Thr Val Asp His Leu Ser Thr
 130 135 140 145
 Leu Gly Cys Asn Met Arg Glu Leu
 150

<210> 373
 <211> 101
 <212> PRT
 <213> Homo sapiens

<220>
 <221> SIGNAL
 <222> -42..-1

<400> 373
 Met Ala His Val Ala Glu Lys Asp Gly Leu Asp Trp Ala Ser Gly Cys
 -40 -35 -30
 Ile Pro Gly Leu Gln Thr Gly Ile Cys Leu Phe Gly Ser Gln Leu Cys
 -25 -20 -15
 Phe His Leu Ser Trp Leu Tyr Ser Trp Ala Ser Gln Cys Gly Pro Thr
 -10 -5 1 5
 Ala Pro Val Ile Asp Lys Lys Ser Ser Pro Leu Leu Thr Glu Leu Leu
 10 15 20
 Asp Leu Val Leu Ile Gly Pro Asp Glu Glu Gly Ile Gln Pro Gln Val
 25 30 35
 Ile Ile Val Ala Arg Lys Met Glu Tyr Thr Lys Trp Thr Gly Leu Ala
 40 45 50

Cys Thr His Arg Asp
55

<210> 374
<211> 85
<212> PRT
<213> Homo sapiens

<220>
<221> SIGNAL
<222> -20...-1

<400> 374
Met Gly Pro Asn Thr Lys Asn Leu Leu Leu Val Thr Leu Val Ala Ser
-20 -15 -10 -5
Thr Val Pro Gly Asn Ser Leu Gly Gln Asp Phe Thr Phe Ala His Leu
1 5 10
Glu Arg Ser Cys Thr Arg Glu Asn Arg Ser Pro Gly Glu Val Phe Gln
15 20 25
Gln Pro Cys Lys Ser Gly Gly Gly Gly Val Gly Glu Pro Asn Ala Gln
30 35 40
Gly Gln Leu Leu Ser Gln His Pro Leu Pro Ala Phe Ile Asn Cys Ser
45 50 55 60
His Gly Gln Ala Phe
65

<210> 375
<211> 90
<212> PRT
<213> Homo sapiens

<220>
<221> SIGNAL
<222> -28...-1

<400> 375
Met Ala Phe Pro Gly Gln Ser Asp Thr Lys Met Gln Trp Pro Glu Val
-25 -20 -15
Pro Ala Leu Pro Leu Leu Ser Ser Leu Cys Met Ala Met Val Arg Lys
-10 -5 1
Ser Ser Ala Leu Gly Lys Glu Val Gly Arg Arg Val Lys Glu Met Val
5 10 15 20
Met Leu Val Ala Pro Phe Arg Gln Ser Ser Ser Leu Ser Arg Thr Phe
25 30 35
Ser Ser Arg Lys Val Val Lys Ala His Ala Ser Leu His Gly Ala Arg
40 45 50
Leu Ser Pro Leu Ser Arg Asn Ile Arg Gly
55 60

<210> 376
<211> 89
<212> PRT
<213> Homo sapiens

<220>
<221> SIGNAL
<222> -33...-1

<220>
 <221> UNSURE
 <222> 47
 <223> Xaa = Ala,Pro,Ser,Thr

<400> 376
 Met Ala Gln Pro Ala Ala Pro Ser Leu Thr Arg Pro Phe Leu Ala Glu
 -30 -25 -20
 Ala Pro Thr Ala Leu Val Pro His Ser Pro Leu Pro Gly Ala Leu Ser
 -15 -10 -5
 Ser Ala Pro Gly Pro Lys Gln Pro Pro Thr Ala Ser Thr Gly Pro Glu
 1 5 10 15
 Leu Leu Leu Leu Pro Leu Ser Ser Phe Met Pro Cys Gly Ala Ala Ala
 20 25 30
 Pro Ala Arg Val Ser Ser Gln Arg Ala Thr Pro Arg Asp Lys Pro Xaa
 35 40 45
 Gly Pro Leu Ile Pro Gly Gln Cys Pro
 50 55

<210> 377
 <211> 132
 <212> PRT
 <213> Homo sapiens

<220>
 <221> SIGNAL
 <222> -15...-1

<400> 377
 Met Asn Arg Val Leu Cys Ala Pro Ala Ala Gly Ala Val Arg Ala Leu
 -15 -10 -5 1
 Arg Leu Ile Gly Trp Ala Ser Arg Ser Leu His Pro Leu Pro Gly Ser
 5 10 15
 Arg Asp Arg Ala His Pro Ala Ala Glu Glu Glu Asp Asp Pro Asp Arg
 20 25 30
 Pro Ile Glu Phe Ser Ser Ser Lys Ala Asn Pro His Arg Trp Ser Val
 35 40 45
 Gly His Thr Met Gly Lys Gly His Gln Arg Pro Trp Trp Lys Val Leu
 50 55 60 65
 Pro Leu Ser Cys Phe Leu Val Ala Leu Ile Ile Trp Cys Tyr Leu Arg
 70 75 80
 Glu Glu Ser Glu Ala Asp Gln Trp Leu Arg Gln Val Trp Gly Glu Val
 85 90 95
 Pro Glu Pro Ser Asp Arg Ser Glu Glu Pro Glu Thr Pro Ala Ala Tyr
 100 105 110
 Arg Ala Arg Thr
 115

<210> 378
 <211> 102
 <212> PRT
 <213> Homo sapiens

<220>
 <221> SIGNAL
 <222> -14...-1

<220>

<221> UNSURE

<222> 50

<223> Xaa = Ala,Gly

<220>

<221> UNSURE

<222> 51

<223> Xaa = Leu,Met,Val

<400> 378

Met	Phe	Leu	Thr	Ala	Leu	Leu	Trp	Arg	Gly	Arg	Ile	Pro	Gly	Arg	Gln	
				-10					-5						1	
Trp	Ile	Gly	Lys	His	Arg	Arg	Pro	Arg	Phe	Val	Ser	Leu	Arg	Ala	Lys	
		5					10					15				
Gln	Asn	Met	Ile	Arg	Arg	Leu	Glu	Ile	Asp	Ala	Glu	Asn	His	Tyr	Trp	
	20					25					30					
Leu	Ser	Met	Pro	Tyr	Met	Thr	Arg	Glu	Gln	Glu	Arg	Gly	His	Ala	Xaa	
	35				40					45					50	
Xaa	Arg	Arg	Arg	Glu	Ala	Phe	Glu	Ala	Ile	Lys	Ala	Ala	Ala	Thr	Ser	
				55					60					65		
Lys	Phe	Pro	Pro	His	Arg	Phe	Ile	Ala	Asp	Gln	Leu	Asp	His	Leu	Asn	
			70					75					80			
Val	Thr	Lys	Lys	Trp	Ser											
			85													

<210> 379

<211> 504

<212> PRT

<213> Homo sapiens

<220>

<221> SIGNAL

<222> -24...-1

<400> 379

Met	Gly	Ile	Lys	Thr	Ala	Leu	Pro	Ala	Ala	Glu	Leu	Gly	Leu	Tyr	Ser	
				-20					-15					-10		
Leu	Val	Leu	Ser	Gly	Ala	Leu	Ala	Tyr	Ala	Gly	Arg	Gly	Leu	Leu	Glu	
			-5					1				5				
Ala	Ser	Gln	Asp	Gly	Ala	His	Arg	Lys	Ala	Phe	Arg	Glu	Ser	Val	Arg	
	10					15				20						
Pro	Gly	Trp	Glu	Tyr	Ile	Gly	Arg	Lys	Met	Asp	Val	Ala	Asp	Phe	Glu	
	25				30					35					40	
Trp	Val	Met	Trp	Phe	Thr	Ser	Phe	Arg	Asn	Val	Ile	Ile	Phe	Ala	Leu	
			45						50					55		
Ser	Gly	His	Val	Leu	Phe	Ala	Lys	Leu	Cys	Thr	Met	Val	Ala	Pro	Lys	
			60					65					70			
Leu	Arg	Ser	Trp	Met	Tyr	Ala	Val	Tyr	Gly	Ala	Leu	Ala	Val	Met	Gly	
		75					80					85				
Thr	Met	Gly	Pro	Trp	Tyr	Leu	Leu	Leu	Leu	Gly	His	Cys	Val	Gly		
	90					95				100						
Leu	Tyr	Val	Ala	Ser	Leu	Gly	Gln	Pro	Trp	Leu	Cys	Leu	Gly	Leu		
	105				110				115						120	
Gly	Leu	Ala	Ser	Leu	Ala	Ser	Phe	Lys	Met	Asp	Pro	Leu	Ile	Ser	Trp	
			125					130						135		
Gln	Ser	Gly	Phe	Val	Thr	Gly	Thr	Phe	Asp	Leu	Gln	Glu	Val	Leu	Phe	
			140					145					150			
His	Gly	Gly	Ser	Ser	Phe	Thr	Val	Leu	Arg	Cys	Thr	Ser	Phe	Ala	Leu	

Arg Ala Leu Tyr Arg Arg His Val Leu Gly Ile Val Leu Gln Gly Pro
 25 30 35
 Ala Leu Cys Phe Ala Ala Ala Ile Phe Ser Leu Phe Phe Val Pro Leu
 40 45 50
 Ser Tyr Leu Leu Met Val Thr Val Ile Leu Leu Pro Tyr Val Ser Lys
 55 60 65 70
 Val Thr Gly Trp Cys Arg Asp Arg Leu Leu Gly His Arg Glu Pro Ser
 75 80 85
 Ala His Pro Val Glu Val Phe Ser Phe Asp Leu His Glu Pro Leu Ser
 90 95 100
 Lys Glu Arg Val Glu Ala Phe Ser Asp Gly Val Tyr Ala Ile Val Ala
 105 110 115
 Thr Leu Leu Ile Leu Asp Ile Trp
 120 125

<210> 381
 <211> 51
 <212> PRT
 <213> Homo sapiens

<220>
 <221> SIGNAL
 <222> -26...-1

<400> 381
 Met Glu Met Leu Phe Asp Glu Arg Ala Pro Leu Leu Phe Ile Leu Phe
 -25 -20 -15
 Lys Phe Ser Leu Cys Pro Tyr Ala Ala Ala Leu Ser Lys Pro Ile Phe
 -10 -5 1 5
 Gly Ser Val Ala Cys Met Thr Lys Glu Ile Leu Ala Arg His Gly Gly
 10 15 20
 Ser Arg Leu
 25

<210> 382
 <211> 72
 <212> PRT
 <213> Homo sapiens

<220>
 <221> SIGNAL
 <222> -23...-1

<400> 382
 Met Leu Arg Pro Ala Leu Pro Trp Leu Tyr Leu Gly Leu Cys Ser Leu
 -20 -15 -10
 Leu Val Gly Glu Ala Glu Ala Pro Ser Pro Val Asp Pro Leu Glu Arg
 -5 1 5
 Ser Arg Pro Tyr Ala Val Leu Arg Gly Gln Asn Leu Val Leu Met Gly
 10 15 20 25
 Thr Ile Phe Ser Ile Leu Leu Val Thr Val Ile Leu Met Ala Phe Cys
 30 35 40
 Val Tyr Lys Pro Ile Arg Arg Arg
 45

<210> 383
 <211> 95
 <212> PRT

<213> Homo sapiens

<220>

<221> SIGNAL

<222> -48...-1

<400> 383

Met	Ala	Ser	Ser	His	Trp	Asn	Glu	Thr	Thr	Thr	Ser	Val	Tyr	Gln	Tyr
			-45					-40					-35		
Leu	Gly	Phe	Gln	Val	Gln	Lys	Ile	Tyr	Pro	Phe	His	Asp	Asn	Trp	Asn
		-30				-25						-20			
Thr	Ala	Cys	Phe	Val	Ile	Leu	Leu	Leu	Phe	Ile	Phe	Thr	Val	Val	Ser
	-15				-10					-5					
Leu	Val	Val	Leu	Ala	Phe	Leu	Tyr	Glu	Val	Leu	Asp	Cys	Cys	Cys	Cys
1			5					10					15		
Val	Lys	Asn	Lys	Thr	Val	Lys	Asp	Leu	Lys	Ser	Glu	Pro	Asn	Pro	Leu
		20					25					30			
Arg	Ser	Met	Met	Asp	Asn	Ile	Arg	Lys	Arg	Glu	Thr	Glu	Val	Val	
		35					40					45			

<210> 384

<211> 150

<212> PRT

<213> Homo sapiens

<220>

<221> SIGNAL

<222> -20...-1

<400> 384

Met	Ala	Arg	His	Gly	Leu	Pro	Leu	Leu	Pro	Leu	Leu	Ser	Leu	Leu	Val
-20				-15					-10						-5
Gly	Ala	Trp	Leu	Lys	Leu	Gly	Asn	Gly	Gln	Ala	Thr	Ser	Met	Val	Gln
			1				5					10			
Leu	Gln	Gly	Gly	Arg	Phe	Leu	Met	Gly	Thr	Asn	Ser	Pro	Asp	Ser	Arg
	15					20					25				
Asp	Gly	Glu	Gly	Pro	Val	Arg	Glu	Ala	Thr	Val	Lys	Pro	Phe	Ala	Ile
	30					35				40					
Asp	Ile	Phe	Pro	Val	Thr	Asn	Lys	Asp	Phe	Arg	Asp	Phe	Val	Arg	Glu
45					50				55						60
Lys	Lys	Tyr	Arg	Thr	Glu	Ala	Glu	Met	Phe	Gly	Trp	Ser	Phe	Val	Phe
				65				70						75	
Glu	Asp	Phe	Val	Ser	Asp	Glu	Leu	Arg	Asn	Lys	Ala	Thr	Gln	Pro	Met
			80				85						90		
Lys	Val	Lys	Phe	Thr	His	Gly	Gly	Thr	Gly	Ser	Ser	Gln	Thr	Ala	Pro
		95				100						105			
Thr	Cys	Gly	Arg	Glu	Ser	Ser	Pro	Arg	Glu	Thr	Lys	Leu	Arg	Met	Ala
	110					115					120				
Ser	Met	Glu	Ser	Pro	Gln										
125					130										

<210> 385

<211> 354

<212> PRT

<213> Homo sapiens

<400> 385

Met Ser Ala Gly Gly Gly Arg Ala Phe Ala Trp Gln Val Phe Pro Pro

1				5					10					15		
Met	Pro	Thr	Cys	Arg	Val	Tyr	Gly	Thr	Val	Ala	His	Gln	Asp	Gly	His	
			20					25					30			
Leu	Leu	Val	Leu	Gly	Gly	Cys	Gly	Arg	Ala	Gly	Leu	Pro	Leu	Asp	Thr	
		35					40					45				
Ala	Glu	Thr	Leu	Asp	Met	Ala	Ser	His	Thr	Trp	Leu	Ala	Leu	Ala	Pro	
	50					55					60					
Leu	Pro	Thr	Ala	Arg	Ala	Gly	Ala	Ala	Ala	Val	Val	Leu	Gly	Lys	Gln	
65				70						75					80	
Val	Leu	Val	Val	Cys	Gly	Val	Asp	Glu	Val	Gln	Ser	Pro	Val	Ala	Ala	
			85					90						95		
Val	Glu	Ala	Phe	Leu	Met	Asp	Glu	Gly	Arg	Trp	Glu	Arg	Arg	Ala	Thr	
		100						105					110			
Leu	Pro	Gln	Ala	Ala	Met	Gly	Val	Ala	Thr	Val	Glu	Arg	Asp	Gly	Met	
	115						120						125			
Val	Tyr	Ala	Leu	Gly	Gly	Met	Gly	Pro	Asp	Thr	Ala	Pro	Gln	Ala	Gln	
	130				135						140					
Val	Arg	Val	Tyr	Asp	Pro	Arg	Arg	Asp	Cys	Trp	Leu	Ser	Leu	Pro	Ser	
145				150					155						160	
Met	Pro	Thr	Pro	Cys	Tyr	Gly	Ala	Ser	Thr	Phe	Leu	His	Gly	Asn	Lys	
			165					170						175		
Ile	Tyr	Val	Leu	Gly	Gly	Arg	Gln	Gly	Lys	Leu	Pro	Val	Thr	Ala	Phe	
		180						185					190			
Glu	Ala	Phe	Asp	Leu	Glu	Ala	Arg	Thr	Trp	Thr	Arg	His	Pro	Ser	Leu	
	195					200						205				
Pro	Ser	Arg	Arg	Ala	Phe	Ala	Gly	Cys	Ala	Met	Ala	Glu	Gly	Ser	Val	
	210				215						220					
Phe	Ser	Leu	Gly	Gly	Leu	Gln	Gln	Pro	Gly	Pro	His	Asn	Phe	Tyr	Ser	
225				230						235					240	
Arg	Pro	His	Phe	Val	Asn	Thr	Val	Glu	Met	Phe	Asp	Leu	Glu	His	Gly	
		245						250						255		
Ser	Trp	Thr	Lys	Leu	Pro	Arg	Ser	Leu	Arg	Met	Arg	Asp	Lys	Arg	Ala	
		260						265					270			
Asp	Phe	Val	Val	Gly	Ser	Leu	Gly	Gly	His	Ile	Val	Ala	Ile	Gly	Gly	
	275						280					285				
Leu	Gly	Asn	Gln	Pro	Cys	Pro	Leu	Gly	Ser	Val	Glu	Ser	Phe	Ser	Leu	
	290					295					300					
Ala	Arg	Arg	Arg	Trp	Glu	Ala	Leu	Pro	Ala	Met	Pro	Thr	Ala	Arg	Cys	
305				310						315					320	
Ser	Cys	Ser	Ser	Leu	Gln	Ala	Gly	Pro	Arg	Leu	Phe	Val	Ile	Gly	Gly	
			325					330						335		
Val	Ala	Gln	Gly	Pro	Ser	Gln	Ala	Val	Glu	Ala	Leu	Cys	Leu	Arg	Asp	
			340					345					350			

<210> 386

<211> 207

<212> PRT

<213> Homo sapiens

<400> 386

Met	Ala	Leu	Leu	Phe	Ala	Arg	Ser	Leu	Arg	Leu	Cys	Arg	Trp	Gly	Ala	
1				5					10					15		
Lys	Arg	Leu	Gly	Val	Ala	Ser	Thr	Glu	Ala	Gln	Arg	Gly	Val	Ser	Phe	
		20						25				30				
Lys	Leu	Glu	Glu	Lys	Thr	Ala	His	Ser	Ser	Leu	Ala	Leu	Phe	Arg	Asp	
	35					40					45					
Asp	Thr	Gly	Val	Lys	Tyr	Gly	Leu	Val	Gly	Leu	Glu	Pro	Thr	Lys	Val	

50		55		60
Ala Leu Asn Val Glu Arg Phe Arg Glu Trp Ala Val Val Leu Ala Asp				
65		70		75
Thr Ala Val Thr Ser Gly Arg His Tyr Trp Glu Val Thr Val Lys Arg				80
	85		90	95
Ser Gln Gln Phe Arg Ile Gly Val Ala Asp Val Asp Met Ser Arg Asp				
	100		105	110
Ser Cys Ile Gly Val Asp Asp Arg Ser Trp Val Phe Thr Tyr Ala Gln				
	115		120	125
Arg Lys Trp Tyr Thr Met Leu Ala Asn Glu Lys Ala Pro Val Glu Gly				
	130		135	140
Ile Gly Gln Pro Glu Lys Val Gly Leu Leu Leu Glu Tyr Glu Ala Gln				
	145		150	155
Lys Leu Ser Leu Val Asp Val Ser Gln Val Ser Val Val His Thr Leu				
	165		170	175
Gln Thr Asp Phe Arg Gly Pro Val Val Pro Ala Phe Ala Leu Trp Asp				
	180		185	190
Gly Glu Leu Leu Thr His Ser Gly Leu Glu Val Pro Glu Gly Leu				
	195		200	205

<210> 387

<211> 210

<212> PRT

<213> Homo sapiens

<400> 387

Met Ala Ala Ser Val Glu Gln Arg Glu Gly Thr Ile Gln Val Gln Gly		
1	5	10
Gln Ala Leu Phe Arg Glu Ala Leu Pro Gly Ser Gly Gln Ala Arg		15
	20	25
Phe Ser Val Leu Leu Leu His Gly Ile Arg Phe Ser Ser Glu Thr Trp		30
	35	40
Gln Asn Leu Gly Thr Leu His Arg Leu Ala Gln Ala Gly Tyr Arg Ala		45
	50	55
Val Ala Ile Asp Leu Pro Gly Leu Gly His Ser Lys Glu Ala Ala Ala		60
	65	70
Pro Ala Pro Ile Gly Glu Leu Ala Pro Gly Ser Phe Leu Ala Ala Val		75
	85	90
Val Asp Ala Leu Glu Leu Gly Pro Pro Val Val Ile Ser Pro Ser Leu		95
	100	105
Ser Gly Met Tyr Ser Leu Pro Phe Leu Thr Ala Pro Gly Ser Gln Leu		110
	115	120
Pro Gly Phe Val Pro Val Ala Pro Ile Cys Thr Asp Lys Ile Asn Ala		125
	130	135
Ala Asn Tyr Ala Ser Val Lys Thr Pro Ala Leu Ile Val Tyr Gly Asp		140
	145	150
Gln Asp Pro Met Gly Gln Thr Ser Phe Glu His Leu Lys Gln Leu Pro		155
	165	170
Asn His Arg Val Leu Ile Met Lys Gly Ala Gly His Pro Cys Tyr Leu		175
	180	185
Asp Lys Pro Glu Glu Trp His Thr Gly Leu Leu Asp Phe Leu Gln Gly		190
	195	200
Leu Gln		205
210		

<210> 388

<211> 375

<212> PRT

<213> Homo sapiens

<400> 388

Met Ala Val Thr Glu Ala Ser Leu Leu Arg Gln Cys Pro Leu Leu Leu
1 5 10 15
Pro Gln Asn Arg Ser Lys Thr Val Tyr Glu Gly Phe Ile Ser Ala Gln
20 25 30
Gly Arg Asp Phe His Leu Arg Ile Val Leu Pro Glu Asp Leu Gln Leu
35 40 45
Lys Asn Ala Arg Leu Leu Cys Ile Trp Gln Leu Arg Thr Ile Leu Ser
50 55 60
Gly Tyr His Arg Ile Val Gln Gln Arg Met Gln His Ser Pro Asp Leu
65 70 75 80
Met Ser Phe Met Met Glu Leu Lys Met Leu Leu Glu Val Ala Leu Lys
85 90 95
Asn Arg Gln Glu Leu Tyr Ala Leu Pro Pro Pro Pro Gln Phe Tyr Ser
100 105 110
Ser Leu Ile Glu Glu Ile Gly Thr Leu Gly Trp Asp Lys Leu Val Tyr
115 120 125
Ala Asp Thr Cys Phe Ser Thr Ile Lys Leu Lys Ala Glu Asp Ala Ser
130 135 140
Gly Arg Glu His Leu Ile Thr Leu Lys Leu Lys Ala Lys Tyr Pro Ala
145 150 155 160
Glu Ser Pro Asp Tyr Phe Val Asp Phe Pro Val Pro Phe Cys Ala Ser
165 170 175
Trp Thr Pro Gln Ser Ser Leu Ile Ser Ile Tyr Ser Gln Phe Leu Ala
180 185 190
Ala Ile Glu Ser Leu Lys Ala Phe Trp Asp Val Met Asp Glu Ile Asp
195 200 205
Glu Lys Thr Trp Val Leu Glu Pro Glu Lys Pro Pro Arg Ser Ala Thr
210 215 220
Ala Arg Arg Ile Ala Leu Gly Asn Asn Val Ser Ile Asn Ile Glu Val
225 230 235 240
Asp Pro Arg His Pro Thr Met Leu Pro Glu Cys Phe Phe Leu Gly Ala
245 250 255
Asp His Val Val Lys Pro Leu Gly Ile Lys Leu Ser Arg Asn Ile His
260 265 270
Leu Trp Asp Pro Glu Asn Ser Val Leu Gln Asn Leu Lys Asp Val Leu
275 280 285
Glu Ile Asp Phe Pro Ala Arg Ala Ile Leu Glu Lys Ser Asp Phe Thr
290 295 300
Met Asp Cys Gly Ile Cys Tyr Ala Tyr Gln Leu Asp Gly Thr Ile Pro
305 310 315 320
Asp Gln Val Cys Asp Asn Ser Gln Cys Gly Gln Pro Phe His Gln Ile
325 330 335
Cys Leu Tyr Glu Trp Leu Arg Gly Leu Leu Thr Ser Arg Gln Ser Phe
340 345 350
Asn Ile Ile Phe Gly Glu Cys Pro Tyr Cys Ser Lys Pro Ile Thr Leu
355 360 365
Lys Met Ser Gly Arg Lys His
370 375

<210> 389

<211> 509

<212> PRT

<213> Homo sapiens

<400> 389

Met	Ala	Ala	Ile	Gly	Val	His	Leu	Gly	Cys	Thr	Ser	Ala	Cys	Val	Ala	1	5	10	15
Val	Tyr	Lys	Asp	Gly	Arg	Ala	Gly	Val	Val	Ala	Asn	Asp	Ala	Gly	Asp	20	25	30	
Arg	Val	Thr	Pro	Ala	Val	Val	Ala	Tyr	Ser	Glu	Asn	Glu	Glu	Ile	Val	35	40	45	
Gly	Leu	Ala	Ala	Lys	Gln	Ser	Arg	Ile	Arg	Asn	Ile	Ser	Asn	Thr	Val	50	55	60	
Met	Lys	Val	Lys	Gln	Ile	Leu	Gly	Arg	Ser	Ser	Ser	Asp	Pro	Gln	Ala	65	70	75	80
Gln	Lys	Tyr	Ile	Ala	Glu	Ser	Lys	Cys	Leu	Val	Ile	Glu	Lys	Asn	Gly	85	90	95	
Lys	Leu	Arg	Tyr	Glu	Ile	Asp	Thr	Gly	Glu	Glu	Thr	Lys	Phe	Val	Asn	100	105	110	
Pro	Glu	Asp	Val	Ala	Arg	Leu	Ile	Phe	Ser	Lys	Met	Lys	Glu	Thr	Ala	115	120	125	
His	Ser	Val	Leu	Gly	Ser	Asp	Ala	Asn	Asp	Val	Val	Ile	Thr	Val	Pro	130	135	140	
Phe	Asp	Phe	Gly	Glu	Lys	Gln	Lys	Asn	Ala	Leu	Gly	Glu	Ala	Ala	Arg	145	150	155	160
Ala	Ala	Gly	Phe	Asn	Val	Leu	Arg	Leu	Ile	His	Glu	Pro	Ser	Ala	Ala	165	170	175	
Leu	Leu	Ala	Tyr	Gly	Ile	Gly	Gln	Asp	Ser	Pro	Thr	Gly	Lys	Ser	Asn	180	185	190	
Ile	Leu	Val	Phe	Lys	Leu	Gly	Gly	Thr	Ser	Leu	Ser	Leu	Ser	Val	Met	195	200	205	
Glu	Val	Asn	Ser	Gly	Ile	Tyr	Arg	Val	Leu	Ser	Thr	Asn	Thr	Asp	Asp	210	215	220	
Asn	Ile	Gly	Gly	Ala	His	Phe	Thr	Glu	Thr	Leu	Ala	Gln	Tyr	Leu	Ala	225	230	235	240
Ser	Glu	Phe	Gln	Arg	Ser	Phe	Lys	His	Asp	Val	Arg	Gly	Asn	Ala	Arg	245	250	255	
Ala	Met	Met	Lys	Leu	Thr	Asn	Ser	Ala	Glu	Val	Ala	Lys	His	Ser	Leu	260	265	270	
Ser	Thr	Leu	Gly	Ser	Ala	Asn	Cys	Phe	Leu	Asp	Ser	Leu	Tyr	Glu	Gly	275	280	285	
Gln	Asp	Phe	Asp	Cys	Asn	Val	Ser	Arg	Ala	Arg	Phe	Glu	Leu	Leu	Cys	290	295	300	
Ser	Pro	Leu	Phe	Asn	Lys	Cys	Ile	Glu	Ala	Ile	Arg	Gly	Leu	Leu	Asp	305	310	315	320
Gln	Asn	Gly	Phe	Thr	Thr	Asp	Asp	Ile	Asn	Lys	Val	Val	Leu	Cys	Gly	325	330	335	
Gly	Ser	Ser	Arg	Ile	Pro	Lys	Leu	Gln	Leu	Ile	Lys	Asp	Leu	Phe		340	345	350	
Pro	Ala	Val	Glu	Leu	Leu	Asn	Ser	Ile	Pro	Pro	Asp	Glu	Val	Ile	Pro	355	360	365	
Ile	Gly	Ala	Ala	Ile	Glu	Ala	Gly	Ile	Leu	Ile	Gly	Lys	Glu	Asn	Leu	370	375	380	
Leu	Val	Glu	Asp	Ser	Leu	Met	Ile	Glu	Cys	Ser	Ala	Arg	Asp	Ile	Leu	385	390	395	400
Val	Lys	Gly	Val	Asp	Glu	Ser	Gly	Ala	Ser	Arg	Phe	Thr	Val	Leu	Phe	405	410	415	
Pro	Ser	Gly	Thr	Pro	Leu	Pro	Ala	Arg	Arg	Gln	His	Thr	Leu	Gln	Ala	420	425	430	
Pro	Gly	Ser	Ile	Ser	Ser	Val	Cys	Leu	Glu	Leu	Tyr	Glu	Ser	Asp	Gly	435	440	445	
Lys	Asn	Ser	Ala	Lys	Glu	Glu	Thr	Lys	Phe	Ala	Gln	Val	Val	Leu	Gln	450	455	460	

Asp Leu Asp Lys Lys Glu Asn Gly Leu Arg Asp Ile Leu Ala Val Leu
 465 470 475 480
 Thr Met Lys Arg Asp Gly Ser Leu His Val Thr Cys Thr Asp Gln Glu
 485 490 495
 Thr Gly Lys Cys Glu Ala Ile Ser Ile Glu Ile Ala Ser
 500 505

<210> 390
 <211> 78
 <212> PRT
 <213> Homo sapiens

<400> 390
 Met Tyr Asn Thr Gly Arg His Val Ser Leu Arg Leu Asp Lys Glu His
 1 5 10 15
 Leu Val Asn Ile Ser Gly Gly Pro Met Thr Tyr Ser His Arg Leu Glu
 20 25 30
 Glu Ile Arg Leu His Phe Gly Ser Glu Asp Ser Gln Gly Ser Glu His
 35 40 45
 Leu Leu Asn Gly Gln Ala Phe Ser Gly Glu Leu Gln Glu Arg Asp Leu
 50 55 60
 Phe Ile Leu Leu Thr Ser Val Ser Gly His Leu Pro Asp Thr
 65 70 75

<210> 391
 <211> 162
 <212> PRT
 <213> Homo sapiens

<400> 391
 Met Ala Thr His Ala Leu Glu Ile Ala Gly Leu Phe Leu Gly Gly Val
 1 5 10 15
 Gly Met Val Gly Thr Val Ala Val Thr Val Met Pro Gln Trp Ile Val
 20 25 30
 Ser Ala Phe Ile Glu Asn Asn Ile Val Val Phe Glu Asn Phe Trp Glu
 35 40 45
 Gly Leu Trp Met Asn Cys Val Arg Gln Ala Asn Ile Arg Met Gln Cys
 50 55 60
 Lys Ile Tyr Asp Ser Leu Leu Ala Leu Ser Pro Asp Leu Gln Ala Ala
 65 70 75 80
 Arg Gly Leu Met Cys Ala Ala Ser Val Met Ser Phe Leu Ala Phe Met
 85 90 95
 Met Ala Ile Leu Gly Met Lys Cys Thr Arg Cys Thr Gly Asp Asn Glu
 100 105 110
 Lys Val Lys Ala His Ile Leu Leu Thr Ala Gly Ile Ile Phe Ile Ile
 115 120 125
 Thr Gly Met Val Val Leu Ile Pro Val Ser Trp Val Ala Asn Ala Ile
 130 135 140
 Ile Arg Asp Phe Tyr Asn Pro Ile Val Asn Val Ala Gln Lys Arg Glu
 145 150 155 160
 Leu Gly

<210> 392
 <211> 146
 <212> PRT
 <213> Homo sapiens

<400> 392

Met Asn Ser Leu Leu His Phe Gly Ile Leu Leu Glu Leu Ser Leu Leu
1 5 10 15
Lys Gln Phe Lys Ser Val Tyr Val Pro Gly Asn His Thr His Gln Ala
20 25 30
Ser Tyr Lys Pro Leu Leu Lys Gln Val Val Glu Glu Ile Phe His Pro
35 40 45
Glu Arg Pro Asp Ser Val Asp Ile Glu His Met Ser Ser Gly Leu Thr
50 55 60
Asp Leu Leu Lys Thr Gly Phe Ser Met Phe Met Lys Val Ser Arg Pro
65 70 75 80
His Pro Ser Asp Tyr Pro Leu Leu Ile Leu Phe Val Val Gly Gly Val
85 90 95
Thr Val Ser Glu Val Lys Met Val Lys Asp Leu Val Ala Ser Leu Lys
100 105 110
Pro Gly Thr Gln Val Ile Val Leu Ser Thr Arg Leu Leu Lys Pro Leu
115 120 125
Asn Ile Pro Glu Leu Leu Phe Ala Thr Asp Arg Leu His Pro Asp Leu
130 135 140
Gly Phe
145

<210> 393

<211> 225

<212> PRT

<213> Homo sapiens

<400> 393

Met Ala Thr His Ala Leu Glu Ile Ala Gly Leu Phe Leu Gly Gly Val
1 5 10 15
Gly Met Val Gly Thr Val Ala Val Thr Val Met Pro Gln Trp Arg Val
20 25 30
Ser Ala Phe Ile Glu Asn Asn Ile Val Val Phe Glu Asn Phe Trp Glu
35 40 45
Gly Leu Trp Met Asn Cys Val Arg Gln Ala Asn Ile Arg Met Gln Cys
50 55 60
Lys Ile Tyr Asp Ser Leu Leu Ala Leu Ser Pro Asp Leu Gln Ala Ala
65 70 75 80
Arg Gly Leu Met Cys Ala Ala Ser Val Met Ser Phe Leu Ala Phe Met
85 90 95
Met Ala Ile Leu Gly Met Lys Cys Thr Arg Cys Thr Gly Asp Asn Glu
100 105 110
Lys Val Lys Ala His Ile Leu Leu Thr Ala Gly Ile Ile Phe Ile Ile
115 120 125
Ala Gly Met Val Val Leu Ile Pro Val Ser Trp Val Ala Asn Ala Ile
130 135 140
Ile Arg Asp Phe Tyr Asn Pro Ile Val Asn Val Ala Gln Lys Arg Glu
145 150 155 160
Leu Gly Glu Ala Leu Tyr Leu Gly Trp Thr Thr Ala Leu Val Leu Ile
165 170 175
Val Gly Gly Ala Leu Phe Cys Cys Val Phe Cys Cys Asn Glu Lys Ser
180 185 190
Ser Ser Tyr Arg Tyr Ser Ile Pro Ser His Arg Thr Thr Gln Lys Ser
195 200 205
Tyr His Thr Gly Lys Lys Ser Pro Ser Val Tyr Ser Arg Ser Gln Tyr
210 215 220
Val
225

<210> 394
 <211> 114
 <212> PRT
 <213> Homo sapiens

<400> 394
 Met Arg Leu Gln Asp Arg Ile Ala Thr Phe Phe Phe Pro Lys Gly Met
 1 5 10 15
 Met Leu Thr Thr Ala Ala Leu Met Leu Phe Phe Leu His Leu Gly Ile
 20 25 30
 Phe Ile Arg Asp Val His Asn Phe Cys Ile Thr Tyr His Tyr Asp His
 35 40 45
 Met Ser Phe His Tyr Thr Val Val Leu Met Phe Ser Gln Val Ile Ser
 50 55 60
 Ile Cys Trp Ala Ala Met Gly Ser Leu Tyr Ala Glu Met Thr Glu Asn
 65 70 75 80
 Asn Ala Gln Arg Ser His Val Leu Gln Pro Pro Val Leu Gly Val Ser
 85 90 95
 Gly His Arg Val Pro Gly Gly Ala Pro Leu Arg Pro Gly Glu Ser Glu
 100 105 110
 Gln Gly

<210> 395
 <211> 367
 <212> PRT
 <213> Homo sapiens

<400> 395
 Met Ala Thr Pro Asn Asn Leu Thr Pro Thr Asn Cys Ser Trp Trp Pro
 1 5 10 15
 Ile Ser Ala Leu Glu Ser Asp Ala Ala Lys Pro Ala Glu Ala Pro Asp
 20 25 30
 Ala Pro Glu Ala Ala Ser Pro Ala His Trp Pro Arg Glu Ser Leu Val
 35 40 45
 Leu Tyr His Trp Thr Gln Ser Phe Ser Ser Gln Lys Val Arg Leu Val
 50 55 60
 Ile Ala Glu Lys Gly Leu Val Cys Glu Glu Arg Asp Val Ser Leu Pro
 65 70 75 80
 Gln Ser Glu His Lys Glu Pro Trp Phe Met Arg Leu Asn Leu Gly Glu
 85 90 95
 Glu Val Pro Val Ile Ile His Arg Asp Asn Ile Ile Ser Asp Tyr Asp
 100 105 110
 Gln Ile Ile Asp Tyr Val Glu Arg Thr Phe Thr Gly Glu His Val Val
 115 120 125
 Ala Leu Met Pro Glu Val Gly Ser Leu Gln His Ala Arg Val Leu Gln
 130 135 140
 Tyr Arg Glu Leu Leu Asp Ala Leu Pro Met Asp Ala Tyr Thr His Gly
 145 150 155 160
 Cys Ile Leu His Pro Glu Leu Thr Thr Asp Ser Met Ile Pro Lys Tyr
 165 170 175
 Ala Thr Ala Glu Ile Arg Arg His Leu Ala Asn Ala Thr Thr Asp Leu
 180 185 190
 Met Lys Leu Asp His Glu Glu Glu Pro Gln Leu Ser Glu Pro Tyr Leu
 195 200 205
 Ser Lys Gln Lys Lys Leu Met Val Lys Ile Leu Glu His Asp Asp Val
 210 215 220
 Ser Tyr Leu Lys Lys Ile Leu Gly Glu Leu Ala Met Val Leu Asp Gln
 225 230 235 240

Ile Glu Ala Glu Leu Glu Lys Arg Lys Leu Glu Asn Glu Gly Gln Lys
245 250 255
Cys Glu Leu Trp Leu Cys Gly Cys Ala Phe Thr Leu Ala Asp Val Leu
260 265 270
Leu Gly Ala Thr Leu His Arg Leu Lys Phe Leu Gly Leu Ser Lys Lys
275 280 285
Tyr Trp Glu Asp Gly Ser Arg Pro Asn Leu Gln Ser Phe Phe Glu Arg
290 295 300
Val Gln Arg Arg Phe Ala Phe Arg Lys Val Leu Gly Asp Ile His Thr
305 310 315 320
Thr Leu Leu Ser Ala Val Ile Pro Asn Ala Phe Arg Leu Val Lys Arg
325 330 335
Lys Pro Pro Ser Phe Phe Gly Ala Ser Phe Leu Met Gly Ser Leu Gly
340 345 350
Gly Met Gly Tyr Phe Ala Tyr Trp Tyr Leu Lys Lys Lys Tyr Ile
355 360 365

<210> 396
<211> 279
<212> PRT
<213> Homo sapiens

<400> 396
Met Pro Val Cys Ala Pro Val Leu Trp Arg Ala Arg Arg Leu Cys Gly
1 5 10 15
Met Pro Val Cys Ala Pro Val Pro Trp Arg Ala Arg Arg Leu Cys Thr
20 25 30
Arg Ala Val Val Cys Pro Ser Ser Val Pro Phe Ile Ala Gly Gln Gly
35 40 45
Cys Thr His Met Cys Lys Pro Ala Thr Asp Pro Arg Phe Thr Arg Ser
50 55 60
Pro Leu Ala Gly Gly Val Ile Leu Gly Val Ala Leu Trp Leu Arg His
65 70 75 80
Asp Pro Gln Thr Thr Asn Leu Leu Tyr Leu Glu Leu Gly Asp Lys Pro
85 90 95
Ala Pro Asn Thr Phe Tyr Val Gly Ile Tyr Ile Leu Ile Ala Val Gly
100 105 110
Ala Val Met Met Phe Val Gly Phe Leu Gly Cys Tyr Gly Ala Ile Gln
115 120 125
Glu Ser Gln Cys Leu Leu Gly Thr Phe Phe Thr Cys Leu Val Ile Leu
130 135 140
Phe Ala Cys Glu Val Ala Ala Gly Ile Trp Gly Phe Val Asn Lys Asp
145 150 155 160
Gln Ile Ala Lys Asp Val Lys Gln Phe Tyr Asp Gln Ala Leu Gln Gln
165 170 175
Ala Val Val Asp Asp Ala Asn Asn Ala Lys Ala Val Val Lys Thr
180 185 190
Phe His Glu Thr Leu Asp Cys Cys Gly Ser Ser Thr Leu Thr Ala Leu
195 200 205
Thr Thr Ser Val Leu Lys Asn Asn Leu Cys Pro Ser Gly Ser Asn Ile
210 215 220
Ile Ser Asn Leu Phe Lys Glu Asp Cys His Gln Lys Ile Asp Asp Leu
225 230 235 240
Phe Ser Gly Lys Leu Tyr Leu Ile Gly Ile Ala Ala Ile Val Val Ala
245 250 255
Val Ile Met Ile Phe Glu Met Ile Leu Ser Met Val Leu Cys Cys Gly
260 265 270
Ile Arg Asn Ser Ser Val Tyr

275

<210> 397
 <211> 173
 <212> PRT
 <213> Homo sapiens

<400> 397
 Met Cys Leu Leu Leu Gly Ala Thr Gly Val Gly Lys Thr Leu Leu Val
 1 5 10 15
 Lys Arg Leu Gln Glu Val Ser Ser Arg Asp Gly Lys Gly Asp Leu Gly
 20 25 30
 Glu Pro Pro Pro Thr Arg Pro Thr Val Gly Thr Asn Leu Thr Asp Ile
 35 40 45
 Val Ala Gln Arg Lys Ile Thr Ile Arg Glu Leu Gly Gly Cys Met Gly
 50 55 60
 Pro Ile Trp Ser Ser Tyr Tyr Gly Asn Cys Arg Ser Leu Leu Phe Val
 65 70 75 80
 Met Asp Ala Ser Asp Pro Thr Gln Leu Ser Ala Ser Cys Val Gln Leu
 85 90 95
 Leu Gly Leu Leu Ser Ala Glu Gln Leu Ala Glu Ala Ser Val Leu Ile
 100 105 110
 Leu Phe Asn Lys Ile Asp Leu Pro Cys Tyr Met Ser Thr Glu Glu Met
 115 120 125
 Lys Ser Leu Ile Arg Leu Pro Asp Ile Ile Ala Cys Ala Lys Gln Asn
 130 135 140
 Ile Thr Thr Ala Glu Ile Ser Ala Arg Glu Gly Thr Gly Leu Ala Gly
 145 150 155 160
 Val Leu Ala Trp Leu Gln Ala Thr His Arg Ala Asn Asp
 165 170

<210> 398
 <211> 205
 <212> PRT
 <213> Homo sapiens

<400> 398
 Met Ala Ala Ala Arg Pro Ser Leu Gly Arg Val Leu Pro Gly Ser Ser
 1 5 10 15
 Val Leu Phe Leu Cys Asp Met Gln Glu Lys Phe Arg His Asn Ile Ala
 20 25 30
 Tyr Phe Pro Gln Ile Val Ser Val Ala Ala Arg Met Leu Lys Val Ala
 35 40 45
 Arg Leu Leu Glu Val Pro Val Met Leu Thr Glu Gln Tyr Pro Gln Gly
 50 55 60
 Leu Gly Pro Thr Val Pro Glu Leu Gly Thr Glu Gly Leu Arg Pro Leu
 65 70 75 80
 Ala Lys Thr Cys Phe Ser Met Val Pro Ala Leu Gln Gln Glu Leu Asp
 85 90 95
 Ser Arg Pro Gln Leu Arg Ser Val Leu Leu Cys Gly Ile Glu Ala Gln
 100 105 110
 Ala Cys Ile Leu Asn Thr Thr Leu Asp Leu Leu Asp Arg Gly Leu Gln
 115 120 125
 Val His Val Val Val Asp Ala Cys Ser Ser Arg Ser Gln Val Asp Arg
 130 135 140
 Leu Val Ala Leu Ala Arg Met Arg Gln Ser Gly Ala Phe Leu Ser Thr
 145 150 155 160
 Ser Glu Gly Leu Ile Leu Gln Leu Val Gly Asp Ala Val His Pro Gln

				165					170					175			
Phe	Lys	Glu	Ile	Gln	Lys	Leu	Ile	Lys	Glu	Pro	Ala	Pro	Asp	Ser	Gly		
			180					185					190				
Leu	Leu	Gly	Leu	Phe	Gln	Gly	Gln	Asn	Ser	Leu	Leu	His					
		195					200					205					

<210> 399
 <211> 180
 <212> PRT
 <213> Homo sapiens

<400> 399

Met	Trp	Leu	Tyr	Arg	Asn	Pro	Tyr	Val	Glu	Ala	Glu	Tyr	Phe	Pro	Thr		
1			5						10				15				
Lys	Pro	Met	Phe	Val	Ile	Ala	Phe	Leu	Ser	Pro	Leu	Ser	Leu	Ile	Phe		
			20					25					30				
Leu	Ala	Lys	Phe	Leu	Lys	Lys	Ala	Asp	Thr	Arg	Asp	Ser	Arg	Gln	Ala		
		35					40					45					
Cys	Leu	Ala	Ala	Ser	Leu	Ala	Leu	Ala	Leu	Asn	Gly	Val	Phe	Thr	Asn		
	50					55					60						
Thr	Ile	Lys	Leu	Ile	Val	Gly	Arg	Pro	Arg	Pro	Asp	Phe	Phe	Tyr	Arg		
65					70					75					80		
Cys	Phe	Pro	Asp	Gly	Leu	Ala	His	Ser	Asp	Leu	Met	Cys	Thr	Gly	Asp		
			85						90					95			
Lys	Asp	Val	Val	Asn	Glu	Gly	Arg	Lys	Ser	Phe	Pro	Ser	Gly	His	Ser		
			100					105					110				
Ser	Phe	Ala	Phe	Ala	Gly	Leu	Ala	Phe	Ala	Ser	Phe	Tyr	Leu	Ala	Gly		
	115					120						125					
Lys	Leu	His	Cys	Phe	Thr	Pro	Gln	Gly	Arg	Gly	Lys	Ser	Trp	Arg	Phe		
	130					135					140						
Cys	Ala	Phe	Leu	Ser	Pro	Leu	Leu	Phe	Ala	Ala	Val	Ile	Ala	Leu	Ser		
145					150				155						160		
Arg	Thr	Cys	Asp	Tyr	Lys	His	His	Trp	Gln	Asp	Leu	Leu	Lys	Cys	Thr		
			165						170					175			
Asn	Thr	Ala	Lys														
			180														

<210> 400
 <211> 150
 <212> PRT
 <213> Homo sapiens

<400> 400

Met	Cys	Thr	Ala	Leu	Leu	Leu	Leu	Tyr	Leu	Arg	Trp	Cys	Phe	Asn	Leu		
1				5					10					15			
Lys	Leu	Val	Asn	Val	Lys	Tyr	Glu	Pro	Lys	Asp	Ser	Leu	Gly	Pro	Glu		
			20					25					30				
Met	Thr	Phe	Val	Ala	Asp	Ala	Ala	Arg	Gly	Pro	Leu	Leu	Ser	Ser	Leu		
		35					40					45					
Asp	Ser	Pro	Ala	Asn	Leu	Met	Ser	Thr	Ala	Ser	Val	Cys	Ile	Ser	Leu		
	50					55					60						
Pro	Glu	Gly	Cys	Ser	Gly	Gly	Arg	Ser	Pro	Cys	Tyr	Ser	Gln	Lys	Trp		
65					70					75					80		
Pro	Pro	Glu	Val	Pro	Glu	Lys	Leu	Thr	Ser	Leu	Gly	Gln	Gln	Ser	Ser		
				85					90					95			
Thr	Ser	Ser	Leu	Thr	Asp	Thr	Asp	Val	Gln	Val	Ser	Pro	Met	Leu	Val		
			100					105					110				
Ala	Gly	Val	Asn	His	Ser	Ser	Ser	Leu	Leu	Asp	Asn	Ile	Pro	Phe	Thr		

130		135		140											
Thr	Glu	Cys	Gly	Gln	Asp	Phe	Ala	Gln	Glu	Ala	Gly	Leu	His	Gln	His
145					150					155					160
Tyr	Ile	Arg	His	Ala	Arg	Gly	Glu	Leu							
				165											

<210> 403
 <211> 367
 <212> PRT
 <213> Homo sapiens

<400> 403

Met	Ala	Thr	Pro	Asn	Asn	Leu	Thr	Pro	Thr	Asn	Cys	Ser	Trp	Trp	Pro
1				5					10					15	
Ile	Ser	Ala	Leu	Glu	Ser	Asp	Ala	Ala	Lys	Pro	Ala	Glu	Ala	Pro	Asp
			20					25					30		
Ala	Pro	Glu	Ala	Ala	Ser	Pro	Ala	His	Trp	Pro	Arg	Glu	Ser	Leu	Val
			35				40					45			
Leu	Tyr	His	Trp	Thr	Gln	Ser	Phe	Ser	Ser	Gln	Lys	Val	Arg	Leu	Val
	50					55					60				
Ile	Ala	Glu	Lys	Gly	Leu	Val	Cys	Glu	Glu	Arg	Asp	Val	Ser	Leu	Pro
65					70					75					80
Gln	Ser	Glu	His	Lys	Glu	Pro	Trp	Phe	Met	Arg	Leu	Asn	Leu	Gly	Glu
				85					90					95	
Glu	Val	Pro	Val	Ile	Ile	His	Arg	Asp	Asn	Ile	Ile	Ser	Asp	Tyr	Asp
			100					105					110		
Gln	Ile	Ile	Asp	Tyr	Val	Glu	Arg	Thr	Phe	Thr	Gly	Glu	His	Val	Val
		115					120					125			
Ala	Leu	Met	Pro	Glu	Val	Gly	Ser	Leu	Gln	His	Ala	Arg	Val	Leu	Gln
	130					135					140				
Tyr	Arg	Glu	Leu	Leu	Asp	Ala	Leu	Pro	Met	Asp	Ala	Tyr	Thr	His	Gly
145					150					155					160
Cys	Ile	Leu	His	Leu	Glu	Leu	Thr	Thr	Asp	Ser	Met	Ile	Pro	Lys	Tyr
				165					170					175	
Ala	Thr	Ala	Glu	Ile	Arg	Arg	His	Leu	Ala	Asn	Ala	Thr	Thr	Asp	Leu
			180					185					190		
Met	Lys	Leu	Asp	His	Glu	Glu	Glu	Pro	Gln	Leu	Ser	Glu	Pro	Tyr	Leu
		195					200						205		
Ser	Lys	Gln	Lys	Lys	Leu	Met	Ala	Lys	Ile	Leu	Glu	His	Asp	Asp	Val
	210					215					220				
Ser	Tyr	Leu	Lys	Lys	Ile	Leu	Gly	Glu	Leu	Ala	Met	Val	Leu	Asp	Gln
225					230					235					240
Ile	Glu	Ala	Glu	Leu	Glu	Lys	Arg	Lys	Leu	Glu	Asn	Glu	Gly	Gln	Lys
			245						250					255	
Cys	Glu	Leu	Trp	Leu	Cys	Gly	Cys	Ala	Phe	Thr	Leu	Ala	Asp	Val	Leu
		260						265					270		
Leu	Gly	Ala	Thr	Leu	His	Arg	Leu	Lys	Phe	Leu	Gly	Leu	Ser	Lys	Lys
		275					280					285			
Tyr	Trp	Glu	Asp	Gly	Ser	Arg	Pro	Asn	Leu	Gln	Ser	Phe	Phe	Glu	Arg
	290					295					300				
Val	Gln	Arg	Arg	Phe	Ala	Phe	Arg	Lys	Val	Leu	Gly	Asp	Ile	His	Thr
305					310					315					320
Thr	Leu	Leu	Ser	Ala	Val	Ile	Pro	Asn	Ala	Phe	Arg	Leu	Val	Lys	Arg
				325					330					335	
Lys	Pro	Pro	Ser	Phe	Phe	Gly	Ala	Ser	Phe	Leu	Met	Gly	Ser	Leu	Gly
			340					345					350		
Gly	Met	Gly	Tyr	Phe	Ala	Tyr	Trp	Tyr	Leu	Lys	Lys	Lys	Tyr	Ile	
		355					360					365			

<210> 404
 <211> 20
 <212> PRT
 <213> Homo sapiens

<400> 404
 Met Ala Ala Ala Arg Pro Ser Leu Gly Arg Val Leu Pro Gly Ser Ser
 1 5 10 15
 Pro Val Pro Val
 20

<210> 405
 <211> 225
 <212> PRT
 <213> Homo sapiens

<400> 405
 Met Ala Thr His Ala Leu Glu Ile Ala Gly Leu Phe Leu Gly Gly Val
 1 5 10 15
 Gly Met Val Gly Thr Val Ala Val Thr Val Met Pro Gln Trp Arg Val
 20 25 30
 Ser Ala Phe Ile Glu Asn Asn Ile Val Val Phe Glu Asn Phe Trp Glu
 35 40 45
 Gly Leu Trp Met Asn Cys Val Arg Gln Ala Asn Ile Arg Met Gln Cys
 50 55 60
 Lys Ile Tyr Asp Ser Leu Leu Ala Leu Ser Pro Asp Leu Gln Ala Ala
 65 70 75 80
 Arg Gly Leu Met Cys Ala Ala Ser Val Met Ser Phe Leu Ala Phe Met
 85 90 95
 Met Ala Ile Leu Gly Met Lys Cys Thr Arg Cys Thr Gly Asp Asn Glu
 100 105 110
 Lys Val Lys Ala His Ile Leu Leu Thr Ala Gly Ile Ile Phe Ile Ile
 115 120 125
 Thr Gly Met Val Val Leu Ile Pro Val Ser Trp Val Ala Asn Ala Ile
 130 135 140
 Ile Arg Asp Phe Tyr Asn Ser Ile Val Asn Val Ala Gln Lys Arg Glu
 145 150 155 160
 Leu Gly Glu Ala Leu Tyr Leu Gly Trp Thr Thr Ala Leu Val Leu Ile
 165 170 175
 Val Gly Gly Ala Leu Phe Cys Cys Val Phe Cys Cys Asn Glu Lys Ser
 180 185 190
 Ser Ser Tyr Arg Tyr Ser Ile Pro Ser His Arg Thr Thr Gln Lys Ser
 195 200 205
 Tyr His Thr Gly Lys Lys Ser Pro Ser Val Tyr Ser Arg Ser Gln Tyr
 210 215 220
 Val
 225

<210> 406
 <211> 378
 <212> PRT
 <213> Homo sapiens

<400> 406
 Met Asp Pro Gly Asp Asp Trp Leu Val Glu Ser Leu Arg Leu Tyr Gln
 1 5 10 15
 Asp Phe Tyr Ala Phe Asp Leu Ser Gly Ala Thr Arg Val Leu Glu Trp

<210> 408
 <211> 345
 <212> PRT
 <213> Homo sapiens

<400> 408
 Met Ala Trp Arg Gly Trp Ala Gln Arg Gly Trp Gly Cys Gly Gln Ala
 1 5 10 15
 Trp Gly Ala Ser Val Gly Gly Arg Ser Cys Glu Glu Leu Thr Ala Val
 20 25 30
 Leu Thr Pro Pro Gln Leu Leu Gly Arg Arg Phe Asn Phe Phe Ile Gln
 35 40 45
 Gln Lys Cys Gly Phe Arg Lys Ala Pro Arg Lys Val Glu Pro Arg Arg
 50 55 60
 Ser Asp Pro Gly Thr Ser Gly Glu Ala Tyr Lys Arg Ser Ala Leu Ile
 65 70 75 80
 Pro Pro Val Glu Glu Thr Val Phe Tyr Pro Ser Pro Tyr Pro Ile Arg
 85 90 95
 Ser Leu Ile Lys Pro Leu Phe Phe Thr Val Gly Phe Thr Gly Cys Ala
 100 105 110
 Phe Gly Ser Ala Ala Ile Trp Gln Tyr Glu Ser Leu Lys Ser Arg Val
 115 120 125
 Gln Ser Tyr Phe Asp Gly Ile Lys Ala Asp Trp Leu Asp Ser Ile Arg
 130 135 140
 Pro Gln Lys Glu Gly Asp Phe Arg Lys Glu Ile Asn Lys Trp Trp Asn
 145 150 155 160
 Asn Leu Ser Asp Gly Gln Arg Thr Val Thr Gly Ile Ile Ala Ala Asn
 165 170 175
 Val Leu Val Phe Cys Leu Trp Arg Val Pro Ser Leu Gln Arg Thr Met
 180 185 190
 Ile Arg Tyr Phe Thr Ser Asn Pro Ala Ser Lys Val Leu Cys Ser Pro
 195 200 205
 Met Leu Leu Ser Thr Phe Ser His Phe Ser Leu Phe His Met Ala Ala
 210 215 220
 Asn Met Tyr Val Leu Trp Ser Phe Ser Ser Ser Ile Val Asn Ile Leu
 225 230 235 240
 Gly Gln Glu Gln Phe Met Ala Val Tyr Leu Ser Ala Gly Val Ile Ser
 245 250 255
 Asn Phe Val Ser Tyr Val Gly Lys Val Ala Thr Gly Arg Tyr Gly Pro
 260 265 270
 Ser Leu Gly Ala Ala Leu Lys Ala Ile Ile Ala Met Asp Thr Ala Gly
 275 280 285
 Met Ile Leu Gly Trp Lys Phe Phe Asp His Ala Ala His Leu Gly Gly
 290 295 300
 Ala Leu Phe Gly Ile Trp Tyr Val Thr Tyr Gly His Glu Leu Ile Trp
 305 310 315 320
 Lys Asn Arg Glu Pro Leu Val Lys Ile Trp His Glu Ile Arg Thr Asn
 325 330 335
 Gly Pro Lys Lys Gly Gly Gly Ser Lys
 340 345

<210> 409
 <211> 236
 <212> PRT
 <213> Homo sapiens

<400> 409

Met	Lys	Arg	Ser	Gly	Asn	Pro	Gly	Ala	Glu	Val	Thr	Asn	Ser	Ser	Val
1				5					10					15	
Ala	Gly	Pro	Asp	Cys	Cys	Gly	Gly	Leu	Gly	Asn	Ile	Asp	Phe	Arg	Gln
			20					25					30		
Ala	Asp	Phe	Cys	Val	Met	Thr	Arg	Leu	Leu	Gly	Tyr	Val	Asp	Pro	Leu
		35					40					45			
Asp	Pro	Ser	Phe	Val	Ala	Ala	Val	Ile	Thr	Ile	Thr	Phe	Asn	Pro	Leu
	50					55					60				
Tyr	Trp	Asn	Val	Val	Ala	Arg	Trp	Glu	His	Lys	Thr	Arg	Lys	Leu	Ser
65					70					75					80
Arg	Ala	Phe	Gly	Ser	Pro	Tyr	Leu	Ala	Cys	Tyr	Ser	Leu	Ser	Ile	Thr
				85					90					95	
Ile	Leu	Leu	Leu	Asn	Phe	Leu	Arg	Ser	His	Cys	Phe	Thr	Gln	Ala	Met
			100					105					110		
Leu	Ser	Gln	Pro	Arg	Met	Glu	Ser	Leu	Asp	Thr	Pro	Ala	Ala	Tyr	Ser
		115					120					125			
Leu	Val	Leu	Ala	Leu	Leu	Gly	Leu	Gly	Val	Val	Leu	Val	Leu	Ser	Ser
	130					135					140				
Phe	Phe	Ala	Leu	Gly	Phe	Ala	Gly	Thr	Phe	Leu	Gly	Asp	Tyr	Phe	Gly
145					150					155					160
Ile	Leu	Lys	Glu	Ala	Arg	Val	Thr	Val	Phe	Pro	Phe	Asn	Ile	Leu	Asp
				165					170					175	
Asn	Pro	Met	Tyr	Trp	Gly	Ser	Thr	Ala	Asn	Tyr	Leu	Gly	Trp	Ala	Ile
			180					185					190		
Met	His	Ala	Ser	Pro	Thr	Gly	Leu	Leu	Leu	Thr	Val	Leu	Val	Ala	Leu
		195					200					205			
Thr	Tyr	Ile	Val	Ala	Leu	Leu	Tyr	Glu	Glu	Pro	Phe	Thr	Ala	Glu	Ile
	210				215						220				
Tyr	Arg	Gln	Lys	Ala	Ser	Gly	Ser	His	Lys	Arg	Ser				
225					230					235					

<210> 410

<211> 121

<212> PRT

<213> Homo sapiens

<400> 410

Met	Asn	Thr	Glu	Ala	Glu	Gln	Gln	Leu	Leu	His	His	Ala	Arg	Asn	Gly
1				5						10				15	
Asn	Ala	Glu	Glu	Val	Arg	Gln	Leu	Leu	Glu	Thr	Met	Ala	Ser	Asn	Glu
			20					25					30		
Val	Ile	Ala	Asp	Ile	Asn	Cys	Lys	Gly	Arg	Ser	Lys	Ser	Asn	Leu	Gly
		35					40					45			
Trp	Thr	Pro	Leu	His	Leu	Ala	Cys	Tyr	Phe	Gly	His	Arg	Gln	Val	Val
	50					55					60				
Gln	Asp	Leu	Leu	Lys	Ala	Gly	Ala	Glu	Val	Asn	Val	Leu	Asn	Asp	Met
65					70					75					80
Gly	Asp	Thr	Pro	Leu	His	Arg	Ala	Ala	Phe	Thr	Gly	Arg	Lys	Val	Lys
				85					90					95	
Ile	Ile	Leu	Cys	Ser	Met	Phe	Val	Ser	Glu	Val	Phe	Gly	Gly	Val	Val
		100						105					110		
Thr	Ile	Val	Phe	Ser	Val	Ile	Thr	Ile							
		115					120								

<210> 411

<211> 170

<212> PRT

<213> Homo sapiens

<400> 411
 Met Arg Leu Gln Gly Ala Ile Phe Val Leu Leu Pro His Leu Gly Pro
 1 5 10 15
 Ile Leu Val Trp Leu Phe Thr Arg Asp His Met Ser Gly Trp Cys Glu
 20 25 30
 Gly Pro Arg Met Leu Ser Trp Cys Pro Phe Tyr Lys Val Leu Leu Leu
 35 40 45
 Val Gln Thr Ala Ile Tyr Ser Val Val Gly Tyr Ala Ser Tyr Leu Val
 50 55 60
 Trp Lys Asp Leu Gly Gly Gly Leu Gly Trp Pro Leu Ala Leu Pro Leu
 65 70 75 80
 Gly Leu Tyr Ala Val Gln Leu Thr Ile Ser Trp Thr Val Leu Val Leu
 85 90 95
 Phe Phe Thr Val His Asn Pro Gly Leu Ala Leu Leu His Leu Leu Leu
 100 105 110
 Leu Tyr Gly Leu Val Val Ser Thr Ala Leu Ile Trp His Pro Ile Asn
 115 120 125
 Lys Leu Ala Ala Leu Leu Leu Leu Pro Tyr Leu Ala Trp Leu Thr Val
 130 135 140
 Thr Ser Ala Leu Thr Tyr His Leu Trp Arg Asp Ser Leu Cys Pro Val
 145 150 155 160
 His Gln Pro Gln Pro Thr Glu Lys Ser Asp
 165 170

<210> 412
 <211> 236
 <212> PRT
 <213> Homo sapiens

<400> 412
 Met Leu Ser Lys Gly Leu Lys Arg Lys Arg Glu Glu Glu Glu Glu Lys
 1 5 10 15
 Glu Pro Leu Ala Val Asp Ser Trp Trp Leu Asp Pro Gly His Thr Ala
 20 25 30
 Val Ala Gln Ala Pro Pro Ala Val Ala Ser Ser Ser Leu Phe Asp Leu
 35 40 45
 Ser Val Leu Lys Leu His His Ser Leu Gln Gln Ser Glu Pro Asp Leu
 50 55 60
 Arg His Leu Val Leu Val Val Asn Thr Leu Arg Arg Ile Gln Ala Ser
 65 70 75 80
 Met Ala Pro Ala Ala Ala Leu Pro Pro Val Pro Ser Pro Pro Ala Ala
 85 90 95
 Pro Ser Val Ala Asp Asn Leu Leu Ala Ser Ser Asp Ala Ala Leu Ser
 100 105 110
 Ala Ser Met Ala Ser Leu Leu Glu Asp Leu Ser His Ile Glu Gly Leu
 115 120 125
 Ser Gln Ala Pro Gln Pro Leu Ala Asp Glu Gly Pro Pro Gly Arg Ser
 130 135 140
 Ile Gly Gly Ala Ala Pro Ser Leu Gly Ala Leu Asp Leu Leu Gly Pro
 145 150 155 160
 Ala Thr Gly Cys Leu Leu Asp Asp Gly Leu Glu Gly Leu Phe Glu Asp
 165 170 175
 Ile Asp Thr Ser Met Tyr Asp Asn Glu Leu Trp Ala Pro Ala Ser Glu
 180 185 190
 Gly Leu Lys Pro Gly Pro Glu Asp Gly Pro Gly Lys Glu Glu Ala Pro
 195 200 205
 Glu Leu Asp Glu Ala Glu Leu Asp Tyr Leu Met Asp Val Leu Val Gly

[illegible][illegible][illegible][illegible][illegible]

130		135		140
Pro Thr Ile Cys His Tyr Phe Met Arg Leu Leu Lys Asp Lys Gly Leu				
145		150		155
Leu Leu Arg Cys Tyr Thr Gln Asn Ile Asp Thr Leu Glu Arg Ile Ala				160
	165		170	
Gly Leu Glu Gln Glu Asp Leu Val Glu Ala His Gly Thr Phe Tyr Thr				175
	180		185	
Ser His Cys Val Ser Ala Ser Cys Arg His Glu Tyr Pro Leu Ser Trp				190
	195		200	
Met Lys Glu Lys Ile Phe Ser Glu Val Thr Pro Lys Cys Glu Asp Cys				205
	210		215	
Gln Ser Leu Val Lys Pro Asp Ile Val Phe Phe Gly Glu Ser Leu Pro				220
225		230		235
Ala Arg Phe Phe Ser Cys Met Gln Ser Asp Phe Leu Lys Val Asp Leu				240
	245		250	
Leu Leu Val Met Gly Thr Ser Leu Gln Val Gln Pro Phe Ala Ser Leu				255
	260		265	
Ile Ser Lys Ala Pro Leu Ser Thr Pro Arg Leu Leu Ile Asn Lys Glu				270
	275		280	
Lys Ala Gly Gln Ser Asp Pro Phe Leu Gly Met Ile Met Gly Leu Gly				285
	290		295	
Gly Gly Met Asp Phe Asp Ser Lys Lys Ala Tyr Arg Asp Val Ala Trp				300
305		310		315
Leu Gly Glu Cys Asp Gln Gly Cys Leu Ala Leu Ala Glu Leu Leu Gly				320
	325		330	
Trp Lys Lys Glu Leu Glu Asp Leu Val Arg Arg Glu His Ala Ser Ile				335
	340		345	
Asp Ala Gln Ser Gly Ala Gly Val Pro Asn Pro Ser Thr Ser Ala Ser				350
	355		360	
Pro Lys Lys Ser Pro Pro Pro Ala Lys Asp Glu Ala Arg Thr Thr Glu				365
	370		375	
Arg Glu Lys Pro Gln				380
385				

<210> 415

<211> 481

<212> PRT

<213> Homo sapiens

<400> 415

Met Ser Leu Asn Leu Pro Glu Ala Ser Leu Leu Ser Arg Ala Ser Trp	
1	5
Pro Glu Gln Ala Lys Glu Pro Arg Arg Glu Gly His Thr Asp Lys Gln	10
	15
	20
Gln Thr Glu Asp Val Leu Ala Ala Gly Leu Arg Cys Leu Pro His Leu	25
	30
	35
Pro Ala Ile Cys Ala Arg Arg Met Ser Pro Ala Phe Arg Ala Met Asp	40
	45
	50
Val Glu Pro Arg Ala Lys Gly Val Leu Leu Glu Pro Phe Val His Gln	55
	60
65	70
Val Gly Gly His Ser Cys Val Leu Arg Phe Asn Glu Thr Thr Leu Cys	75
	80
	85
Lys Pro Leu Val Pro Arg Glu His Gln Phe Tyr Glu Thr Leu Pro Ala	90
	95
	100
Glu Met Arg Lys Phe Thr Pro Gln Tyr Lys Gly Val Val Ser Val Arg	105
	110
	115
Phe Glu Glu Asp Glu Asp Arg Asn Leu Cys Leu Ile Ala Tyr Pro Leu	120
	125
	130
	135
	140

Lys Gly Asp His Gly Ile Val Asp Ile Val Asp Asn Ser Asp Cys Glu
 145 150 155 160
 Pro Lys Ser Lys Leu Leu Arg Trp Thr Thr Asn Lys Lys His His Val
 165 170 175
 Leu Glu Thr Glu Lys Thr Pro Lys Asp Trp Val Arg Gln His Arg Lys
 180 185 190
 Glu Glu Lys Met Lys Ser His Lys Leu Glu Glu Glu Phe Glu Trp Leu
 195 200 205
 Lys Lys Ser Glu Val Leu Tyr Tyr Thr Val Glu Lys Lys Gly Asn Ile
 210 215 220
 Ser Ser Gln Leu Lys His Tyr Asn Pro Trp Ser Met Lys Cys His Gln
 225 230 235 240
 Gln Gln Leu Gln Arg Met Lys Glu Asn Ala Lys His Arg Asn Gln Tyr
 245 250 255
 Lys Phe Ile Leu Leu Glu Asn Leu Thr Ser Arg Tyr Glu Val Pro Cys
 260 265 270
 Val Leu Asp Leu Lys Met Gly Thr Arg Gln His Gly Asp Asp Ala Ser
 275 280 285
 Glu Glu Lys Ala Ala Asn Gln Ile Arg Lys Cys Gln Gln Ser Thr Ser
 290 295 300
 Ala Val Ile Gly Val Arg Val Cys Gly Met Gln Val Tyr Gln Ala Gly
 305 310 315 320
 Ser Gly Gln Leu Met Phe Met Asn Lys Tyr His Gly Arg Lys Leu Ser
 325 330 335
 Val Gln Gly Phe Lys Glu Ala Leu Phe Gln Phe Phe His Asn Gly Arg
 340 345 350
 Tyr Leu Arg Arg Glu Leu Leu Gly Pro Val Leu Lys Lys Leu Thr Glu
 355 360 365
 Leu Lys Ala Val Leu Glu Arg Gln Glu Ser Tyr Arg Phe Tyr Ser Ser
 370 375 380
 Ser Leu Leu Val Ile Tyr Asp Gly Lys Glu Arg Pro Glu Val Val Leu
 385 390 395 400
 Asp Ser Asp Ala Glu Asp Leu Glu Asp Leu Ser Glu Glu Ser Ala Asp
 405 410 415
 Glu Ser Ala Gly Ala Tyr Ala Tyr Lys Pro Ile Gly Ala Ser Ser Val
 420 425 430
 Asp Val Arg Met Ile Asp Phe Ala His Thr Thr Cys Arg Leu Tyr Gly
 435 440 445
 Glu Asp Thr Val Val His Glu Gly Gln Asp Ala Gly Tyr Ile Phe Gly
 450 455 460
 Leu Gln Ser Leu Ile Asp Ile Val Thr Glu Ile Ser Glu Glu Ser Gly
 465 470 475 480
 Glu

<210> 416
 <211> 354
 <212> PRT
 <213> Homo sapiens

<400> 416
 Met Ser Ala Gly Gly Gly Arg Ala Phe Ala Trp Gln Val Phe Pro Pro
 1 5 10 15
 Met Pro Thr Cys Arg Val Tyr Gly Thr Val Ala His Gln Asp Gly His
 20 25 30
 Leu Leu Val Leu Gly Gly Cys Gly Arg Ala Gly Leu Pro Leu Asp Thr
 35 40 45
 Ala Glu Thr Leu Asp Met Ala Ser His Thr Trp Leu Ala Leu Ala Pro
 50 55 60

Leu Pro Thr Ala Arg Ala Gly Ala Ala Ala Val Val Leu Gly Lys Gln
 65 70 75 80
 Val Leu Val Val Gly Gly Val Asp Glu Val Gln Ser Pro Val Ala Ala
 85 90 95
 Val Glu Ala Phe Leu Met Asp Glu Gly Arg Trp Glu Arg Arg Ala Thr
 100 105 110
 Leu Pro Gln Ala Ala Met Gly Val Ala Thr Val Glu Arg Asp Gly Met
 115 120 125
 Val Tyr Ala Leu Gly Gly Met Gly Pro Asp Thr Ala Pro Gln Ala Gln
 130 135 140
 Val Arg Val Tyr Glu Pro Arg Arg Asp Cys Trp Leu Ser Leu Pro Ser
 145 150 155 160
 Met Pro Thr Pro Cys Tyr Gly Ala Ser Thr Phe Leu His Gly Asn Lys
 165 170 175
 Ile Tyr Val Leu Gly Gly Arg Gln Gly Lys Leu Pro Val Thr Ala Phe
 180 185 190
 Glu Ala Phe Asp Leu Glu Ala Arg Thr Trp Thr Arg His Pro Ser Leu
 195 200 205
 Pro Ser Arg Arg Ala Phe Ala Gly Cys Ala Met Ala Glu Gly Ser Val
 210 215 220
 Phe Ser Leu Gly Gly Leu Gln Gln Pro Gly Pro His Asn Phe Tyr Ser
 225 230 235 240
 Arg Pro His Phe Val Asn Thr Val Glu Met Phe Asp Leu Glu His Gly
 245 250 255
 Ser Trp Thr Lys Leu Pro Arg Ser Leu Arg Met Arg Asp Lys Arg Ala
 260 265 270
 Asp Phe Val Val Gly Ser Leu Gly Gly His Ile Val Ala Ile Gly Gly
 275 280 285
 Leu Gly Asn Gln Pro Cys Pro Leu Gly Ser Val Glu Ser Phe Ser Leu
 290 295 300
 Ala Arg Arg Arg Trp Glu Ala Leu Pro Ala Met Pro Thr Ala Arg Cys
 305 310 315 320
 Ser Cys Ser Ser Leu Gln Ala Gly Pro Arg Leu Phe Val Ile Gly Gly
 325 330 335
 Val Ala Gln Gly Pro Ser Gln Ala Val Glu Ala Leu Cys Leu Arg Asp
 340 345 350
 Gly Val

<210> 417

<211> 20

<212> PRT

<213> Homo sapiens

<400> 417

Met Lys Gly Leu Tyr Phe Gln Gln Ser Ser Thr Asp Glu Glu Ile Thr
 1 5 10 15

Phe Val Phe Gln
 20

<210> 418

<211> 320

<212> PRT

<213> Homo sapiens

<400> 418

Met Lys Gly Leu Tyr Phe Gln Gln Ser Ser Thr Asp Glu Glu Ile Thr
 1 5 10 15

Phe Val Phe Gln Glu Lys Glu Asp Leu Pro Val Thr Glu Asp Asn Phe

Val	Lys	Leu	Gln	Val	Lys	Ala	Cys	Ala	Leu	Ser	Gln	Ile	Asn	Thr	Lys
		35					40					45			
Leu	Leu	Ala	Glu	Met	Lys	Met	Lys	Lys	Asp	Leu	Phe	Pro	Val	Gly	Arg
		50				55					60				
Glu	Ile	Ala	Gly	Ile	Val	Leu	Asp	Val	Gly	Ser	Lys	Val	Ser	Phe	Phe
65				70					75						80
Gln	Pro	Asp	Asp	Glu	Val	Val	Gly	Ile	Leu	Pro	Leu	Asp	Ser	Glu	Asp
			85					90						95	
Pro	Gly	Leu	Cys	Glu	Val	Val	Arg	Val	His	Glu	His	Tyr	Leu	Val	His
			100					105					110		
Lys	Pro	Glu	Lys	Val	Thr	Trp	Thr	Glu	Ala	Ala	Gly	Ser	Ile	Arg	Asp
		115					120					125			
Gly	Val	Arg	Ala	Tyr	Thr	Ala	Leu	His	Tyr	Leu	Ser	His	Leu	Ser	Pro
		130				135					140				
Gly	Lys	Ser	Val	Leu	Ile	Met	Asp	Gly	Ala	Ser	Ala	Phe	Gly	Thr	Ile
145				150					155						160
Ala	Ile	Gln	Leu	Ala	His	His	Arg	Gly	Ala	Lys	Val	Ile	Ser	Thr	Ala
				165				170						175	
Cys	Ser	Leu	Glu	Asp	Lys	Gln	Cys	Leu	Glu	Arg	Phe	Arg	Pro	Pro	Ile
			180				185						190		
Ala	Arg	Val	Ile	Asp	Val	Ser	Asn	Gly	Lys	Val	His	Val	Ala	Glu	Ser
		195					200					205			
Cys	Leu	Glu	Glu	Thr	Gly	Gly	Leu	Gly	Val	Asp	Ile	Val	Leu	Asp	Ala
		210				215					220				
Gly	Val	Arg	Leu	Tyr	Ser	Lys	Asp	Asp	Glu	Pro	Ala	Val	Lys	Leu	Gln
225				230					235						240
Leu	Leu	Pro	His	Lys	His	Asp	Ile	Ile	Thr	Leu	Leu	Gly	Val	Gly	Gly
			245					250						255	
His	Trp	Val	Thr	Thr	Glu	Glu	Asn	Leu	Gln	Leu	Asp	Pro	Pro	Asp	Ser
			260				265						270		
His	Cys	Leu	Phe	Leu	Lys	Gly	Ala	Thr	Leu	Ala	Phe	Leu	Asn	Asp	Glu
		275					280					285			
Val	Trp	Asn	Leu	Ser	Asn	Val	Gln	Gln	Gly	Lys	Tyr	Leu	Tyr	Leu	Lys
		290			295						300				
Gly	Cys	Asp	Gly	Glu	Val	Ile	Asn	Trp	Cys	Phe	Gln	Thr	Ser	Val	Gly
305				310					315						320

<210> 419

<211> 159

<212> PRT

<213> Homo sapiens

<400> 419

Met	Glu	Lys	Leu	Arg	Arg	Val	Leu	Ser	Gly	Gln	Asp	Asp	Glu	Glu	Gln
1			5						10				15		
Gly	Leu	Thr	Ala	Gln	Val	Leu	Asp	Ala	Ser	Ser	Leu	Ser	Phe	Asn	Thr
		20						25					30		
Arg	Leu	Lys	Trp	Phe	Ala	Ile	Cys	Phe	Val	Cys	Gly	Val	Phe	Phe	Ser
		35				40					45				
Ile	Leu	Gly	Thr	Gly	Leu	Leu	Trp	Leu	Pro	Gly	Gly	Ile	Lys	Leu	Phe
	50				55					60					
Ala	Val	Phe	Tyr	Thr	Leu	Gly	Asn	Leu	Ala	Ala	Leu	Ala	Ser	Thr	Cys
65				70					75						80
Phe	Leu	Met	Gly	Pro	Val	Lys	Gln	Leu	Lys	Lys	Met	Phe	Glu	Ala	Thr
			85					90					95		
Arg	Leu	Leu	Ala	Thr	Ile	Val	Met	Leu	Leu	Cys	Phe	Ile	Phe	Thr	Leu
		100						105					110		

Cys Ala Ala Leu Trp Trp His Lys Lys Gly Leu Ala Val Leu Phe Cys
 115 120 125
 Ile Leu Gln Phe Leu Ser Met Thr Trp Tyr Ser Leu Ser Tyr Ile Pro
 130 135 140
 Tyr Ala Arg Asp Ala Val Ile Lys Cys Cys Ser Ser Leu Leu Ser
 145 150 155

<210> 420
 <211> 183
 <212> PRT
 <213> Homo sapiens

<400> 420
 Met Glu Gln Arg Leu Ala Glu Phe Arg Ala Ala Arg Lys Arg Ala Gly
 1 5 10 15
 Leu Ala Ala Gln Pro Pro Ala Ala Ser Gln Gly Ala Gln Thr Pro Gly
 20 25 30
 Glu Lys Ala Glu Ala Ala Ala Thr Leu Lys Ala Ala Pro Gly Trp Leu
 35 40 45
 Lys Arg Phe Leu Val Trp Lys Pro Arg Pro Ala Ser Ala Arg Ala Gln
 50 55 60
 Pro Gly Leu Val Gln Glu Ala Ala Gln Pro Gln Gly Ser Thr Ser Glu
 65 70 75 80
 Thr Pro Trp Asn Thr Ala Ile Pro Leu Pro Ser Cys Trp Asp Gln Ser
 85 90 95
 Phe Leu Thr Asn Ile Thr Phe Leu Lys Val Leu Leu Trp Leu Val Leu
 100 105 110
 Leu Gly Leu Phe Val Glu Leu Glu Phe Gly Leu Ala Tyr Phe Val Leu
 115 120 125
 Ser Leu Phe Tyr Trp Met Tyr Val Gly Thr Arg Gly Pro Glu Glu Lys
 130 135 140
 Lys Glu Gly Glu Lys Ser Ala Tyr Ser Val Phe Asn Pro Gly Cys Glu
 145 150 155 160
 Ala Ile Gln Gly Thr Leu Thr Ala Glu Gln Leu Glu Arg Glu Leu Gln
 165 170 175
 Leu Arg Pro Leu Ala Gly Arg
 180

<210> 421
 <211> 143
 <212> PRT
 <213> Homo sapiens

<400> 421
 Met Ala Ala Pro Arg Arg Gly Arg Gly Ser Ser Thr Val Leu Ser Ser
 1 5 10 15
 Val Pro Leu Gln Met Leu Phe Tyr Leu Ser Gly Thr Tyr Tyr Ala Leu
 20 25 30
 Tyr Phe Leu Ala Thr Leu Leu Met Ile Thr Tyr Lys Ser Gln Val Phe
 35 40 45
 Ser Tyr Pro His Arg Tyr Leu Val Leu Asp Leu Ala Leu Leu Phe Leu
 50 55 60
 Met Gly Ile Leu Glu Ala Val Arg Leu Tyr Leu Gly Thr Arg Gly Asn
 65 70 75 80
 Leu Thr Glu Ala Glu Arg Pro Leu Ala Ala Ser Leu Ala Leu Thr Ala
 85 90 95
 Gly Thr Ala Leu Leu Ser Ala His Phe Leu Leu Trp Gln Ala Leu Val
 100 105 110

Leu Trp Ala Asp Trp Ala Leu Ser Ala Thr Leu Leu Ala Leu His Gly
115 120 125
Leu Glu Ala Val Leu Gln Val Val Ala Ile Ala Ala Phe Thr Arg
130 135 140

<210> 422
<211> 73
<212> PRT
<213> Homo sapiens

<400> 422
Met Ser Gly Val Pro Ala Glu Met Thr Gly Ala Val Glu Ala Phe Leu
1 5 10 15
Pro Val Val Ser Ser Arg Arg Leu Pro Arg Phe Val His Met Val
20 25 30
Ala Gly Val Ser Ser Lys Gln Glu Arg Ala Arg Ser Asn Thr Glu Ala
35 40 45
Leu Phe Lys Leu Cys Phe His His Ile Cys Gln Cys Leu Thr Asp Glu
50 55 60
His Lys Phe His Gly Gln Val Gln Phe
65 70

<210> 423
<211> 142
<212> PRT
<213> Homo sapiens

<400> 423
Met Pro Pro Phe Gly Gly His Pro Leu Ser Gln Glu Glu Asp Gly Ser
1 5 10 15
Gln Arg Cys Cys Cys Leu Ser Ser Leu Arg Ser Val Asp Asp Ser Asn
20 25 30
Gly Glu Thr Val Val Ile Met Ala Leu Phe Leu Ala Val Ser Tyr His
35 40 45
His Lys Thr Gln Ser Lys Arg Trp Pro Gly Leu Thr Pro Pro His Ser
50 55 60
Ser Leu Leu Cys Arg Pro Leu Gln Leu Ser Phe Leu Val Ile Gln Ser
65 70 75 80
Val Arg Met Arg Ala Cys Gly Cys Asp Ser Gly His Cys Arg Ile Leu
85 90 95
Gly Arg Tyr Ser Leu Leu Gly Trp Ser Gln Gly His Arg Ala Arg Gly
100 105 110
Arg Gly Gly Val Ser Leu Arg Asp Asn Thr Phe Phe Gln Glu Ala Ser
115 120 125
Glu Gly Gln Gly Gln Trp Leu Met Pro Val Ile Pro Ala Phe
130 135 140

<210> 424
<211> 149
<212> PRT
<213> Homo sapiens

<400> 424
Met Leu Ser Ile Leu Lys Pro Arg Arg Ser Gln Glu Trp Arg Thr Ala
1 5 10 15
Leu Arg Arg Tyr Cys Cys Pro Thr Asp Leu Gln Ala Pro Arg Ser Pro
20 25 30
Val Pro Pro Ile Arg Lys Val Gly Ile Ser Asp Val Ile Val His Ala

$\frac{1}{\sqrt{2}} \begin{pmatrix} 1 & i \\ 0 & 1 \end{pmatrix}$

[illegible][illegible][illegible][illegible][illegible]

$\frac{1}{\sqrt{2}} \begin{pmatrix} 1 & i \\ 0 & 1 \end{pmatrix}$

Leu Ile Arg His Leu Arg Thr Phe Ser Ala Ala Ala Ala Leu Ala Pro
 20 25 30
 Arg Tyr Pro Thr Arg Leu Pro Ser Ser Leu Leu Leu Trp His Leu Cys
 35 40 45
 Gln Cys Leu His Leu Leu Tyr Ala Val Ser Thr Ser Cys Asn Ser His
 50 55 60
 Gly Lys Arg Ser Ala Ala Trp Ala Met Thr Arg Thr Glu Asp Thr Asp
 65 70 75 80
 Ala Leu Thr Asp Ser Phe Asp Asp Ser Phe Ile Ser Ser Ala Asp
 85 90 95

<210> 430
 <211> 99
 <212> PRT
 <213> Homo sapiens

<400> 430
 Met Lys Lys Lys Glu Glu Thr Thr Leu Ser Glu Met Glu Pro Val Glu
 1 5 10 15
 Pro Gln Tyr Gln Leu Val Asn Ala Glu Ser Thr Ser Pro Phe Leu His
 20 25 30
 Cys Leu Arg Glu Val Ile Gly Glu Tyr Ser Val His Glu Phe Ser Leu
 35 40 45
 Leu Gly Lys Thr Glu Ser Gln Gly Ile Gly Leu Trp Ile Ala Leu Val
 50 55 60
 Val Phe Leu Ser Phe Leu Ile Phe Ser Thr Ser Phe Tyr Ile Ser Asn
 65 70 75 80
 Ala Glu Gln Pro Phe Phe Lys Glu Pro Pro Thr Glu Ala Ala Lys Glu
 85 90 95
 Leu Ser Leu

<210> 431
 <211> 122
 <212> PRT
 <213> Homo sapiens

<400> 431
 Ile Arg Ala Thr Met Val Ala Arg Val Trp Ser Leu Met Arg Phe Leu
 1 5 10 15
 Ile Lys Gly Ser Val Ala Gly Gly Ala Val Tyr Leu Val Tyr Asp Gln
 20 25 30
 Glu Leu Leu Gly Pro Ser Asp Lys Ser Gln Ala Ala Leu Gln Lys Ala
 35 40 45
 Gly Glu Val Val Pro Pro Ala Met Tyr Gln Phe Ser Gln Tyr Val Cys
 50 55 60
 Gln Gln Thr Gly Leu Gln Ile Pro Gln Leu Pro Ala Pro Pro Lys Ile
 65 70 75 80
 Tyr Phe Pro Ile Arg Asp Ser Trp Asn Ala Gly Ile Met Thr Val Met
 85 90 95
 Ser Ala Leu Ser Val Ala Pro Ser Lys Ala Arg Glu Tyr Ser Lys Glu
 100 105 110
 Gly Trp Glu Tyr Val Lys Ala Arg Thr Lys
 115 120

<210> 432
 <211> 118
 <212> PRT
 <213> Homo sapiens

<400> 432

Met Gln Pro Ser Leu Leu Arg Ser Tyr Arg Leu Lys Ala Gln Leu Ser
1 5 10 15
Leu Ser Ser Thr Val Pro Arg Arg Ile Thr Asp Lys Pro Ala Thr Lys
20 25 30
Ser Trp Glu Gly Gly Arg Arg Glu Leu Cys Pro Arg Val Leu Phe Thr
35 40 45
Gln Leu Leu Leu Trp Val Trp Pro Gly Asp Pro Gly Pro Glu Leu Gln
50 55 60
Glu Thr Gly Phe Pro Gly Pro Pro Arg Pro Ala His Leu Lys Thr Asp
65 70 75 80
Arg Ala Ile Met Val Gly Val Lys Gly Ile Glu Glu Lys Ser Gly Ile
85 90 95
Gly Ala Gly Val Cys Arg Val Ser Val Glu Lys Leu Ala Ser Thr Gln
100 105 110
Glu Arg Thr Ser Ser Leu
115

<210> 433

<211> 49

<212> PRT

<213> Homo sapiens

<400> 433

Met Glu Leu Glu Ala Met Ser Arg Tyr Thr Ser Pro Val Asn Pro Pro
1 5 10 15
Val Phe Pro His Leu Thr Val Val Leu Ala Ile Gly Met Phe Phe
20 25 30
Thr Ala Trp Phe Phe Val Tyr Pro Phe Thr Glu Gln Pro Glu Asp Gln
35 40 45
His

<210> 434

<211> 89

<212> PRT

<213> Homo sapiens

<400> 434

Met Leu Ala Leu Phe His Phe His Leu Pro Pro Trp Asp Asp Ala Val
1 5 10 15
Arg Arg Pro Ser Val Asp Ala Ser Pro Ser Thr Leu Asn Phe Pro Asp
20 25 30
Ala Glu Leu Tyr Ala Ser Ile Phe Leu Cys Cys Met Ala Pro Gly Glu
35 40 45
Ile Leu Ile Ser Phe Leu Thr Leu Val Gln Ile Ala His Ala Asn Gly
50 55 60
Arg Gly Cys Asn Thr Pro Ala Cys Gly Ala Ala Ala Cys Val Trp His
65 70 75 80
Glu Asn Ser Gln Glu Glu Arg Lys Tyr
85

<210> 435

<211> 87

<212> PRT

<213> Homo sapiens

<400> 435

Met Ser Gln Gln His Arg Arg Lys Arg Pro Ser Ser Glu Arg Lys Ser
 1 5 10 15
 Thr Arg Lys Met Asp Thr Trp Gln Ser Leu Lys Val Lys Glu Val Phe
 20 25 30
 Cys Lys His Asn Ser Ser Tyr Glu Cys Leu Leu Tyr Lys Glu Val Glu
 35 40 45
 Ala Arg Gln Val Ser Lys Thr Ala Thr Asp Gly Ser Tyr Leu Leu Val
 50 55 60
 Phe Thr Ser Tyr Val Ile Ser Ser Pro Val Trp Thr Gly Pro Gly Asp
 65 70 75 80
 Leu Leu Pro Val Asn Arg Ile
 85

<210> 436
 <211> 45
 <212> PRT
 <213> Homo sapiens

<400> 436
 Met Pro Arg Ser Ser Arg Ser Pro Gly Asp Pro Gly Ala Leu Leu Glu
 1 5 10 15
 Asp Gly Pro Gln Ser Gln Thr Pro Glu Asp Cys Pro Ala Arg Pro Glu
 20 25 30
 His Gln Gln Asp Gly Arg Gly His Leu Pro Lys His Glu
 35 40 45

<210> 437
 <211> 65
 <212> PRT
 <213> Homo sapiens

<400> 437
 Met Ala Tyr Leu Asp Asp Lys Gly Ser Leu Leu Ala Ile His Ser His
 1 5 10 15
 Ala Arg Gln His Ser His Glu Thr Asn Gln Val His Gln Trp Leu Pro
 20 25 30
 Arg Asn Thr Phe Ala Phe Leu Ile Lys Glu Asp Arg Cys Ser Cys Arg
 35 40 45
 Ser Thr Cys Ala Ser Phe Ser Phe Ser Ser Ser Phe Ser Phe Leu Ile
 50 55 60
 Ser
 65

<210> 438
 <211> 112
 <212> PRT
 <213> Homo sapiens

<400> 438
 Met Arg Lys Lys Cys Lys Cys Phe Thr Ile Lys Lys Thr Asn Thr Tyr
 1 5 10 15
 Glu Glu Ser Asn Ala Gly Asn Glu Gly Gln Lys Glu Ala Ile Ser Ile
 20 25 30
 Cys Ile Cys Arg Arg Asp Gly Leu Leu Pro Leu Trp Val Thr Arg Leu
 35 40 45
 Ser Asp Leu Val Phe Ser Lys Glu Lys Ala His Gly Met Ile Pro Leu
 50 55 60
 Leu Gly Ser His Arg Glu Lys Lys Thr Ser Lys Glu Met Lys Thr Ser

65					70					75					80
Ser	Arg	Asn	Leu	Arg	Tyr	Phe	Ile	Val	Cys	Arg	Asp	Ala	Ser	Ser	Tyr
				85					90					95	
Thr	Pro	Gln	Ser	Leu	Ile	Ser	Gly	Tyr	Ile	Gly	Pro	Cys	Gln	His	Gln
			100					105					110		

<210> 439
 <211> 110
 <212> PRT
 <213> Homo sapiens

<400> 439	Met	Val	Phe	Gly	Ala	Met	Val	Leu	Leu	Val	Gly	Leu	Glu	Glu	Leu	Thr
1				5						10					15	
	Asn	Ile	Arg	Asn	Val	Glu	Arg	Leu	Lys	Lys	Asp	Leu	Arg	Ala	Ser	Tyr
				20					25					30		
	Cys	Leu	Ile	Asp	Ser	Phe	Leu	Gly	Asp	Ser	Glu	Leu	Ile	Gly	Asp	Leu
			35					40					45			
	Thr	Gln	Cys	Val	Asp	Cys	Val	Ile	Pro	Pro	Glu	Gly	Ser	Leu	Leu	Gln
			50				55					60				
	Ile	Ser	Ser	Tyr	Leu	Tyr	Leu	Asn	Thr	Ala	Leu	Val	Asp	Leu	Pro	Gly
65					70					75					80	
	Val	Ala	Ala	Ser	Gln	Ala	Cys	Asp	Ser	Gln	Gln	Val	Thr	Trp	Leu	Leu
				85						90					95	
	Tyr	Val	Ala	Asn	Gly	Ala	Tyr	Ser	Ala	Cys	Asn	Arg	Pro	Gly		
				100					105					110		

<210> 440
 <211> 121
 <212> PRT
 <213> Homo sapiens

<400> 440	Thr	Ser	Ser	Ser	Gly	Ala	Glu	Val	Thr	Met	Ala	Ala	Ala	Leu	Ala	Arg
1					5					10					15	
	Leu	Gly	Leu	Arg	Pro	Val	Lys	Gln	Val	Arg	Val	Gln	Phe	Cys	Pro	Phe
				20					25					30		
	Glu	Lys	Asn	Val	Glu	Ser	Thr	Arg	Thr	Phe	Leu	Gln	Thr	Val	Ser	Ser
			35					40					45			
	Glu	Lys	Val	Arg	Ser	Thr	Asn	Leu	Asn	Cys	Ser	Val	Ile	Ala	Asp	Val
			50				55					60				
	Arg	His	Asp	Gly	Ser	Glu	Pro	Cys	Val	Asp	Val	Leu	Phe	Gly	Asp	Gly
65					70					75					80	
	His	Arg	Leu	Ile	Met	Arg	Gly	Ala	His	Leu	Thr	Ala	Leu	Glu	Met	Leu
				85						90					95	
	Thr	Ala	Phe	Ala	Ser	His	Ile	Arg	Ala	Arg	Asp	Ala	Ala	Gly	Ser	Gly
				100					105					110		
	Asp	Lys	Pro	Gly	Ala	Asp	Thr	Gly	Arg							
				115					120							

<210> 441
 <211> 99
 <212> PRT
 <213> Homo sapiens

<400> 441	Met	Leu	Ala	Arg	Ala	Thr	Phe	Arg	Ala	Ala	Ser	Ala	Pro	Thr	Leu	Val
1				5						10					15	

Ala Arg Arg Gly Phe Gln Ser Thr Arg Ala Gln Met Ala Ser Pro Tyr
20 25 30
His Tyr Pro Glu Gly Pro Arg Ser Asn Leu Pro Phe Asp Pro Leu Lys
35 40 45
Lys Gly Phe Ala Phe Lys Tyr Trp Gly Phe Met Gly Thr Gly Phe Ala
50 55 60
Leu Pro Phe Leu Leu Ala Val Trp Gln Thr Glu Gln Ala Val Asn Ala
65 70 75 80
Leu Arg His Gly Val Asp Met Arg Ile Gly Ile Pro Gly Asn Thr Ala
85 90 95
Phe Val Asp

<210> 442

<211> 183

<212> PRT

<213> Homo sapiens

<400> 442

Arg Glu Gly Ala Arg Ala Arg Pro Ser Pro Thr Met Ser Asp Glu Ala
1 5 10 15
Ser Ala Ile Thr Ser Tyr Glu Lys Phe Leu Thr Pro Glu Glu Pro Phe
20 25 30
Pro Leu Leu Gly Pro Pro Arg Gly Val Gly Thr Cys Pro Ser Glu Glu
35 40 45
Pro Gly Cys Leu Asp Ile Ser Asp Phe Gly Cys Gln Leu Ser Ser Cys
50 55 60
His Arg Thr Asp Pro Leu His Arg Phe His Thr Asn Arg Trp Asn Leu
65 70 75 80
Thr Ser Cys Gly Thr Ser Val Ala Ser Ser Glu Gly Ser Glu Glu Leu
85 90 95
Phe Ser Ser Val Ser Val Gly Asp Gln Asp Asp Cys Tyr Ser Leu Leu
100 105 110
Asp Asp Gln Asp Phe Thr Ser Phe Asp Leu Phe Pro Glu Gly Ser Val
115 120 125
Cys Ser Asp Val Ser Ser Ser Ile Ser Thr Tyr Trp Asp Trp Ser Asp
130 135 140
Ser Glu Phe Glu Trp Gln Leu Pro Gly Ser Asp Ile Ala Ser Gly Ser
145 150 155 160
Asp Val Leu Ser Asp Val Ile Pro Ser Ile Pro Ser Ser Pro Cys Leu
165 170 175
Leu Pro Lys Lys Lys Lys Lys
180

<210> 443

<211> 94

<212> PRT

<213> Homo sapiens

<400> 443

Met Ser Asp Glu Ala Ser Ala Ile Thr Ser Tyr Glu Lys Phe Leu Thr
1 5 10 15
Pro Glu Glu Pro Phe Pro Leu Leu Gly Pro Pro Arg Gly Val Gly Thr
20 25 30
Cys Pro Ser Glu Glu Pro Gly Cys Leu Asp Ile Ser Asp Phe Gly Cys
35 40 45
Gln Leu Ser Ser Cys His Arg Thr Asp Pro Leu His Arg Phe His Thr
50 55 60
Asn Arg Trp Asn Leu Thr Ser Cys Gly Thr Ser Val Ala Ser Ser Glu

Figure 1. The effect of the number of trials on the number of correct responses. The number of correct responses was significantly higher for the 10-trial condition than for the 5-trial condition ($p < 0.05$).

Figure 1. The effect of the concentration of the *Agaricus bisporus* spores on the growth of *Agaricus bisporus* on the substrate. The concentration of the spores was 10⁴, 10⁵, 10⁶, 10⁷, 10⁸, 10⁹, 10¹⁰, 10¹¹, 10¹², 10¹³, 10¹⁴, 10¹⁵, 10¹⁶, 10¹⁷, 10¹⁸, 10¹⁹, 10²⁰, 10²¹, 10²², 10²³, 10²⁴, 10²⁵, 10²⁶, 10²⁷, 10²⁸, 10²⁹, 10³⁰, 10³¹, 10³², 10³³, 10³⁴, 10³⁵, 10³⁶, 10³⁷, 10³⁸, 10³⁹, 10⁴⁰, 10⁴¹, 10⁴², 10⁴³, 10⁴⁴, 10⁴⁵, 10⁴⁶, 10⁴⁷, 10⁴⁸, 10⁴⁹, 10⁵⁰, 10⁵¹, 10⁵², 10⁵³, 10⁵⁴, 10⁵⁵, 10⁵⁶, 10⁵⁷, 10⁵⁸, 10⁵⁹, 10⁶⁰, 10⁶¹, 10⁶², 10⁶³, 10⁶⁴, 10⁶⁵, 10⁶⁶, 10⁶⁷, 10⁶⁸, 10⁶⁹, 10⁷⁰, 10⁷¹, 10⁷², 10⁷³, 10⁷⁴, 10⁷⁵, 10⁷⁶, 10⁷⁷, 10⁷⁸, 10⁷⁹, 10⁸⁰, 10⁸¹, 10⁸², 10⁸³, 10⁸⁴, 10⁸⁵, 10⁸⁶, 10⁸⁷, 10⁸⁸, 10⁸⁹, 10⁹⁰, 10⁹¹, 10⁹², 10⁹³, 10⁹⁴, 10⁹⁵, 10⁹⁶, 10⁹⁷, 10⁹⁸, 10⁹⁹, 10¹⁰⁰, 10¹⁰¹, 10¹⁰², 10¹⁰³, 10¹⁰⁴, 10¹⁰⁵, 10¹⁰⁶, 10¹⁰⁷, 10¹⁰⁸, 10¹⁰⁹, 10¹¹⁰, 10¹¹¹, 10¹¹², 10¹¹³, 10¹¹⁴, 10¹¹⁵, 10¹¹⁶, 10¹¹⁷, 10¹¹⁸, 10¹¹⁹, 10¹²⁰, 10¹²¹, 10¹²², 10¹²³, 10¹²⁴, 10¹²⁵, 10¹²⁶, 10¹²⁷, 10¹²⁸, 10¹²⁹, 10¹³⁰, 10¹³¹, 10¹³², 10¹³³, 10¹³⁴, 10¹³⁵, 10¹³⁶, 10¹³⁷, 10¹³⁸, 10¹³⁹, 10¹⁴⁰, 10¹⁴¹, 10¹⁴², 10¹⁴³, 10¹⁴⁴, 10¹⁴⁵, 10¹⁴⁶, 10¹⁴⁷, 10¹⁴⁸, 10¹⁴⁹, 10¹⁵⁰, 10¹⁵¹, 10¹⁵², 10¹⁵³, 10¹⁵⁴, 10¹⁵⁵, 10¹⁵⁶, 10¹⁵⁷, 10¹⁵⁸, 10¹⁵⁹, 10¹⁶⁰, 10¹⁶¹, 10¹⁶², 10¹⁶³, 10¹⁶⁴, 10¹⁶⁵, 10¹⁶⁶, 10¹⁶⁷, 10¹⁶⁸, 10¹⁶⁹, 10¹⁷⁰, 10¹⁷¹, 10¹⁷², 10¹⁷³, 10¹⁷⁴, 10¹⁷⁵, 10¹⁷⁶, 10¹⁷⁷, 10¹⁷⁸, 10¹⁷⁹, 10¹⁸⁰, 10¹⁸¹, 10¹⁸², 10¹⁸³, 10¹⁸⁴, 10¹⁸⁵, 10¹⁸⁶, 10¹⁸⁷, 10¹⁸⁸, 10¹⁸⁹, 10¹⁹⁰, 10¹⁹¹, 10¹⁹², 10¹⁹³, 10¹⁹⁴, 10¹⁹⁵, 10¹⁹⁶, 10¹⁹⁷, 10¹⁹⁸, 10¹⁹⁹, 10²⁰⁰, 10²⁰¹, 10²⁰², 10²⁰³, 10²⁰⁴, 10²⁰⁵, 10²⁰⁶, 10²⁰⁷, 10²⁰⁸, 10²⁰⁹, 10²¹⁰, 10²¹¹, 10²¹², 10²¹³, 10²¹⁴, 10²¹⁵, 10²¹⁶, 10²¹⁷, 10²¹⁸, 10²¹⁹, 10²²⁰, 10²²¹, 10²²², 10²²³, 10²²⁴, 10²²⁵, 10²²⁶, 10²²⁷, 10²²⁸, 10²²⁹, 10²³⁰, 10²³¹, 10²³², 10²³³, 10²³⁴, 10²³⁵, 10²³⁶, 10²³⁷, 10²³⁸, 10²³⁹, 10²⁴⁰, 10²⁴¹, 10²⁴², 10²⁴³, 10²⁴⁴, 10²⁴⁵, 10²⁴⁶, 10²⁴⁷, 10²⁴⁸, 10²⁴⁹, 10²⁵⁰, 10²⁵¹, 10²⁵², 10²⁵³, 10²⁵⁴, 10²⁵⁵, 10²⁵⁶, 10²⁵⁷, 10²⁵⁸, 10²⁵⁹, 10²⁶⁰, 10²⁶¹, 10²⁶², 10²⁶³, 10²⁶⁴, 10²⁶⁵, 10²⁶⁶, 10²⁶⁷, 10²⁶⁸, 10²⁶⁹, 10²⁷⁰, 10²⁷¹, 10²⁷², 10²⁷³, 10²⁷⁴, 10²⁷⁵, 10²⁷⁶, 10²⁷⁷, 10²⁷⁸, 10²⁷⁹, 10²⁸⁰, 10²⁸¹, 10²⁸², 10²⁸³, 10²⁸⁴, 10²⁸⁵, 10²⁸⁶, 10²⁸⁷, 10²⁸⁸, 10²⁸⁹, 10²⁹⁰, 10²⁹¹, 10²⁹², 10²⁹³, 10²⁹⁴, 10²⁹⁵, 10²⁹⁶, 10²⁹⁷, 10²⁹⁸, 10²⁹⁹, 10³⁰⁰, 10³⁰¹, 10³⁰², 10³⁰³, 10³⁰⁴, 10³⁰⁵, 10³⁰⁶, 10³⁰⁷, 10³⁰⁸, 10³⁰⁹, 10³¹⁰, 10³¹¹, 10³¹², 10³¹³, 10³¹⁴, 10³¹⁵, 10³¹⁶, 10³¹⁷, 10³¹⁸, 10³¹⁹, 10³²⁰, 10³²¹, 10³²², 10³²³, 10³²⁴, 10³²⁵, 10³²⁶, 10³²⁷, 10³²⁸, 10³²⁹, 10³³⁰, 10³³¹, 10³³², 10³³³, 10³³⁴, 10³³⁵, 10³³⁶, 10³³⁷, 10³³⁸, 10³³⁹, 10³⁴⁰, 10³⁴¹, 10³⁴², 10³⁴³, 10³⁴⁴, 10³⁴⁵, 10³⁴⁶, 10³⁴⁷, 10³⁴⁸, 10<

Figure 1. The effect of the number of trials on the number of correct responses. The number of correct responses was significantly higher for the 10-trial condition than for the 5-trial condition ($p < 0.05$).

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<400> 446

```
Met Glu Asp Lys Glu Ile Pro Ile Lys Ser Glu Pro Leu Pro Lys Pro
1      5      10      15
Pro Ala Ser Ala Pro Pro Ser Ile Leu Val Lys Pro Glu Asn Ser Arg
20     25     30
Asn Gly Ile Glu Lys Gln Val Lys Thr Val Arg Phe Gln Asn Tyr Ser
35     40     45
Pro Pro Pro Thr Lys His Tyr Thr Ser His Pro Thr Ser Gly Lys Pro
50     55     60
Glu Gln Pro Ala Thr Leu Lys Ala Ser Gln Pro Glu Ala Ala Ser Leu
65     70     75     80
Gly Pro Glu Met Thr Val Leu Phe Ala His Arg Ser Gly Cys His Ser
85     90     95
Gly Gln Gln Thr Asp Leu Arg Arg Lys Ser Ala Leu Ala Lys Ala Thr
100    105    110
Thr Leu Val Ser Thr Ala Ser Gly Thr Gln Thr Val Phe Pro Ser Lys
115    120    125
```

<210> 447

<211> 96

<212> PRT

<213> Homo sapiens

<400> 447

```
Met Leu Thr Arg Val Glu Glu Gln Lys Lys Met Val Lys Ala Cys Arg
1      5      10      15
Tyr Arg Cys Ser Ala Cys His Leu Lys Tyr Ser Pro Gln Arg Gln Lys
20     25     30
Glu Arg Lys Leu Ser Leu Lys Arg Gly Arg Thr Ser Gln Gln Asn Met
35     40     45
Ser Met Phe Trp Leu Lys Lys Leu Leu Glu Ser Gly Leu Phe Cys Ala
50     55     60
Met Cys Ser Pro Arg Ala Ser Thr Lys Lys Gly Phe Trp Cys Arg Pro
65     70     75     80
Lys Thr Thr Ile Ile Ile Asp Tyr Ser Ser Pro Arg Gln Cys Leu
85     90     95
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<210> 448

<211> 160

<212> PRT

<213> Homo sapiens

<220>

<221> UNSURE

<222> 114

<223> Xaa = Glu,Val

<220>

<221> UNSURE

<222> 113

<223> Xaa = His,Gln

<220>

<221> UNSURE

<222> 115

<223> Xaa = Ile,Val

<400> 448

Met Gly Lys Ile Ala Leu Gln Leu Lys Ala Thr Leu Glu Asn Ile Thr
1 5 10 15
Asn Leu Arg Pro Val Gly Glu Asp Phe Arg Trp Tyr Leu Lys Met Lys
20 25 30
Cys Gly Asn Cys Gly Glu Ile Ser Asp Lys Trp Gln Tyr Ile Arg Leu
35 40 45
Met Asp Ser Val Ala Leu Lys Gly Gly Arg Gly Ser Ala Ser Met Val
50 55 60
Gln Lys Cys Lys Leu Cys Ala Arg Glu Asn Ser Ile Glu Ile Leu Ser
65 70 75 80
Ser Thr Ile Lys Pro Tyr Asn Ala Glu Asp Asn Glu Asn Phe Lys Thr
85 90 95
Ile Val Glu Phe Glu Cys Arg Gly Leu Glu Pro Val Asp Phe Gln Pro
100 105 110
Xaa Xaa Xaa Leu Leu Leu Lys Val Trp Ser Gln Gly Gln Pro Ser Val
115 120 125
Thr Leu Ile Cys Arg Arg Arg Thr Gly Thr Asp Tyr Asp Glu Lys Ala
130 135 140
Gln Glu Ser Val Gly Ile Tyr Glu Val Thr His Gln Phe Val Lys Cys
145 150 155 160

<210> 449

<211> 117

<212> PRT

<213> Homo sapiens

<400> 449

Met Asp Ser Leu Ala Ala Gly Glu Leu Asn Ala Ser His Gln Pro Trp
1 5 10 15
Val Pro Glu Phe Val Ala Tyr Trp Arg Lys Thr His Gln Asp His Leu
20 25 30
Cys Ser Leu His Ser Arg Ala Phe Gly Leu Leu Asp Ala Arg Val Thr
35 40 45
Trp Ala Leu Arg Arg Ala Pro Glu Pro Val Pro Gly Lys Asp Arg Leu
50 55 60
Leu Leu Ala Ala Phe Pro Ala Glu Ala Ser Pro Val Asp Thr Ala Ser
65 70 75 80
Val Ser Val Tyr Gly Arg Ala Pro Arg Tyr Met His Lys Gly Val Lys
85 90 95
Lys Cys Val Cys Thr Pro Val Ser Lys Asn Ser Thr Ala Trp Leu Leu
100 105 110
Leu Gly Gly Ile Ser
115

<210> 450

<211> 335

<212> PRT

<213> Homo sapiens

<400> 450

Met Cys Cys Gln Val Cys Glu Ala Val Arg Ser Gly Asn Glu Glu Val
1 5 10 15
Leu Ala Asp Val Arg Thr Ile Val Asn Gln Ile Ser Tyr Thr Pro Gln
20 25 30
Asp Pro Arg Asp Leu Cys Gly Arg Ile Leu Thr Thr Cys Tyr Met Ala
35 40 45
Ser Lys Asn Ser Ser Gln Glu Thr Cys Thr Arg Ala Arg Glu Leu Ala
50 55 60

Gln	Gln	Ile	Gly	Ser	His	His	Ile	Ser	Leu	Asn	Ile	Asp	Pro	Ala	Val
65					70					75					80
Lys	Ala	Val	Met	Gly	Ile	Phe	Ser	Leu	Val	Thr	Gly	Lys	Ser	Pro	Leu
				85					90					95	
Phe	Ala	Ala	His	Gly	Gly	Ser	Ser	Arg	Glu	Asn	Leu	Ala	Leu	Gln	Asn
			100					105					110		
Val	Gln	Ala	Arg	Ile	Arg	Met	Val	Leu	Ala	Tyr	Leu	Phe	Ala	Gln	Leu
		115					120					125			
Ser	Leu	Trp	Ser	Arg	Gly	Val	His	Gly	Gly	Leu	Leu	Val	Leu	Gly	Ser
	130					135					140				
Ala	Asn	Val	Asp	Glu	Ser	Leu	Leu	Gly	Tyr	Leu	Thr	Lys	Tyr	Asp	Cys
145					150					155					160
Ser	Ser	Ala	Asp	Ile	Asn	Pro	Ile	Gly	Gly	Ile	Ser	Lys	Thr	Asp	Leu
			165					170						175	
Arg	Ala	Phe	Val	Gln	Phe	Cys	Ile	Gln	Arg	Phe	Gln	Leu	Pro	Ala	Leu
		180						185					190		
Gln	Ser	Ile	Leu	Leu	Ala	Pro	Ala	Thr	Ala	Glu	Leu	Glu	Pro	Leu	Ala
	195						200					205			
Asp	Gly	Gln	Val	Ser	Gln	Thr	Asp	Glu	Glu	Asp	Met	Gly	Met	Thr	Tyr
	210					215					220				
Ala	Glu	Leu	Ser	Val	Tyr	Gly	Lys	Leu	Arg	Lys	Val	Ala	Lys	Met	Gly
225				230						235					240
Pro	Tyr	Ser	Met	Phe	Cys	Lys	Leu	Leu	Gly	Met	Trp	Arg	His	Ile	Cys
			245						250					255	
Thr	Pro	Arg	Gln	Val	Ala	Asp	Lys	Val	Lys	Arg	Phe	Phe	Ser	Lys	Tyr
		260						265						270	
Ser	Met	Asn	Arg	His	Lys	Met	Thr	Thr	Leu	Thr	Pro	Ala	Tyr	His	Ala
	275						280					285			
Glu	Asn	Tyr	Ser	Pro	Glu	Asp	Asn	Arg	Phe	Asp	Leu	Arg	Pro	Phe	Leu
	290					295					300				
Tyr	Asn	Thr	Ser	Trp	Pro	Trp	Gln	Phe	Arg	Cys	Ile	Glu	Asn	Gln	Val
305				310						315					320
Leu	Gln	Leu	Glu	Arg	Ala	Glu	Pro	Gln	Ser	Leu	Asp	Gly	Val	Asp	
			325						330					335	

<210> 451

<211> 86

<212> PRT

<213> Homo sapiens

<220>

<221> UNSURE

<222> 76

<223> Xaa = Lys,Asn

<400> 451

Met	Cys	Trp	Val	Ile	Asn	His	Ala	Ile	Leu	Pro	Arg	Met	Arg	Met	His
1				5					10					15	
Ser	Lys	Arg	Gln	Thr	Ile	Thr	Arg	His	Ser	Ala	Ser	Leu	Ser	Phe	His
			20					25					30		
Ala	Leu	Pro	Arg	Ser	Ala	Phe	Leu	Gln	Leu	Cys	Leu	Leu	Arg	Gln	Ile
		35					40					45			
His	Gln	Ile	Pro	Cys	Leu	Ser	Ile	Phe	Ser	Ser	Thr	Leu	Arg	Ala	Gln
	50					55					60				
Thr	His	Asp	Ser	Gly	Ile	Gly	Cys	Thr	Thr	Ala	Xaa	Pro	Gly	Gly	Arg
65					70					75					80
Arg	Gln	Glu	Gln	Leu	Arg										
				85											

<210> 452
 <211> 93
 <212> PRT
 <213> Homo sapiens

<400> 452
 Met Lys Ile Ala Leu Cys Gln Arg Glu Leu Pro Ser Pro Arg Ser Cys
 1 5 10 15
 Leu Leu Ser Arg Asp Val Thr Gly Val Ile Cys Thr Arg Met Pro Arg
 20 25 30
 Leu Ala Ile Cys Ser Lys Thr Ala Gln Lys Ala Leu Pro Cys Ile Pro
 35 40 45
 Leu Leu His Thr Ser Pro Leu Cys Leu Gln Leu Leu Ser Ala Gly Leu
 50 55 60
 His Ile Tyr Ala Thr Leu Cys Lys Ser Cys Ala Ser Arg Asn His Lys
 65 70 75 80
 Asn Ile Phe Leu His Leu Leu His Ser Leu Ser Ala Ala
 85 90

<210> 453
 <211> 108
 <212> PRT
 <213> Homo sapiens

<400> 453
 Met Ala Val Arg Ala Ser Phe Glu Asn Asn Cys Glu Ile Gly Cys Phe
 1 5 10 15
 Ala Lys Leu Thr Asn Thr Tyr Cys Leu Val Ala Ile Gly Gly Ser Glu
 20 25 30
 Asn Phe Tyr Ser Val Phe Glu Gly Glu Leu Ser Asp Thr Ile Pro Val
 35 40 45
 Val His Ala Ser Ile Ala Gly Cys Arg Ile Ile Gly Arg Met Cys Val
 50 55 60
 Gly Asp Arg Arg Asn Ser Gly Arg Cys Ala Gln Gly Gly Ser Leu Gln
 65 70 75 80
 Thr Asp Ser Gly Arg Pro Gly Ala Ser Arg Lys Leu Leu Cys Leu Gln
 85 90 95
 Gln Ser Gly Arg Ala Gly Ala Ser Gln Asp Phe Asn
 100 105

<210> 454
 <211> 277
 <212> PRT
 <213> Homo sapiens

<400> 454
 Met Ser Leu Cys Glu Asp Met Leu Leu Cys Asn Tyr Arg Lys Cys Arg
 1 5 10 15
 Ile Lys Leu Ser Gly Tyr Ala Trp Val Thr Ala Cys Ser His Ile Phe
 20 25 30
 Cys Asp Gln His Gly Ser Gly Glu Phe Ser Arg Ser Pro Ala Ile Cys
 35 40 45
 Pro Ala Cys Asn Ser Thr Leu Ser Gly Lys Leu Asp Ile Val Arg Thr
 50 55 60
 Glu Leu Ser Pro Ser Glu Glu Tyr Lys Ala Met Val Leu Ala Gly Leu
 65 70 75 80
 Arg Pro Glu Ile Val Leu Asp Ile Ser Ser Arg Ala Leu Ala Phe Trp

				85					90					95			
Thr	Tyr	Gln	Val	His	Gln	Glu	Arg	Leu	Tyr	Gln	Glu	Tyr	Asn	Phe	Ser		
			100					105					110				
Lys	Ala	Glu	Gly	His	Leu	Lys	Gln	Met	Glu	Lys	Ile	Tyr	Thr	Gln	Gln		
		115					120					125					
Ile	Gln	Ser	Lys	Asp	Val	Glu	Leu	Thr	Ser	Met	Lys	Gly	Glu	Val	Thr		
	130					135					140						
Ser	Met	Lys	Lys	Val	Leu	Glu	Glu	Tyr	Lys	Lys	Lys	Phe	Ser	Asp	Ile		
145					150					155				160			
Ser	Glu	Lys	Leu	Met	Glu	Arg	Asn	Arg	Gln	Tyr	Gln	Lys	Leu	Gln	Gly		
			165					170						175			
Leu	Tyr	Asp	Ser	Leu	Arg	Leu	Arg	Asn	Ile	Thr	Ile	Ala	Asn	His	Glu		
		180						185					190				
Gly	Thr	Leu	Glu	Pro	Ser	Met	Ile	Ala	Gln	Ser	Gly	Val	Leu	Gly	Phe		
	195						200					205					
Pro	Leu	Gly	Asn	Asn	Ser	Lys	Phe	Pro	Leu	Asp	Asn	Thr	Pro	Val	Arg		
	210					215					220						
Asn	Arg	Gly	Asp	Gly	Asp	Gly	Asp	Phe	Gln	Phe	Arg	Pro	Phe	Phe	Ala		
225				230						235					240		
Gly	Ser	Pro	Thr	Ala	Pro	Glu	Pro	Ser	Asn	Ser	Phe	Phe	Ser	Phe	Val		
				245					250					255			
Ser	Pro	Ser	Arg	Glu	Leu	Glu	Gln	Gln	Gln	Val	Ser	Ser	Arg	Ala	Phe		
			260				265						270				
Lys	Val	Lys	Arg	Ile													
		275															

<210> 455

<211> 173

<212> PRT

<213> Homo sapiens

<400> 455

Met	Leu	Val	Met	Tyr	Leu	Leu	Ala	Ala	Leu	Phe	Gly	Tyr	Leu	Thr	Phe		
1				5					10					15			
Tyr	Gly	Glu	Val	Glu	Asp	Glu	Leu	Leu	His	Ala	Tyr	Ser	Lys	Val	Tyr		
		20					25						30				
Thr	Leu	Asp	Ile	Pro	Leu	Leu	Met	Val	Arg	Leu	Ala	Val	Leu	Val	Ala		
	35					40					45						
Val	Thr	Leu	Thr	Val	Pro	Ile	Val	Leu	Phe	Pro	Ile	Arg	Thr	Ser	Val		
	50					55					60						
Ile	Thr	Leu	Leu	Phe	Pro	Lys	Arg	Pro	Phe	Ser	Trp	Ile	Arg	His	Phe		
65				70					75					80			
Leu	Ile	Ala	Ala	Val	Leu	Ile	Ala	Leu	Asn	Asn	Val	Leu	Val	Ile	Leu		
			85						90				95				
Val	Pro	Thr	Ile	Lys	Tyr	Ile	Phe	Gly	Phe	Ile	Gly	Ala	Ser	Ser	Ala		
		100						105					110				
Thr	Met	Leu	Ile	Phe	Ile	Leu	Pro	Ala	Val	Phe	Tyr	Leu	Lys	Leu	Val		
	115					120						125					
Lys	Lys	Glu	Thr	Phe	Arg	Ser	Pro	Gln	Lys	Val	Gly	Ala	Leu	Ile	Phe		
	130					135					140						
Leu	Val	Val	Gly	Ile	Phe	Phe	Met	Ile	Gly	Ser	Met	Ala	Leu	Ile	Ile		
145				150						155				160			
Ile	Asp	Trp	Ile	Tyr	Asp	Pro	Pro	Asn	Ser	Lys	His	His					
			165					170									

<210> 456

<211> 370

<212> PRT

<213> Homo sapiens

<400> 456

Met Ser Ala Ser Ala Ala Thr Gly Val Phe Val Leu Ser Leu Ser Ala
1 5 10 15
Ile Pro Val Thr Tyr Val Phe Asn His Leu Ala Ala Gln His Asp Ser
20 25 30
Trp Thr Ile Val Gly Val Ala Ala Leu Ile Leu Phe Leu Val Ala Leu
35 40 45
Leu Ala Arg Val Leu Val Lys Arg Lys Pro Pro Arg Asp Pro Leu Phe
50 55 60
Tyr Val Tyr Ala Val Phe Gly Phe Thr Ser Val Val Asn Leu Ile Ile
65 70 75 80
Gly Leu Glu Gln Asp Gly Ile Ile Asp Gly Phe Met Thr His Tyr Leu
85 90 95
Arg Glu Gly Glu Pro Tyr Leu Asn Thr Ala Tyr Gly His Met Ile Cys
100 105 110
Tyr Trp Asp Gly Ser Ala His Tyr Leu Met Tyr Leu Val Met Val Ala
115 120 125
Ala Ile Ala Trp Glu Glu Thr Tyr Arg Thr Ile Gly Leu Tyr Trp Val
130 135 140
Gly Ser Ile Ile Met Ser Val Val Val Phe Val Pro Gly Asn Ile Val
145 150 155 160
Gly Lys Tyr Gly Thr Arg Ile Cys Pro Ala Phe Phe Leu Ser Ile Pro
165 170 175
Tyr Thr Cys Leu Pro Val Trp Ala Gly Phe Arg Ile Tyr Asn Gln Pro
180 185 190
Ser Glu Asn Tyr Asn Tyr Pro Ser Lys Val Ile Gln Glu Ala Gln Ala
195 200 205
Lys Asp Leu Leu Arg Arg Pro Phe Asp Leu Met Leu Val Val Cys Leu
210 215 220
Leu Leu Ala Thr Gly Phe Cys Leu Phe Arg Gly Leu Ile Ala Leu Asp
225 230 235 240
Cys Pro Ser Glu Leu Cys Arg Leu Tyr Thr Gln Phe Gln Glu Pro Tyr
245 250 255
Leu Lys Asp Pro Ala Ala Tyr Pro Lys Ile Gln Met Leu Ala Tyr Met
260 265 270
Phe Tyr Ser Val Pro Tyr Phe Val Thr Ala Leu Tyr Gly Leu Val Val
275 280 285
Pro Gly Cys Ser Trp Met Pro Asp Ile Thr Leu Ile His Ala Gly Gly
290 295 300
Leu Ala Gln Ala Gln Phe Ser His Ile Gly Ala Ser Leu His Ala Arg
305 310 315 320
Thr Ala Tyr Val Tyr Arg Val Pro Glu Glu Ala Lys Ile Leu Phe Leu
325 330 335
Ala Leu Asn Ile Ala Tyr Gly Val Leu Pro Gln Leu Leu Ala Tyr Arg
340 345 350
Cys Ile Tyr Lys Pro Glu Phe Phe Ile Lys Thr Lys Ala Glu Glu Lys
355 360 365
Val Glu
370

<210> 457

<211> 393

<212> PRT

<213> Homo sapiens

<400> 457

Met Thr Tyr Arg Trp Gly Thr Leu Leu Met Lys Arg Lys Phe Glu Glu
 1 5 10 15
 Pro Arg Pro Gly Phe His Gly Val Leu Gly Ile Asn Ser Ile Thr Gly
 20 25 30
 Lys Glu Glu Pro Leu Tyr Pro Ser Tyr Lys Arg Gln Leu Arg Ile Tyr
 35 40 45
 Leu Val Ser Leu Pro Phe Val Cys Leu Cys Leu Tyr Phe Ser Leu Tyr
 50 55 60
 Val Met Met Ile Tyr Phe Asp Met Glu Val Trp Ala Leu Gly Leu His
 65 70 75 80
 Glu Asn Ser Gly Ser Glu Trp Thr Ser Val Leu Leu Tyr Val Pro Ser
 85 90 95
 Ile Ile Tyr Ala Ile Val Ile Glu Ile Met Asn Arg Leu Tyr Arg Tyr
 100 105 110
 Ala Ala Glu Phe Leu Thr Ser Trp Glu Asn His Arg Leu Glu Ser Ala
 115 120 125
 Tyr Gln Asn His Leu Ile Leu Lys Val Leu Val Phe Asn Phe Leu Asn
 130 135 140
 Cys Phe Ala Ser Leu Phe Tyr Ile Ala Phe Val Leu Lys Asp Met Lys
 145 150 155 160
 Leu Leu Arg Gln Ser Leu Ala Thr Leu Leu Ile Thr Ser Gln Ile Leu
 165 170 175
 Asn Gln Ile Met Glu Ser Phe Leu Pro Tyr Trp Leu Gln Arg Lys His
 180 185 190
 Gly Val Arg Val Lys Arg Lys Val Gln Ala Leu Lys Ala Asp Ile Asp
 195 200 205
 Ala Thr Leu Tyr Glu Gln Val Ile Leu Glu Lys Glu Met Gly Thr Tyr
 210 215 220
 Leu Gly Thr Phe Asp Asp Tyr Leu Glu Leu Phe Leu Gln Phe Gly Tyr
 225 230 235 240
 Val Ser Leu Phe Ser Cys Val Tyr Pro Leu Ala Ala Ala Phe Ala Val
 245 250 255
 Leu Asn Asn Phe Thr Glu Val Asn Ser Asp Ala Leu Lys Met Cys Arg
 260 265 270
 Val Phe Lys Arg Pro Phe Ser Glu Pro Ser Ala Asn Ile Gly Val Trp
 275 280 285
 Gln Leu Ala Phe Glu Thr Met Ser Val Ile Ser Val Val Thr Asn Cys
 290 295 300
 Ala Leu Ile Gly Met Ser Pro Gln Val Asn Ala Val Phe Pro Glu Ser
 305 310 315 320
 Lys Ala Asp Leu Ile Leu Ile Val Val Ala Val Glu His Ala Leu Leu
 325 330 335
 Ala Leu Lys Phe Ile Leu Ala Phe Ala Ile Pro Asp Lys Pro Arg His
 340 345 350
 Ile Gln Met Lys Leu Ala Arg Leu Glu Phe Glu Ser Leu Glu Ala Leu
 355 360 365
 Lys Gln Gln Gln Met Lys Leu Val Thr Glu Asn Leu Lys Glu Glu Pro
 370 375 380
 Met Glu Ser Gly Lys Glu Lys Ala Thr
 385 390

<210> 458
 <211> 116
 <212> PRT
 <213> Homo sapiens

<400> 458
 Met Val Gly Gly Glu Ala Ala Ala Ala Val Glu Glu Leu Val Ser Gly

1				5					10					15			
Val	Arg	Gln	Ala	Ala	Asp	Phe	Ala	Glu	Gln	Phe	Arg	Ser	Tyr	Ser	Glu		
			20					25					30				
Ser	Glu	Lys	Gln	Trp	Lys	Ala	Arg	Met	Glu	Phe	Ile	Leu	Arg	His	Leu		
		35					40					45					
Pro	Asp	Tyr	Arg	Asp	Pro	Pro	Asp	Gly	Ser	Gly	Arg	Leu	Asp	Gln	Leu		
	50					55					60						
Leu	Ser	Leu	Ser	Met	Val	Trp	Ala	Asn	His	Leu	Phe	Leu	Gly	Cys	Ser		
65				70						75					80		
Tyr	Asn	Lys	Asp	Leu	Leu	Asp	Lys	Val	Met	Glu	Met	Ala	Asp	Gly	Ile		
			85					90					95				
Glu	Val	Glu	Asp	Leu	Pro	Gln	Phe	Thr	Arg	Ser	Glu	Leu	Met	Lys			
			100					105					110				
Lys	His	Gln	Ser														
		115															

<210> 459

<211> 163

<212> PRT

<213> Homo sapiens

<400> 459

Met	Glu	His	Tyr	Arg	Lys	Ala	Gly	Ser	Val	Glu	Leu	Pro	Ala	Pro	Ser		
1				5					10					15			
Pro	Met	Pro	Gln	Leu	Pro	Pro	Asp	Thr	Leu	Glu	Met	Arg	Val	Arg	Asp		
			20					25				30					
Gly	Ser	Lys	Ile	Arg	Asn	Leu	Leu	Gly	Leu	Ala	Leu	Gly	Arg	Leu	Glu		
		35				40						45					
Gly	Gly	Ser	Ala	Arg	His	Val	Val	Phe	Ser	Gly	Ser	Gly	Arg	Ala	Ala		
	50					55					60						
Gly	Lys	Ala	Val	Ser	Cys	Ala	Glu	Ile	Val	Lys	Arg	Arg	Val	Pro	Gly		
65				70						75					80		
Leu	His	Gln	Leu	Thr	Lys	Leu	Arg	Phe	Leu	Gln	Thr	Glu	Asp	Ser	Trp		
				85				90					95				
Val	Pro	Ala	Ser	Pro	Asp	Thr	Gly	Leu	Asp	Pro	Leu	Thr	Val	Arg	Arg		
			100				105						110				
His	Val	Pro	Ala	Val	Trp	Val	Leu	Ser	Arg	Asp	Pro	Leu	Asp	Pro			
		115				120					125						
Asn	Glu	Cys	Gly	Tyr	Gln	Pro	Pro	Gly	Ala	Pro	Pro	Gly	Leu	Gly	Ser		
	130					135					140						
Met	Pro	Ser	Ser	Ser	Cys	Gly	Pro	Arg	Ser	Arg	Arg	Arg	Ala	Arg	Asp		
145					150					155					160		
Thr	Arg	Ser															

<210> 460

<211> 230

<212> PRT

<213> Homo sapiens

<400> 460

Met	Val	Val	Phe	Gly	Tyr	Glu	Ala	Gly	Thr	Lys	Pro	Arg	Asp	Ser	Gly		
1			5						10					15			
Val	Val	Pro	Val	Gly	Thr	Glu	Glu	Ala	Pro	Lys	Val	Phe	Lys	Met	Ala		
			20					25					30				
Ala	Ser	Met	His	Gly	Gln	Pro	Ser	Pro	Ser	Leu	Glu	Asp	Ala	Lys	Leu		
		35				40						45					
Arg	Arg	Pro	Met	Val	Ile	Glu	Ile	Ile	Glu	Lys	Asn	Phe	Asp	Tyr	Leu		
	50					55					60						

Arg	Lys	Glu	Met	Thr	Gln	Asn	Ile	Tyr	Gln	Met	Ala	Thr	Phe	Gly	Thr
65					70					75					80
Thr	Ala	Gly	Phe	Ser	Gly	Ile	Phe	Ser	Asn	Phe	Leu	Phe	Arg	Arg	Cys
				85					90					95	
Phe	Lys	Val	Lys	His	Asp	Ala	Leu	Lys	Thr	Tyr	Ala	Ser	Leu	Ala	Thr
			100					105					110		
Leu	Pro	Phe	Leu	Ser	Thr	Val	Val	Thr	Asp	Lys	Leu	Phe	Val	Ile	Asp
		115					120					125			
Ala	Leu	Tyr	Ser	Asp	Asn	Ile	Ser	Lys	Glu	Asn	Cys	Val	Phe	Arg	Ser
	130					135				140					
Ser	Leu	Ile	Gly	Ile	Val	Cys	Gly	Val	Phe	Tyr	Pro	Ser	Ser	Leu	Ala
145					150					155					160
Phe	Thr	Lys	Asn	Gly	Arg	Leu	Ala	Thr	Lys	Tyr	His	Thr	Val	Pro	Leu
				165					170					175	
Pro	Pro	Lys	Gly	Arg	Val	Leu	Ile	His	Trp	Met	Thr	Leu	Cys	Gln	Thr
			180					185					190		
Gln	Met	Lys	Leu	Met	Ala	Ile	Pro	Leu	Val	Phe	Gln	Ile	Met	Phe	Gly
		195					200					205			
Ile	Leu	Asn	Gly	Leu	Tyr	His	Tyr	Ala	Val	Phe	Glu	Glu	Thr	Leu	Glu
	210					215					220				
Lys	Thr	Ile	His	Glu	Glu										
225					230										

<210> 461

<211> 101

<212> PRT

<213> Homo sapiens

<220>

<221> UNSURE

<222> 95

<223> Xaa = Cys,Trp

<400> 461

Met	Glu	Arg	Pro	Asp	Lys	Ala	Ala	Leu	Asn	Ala	Leu	Gln	Pro	Pro	Glu
1				5					10					15	
Phe	Arg	Asn	Glu	Ser	Ser	Leu	Ala	Ser	Thr	Leu	Lys	Thr	Leu	Leu	Phe
		20						25					30		
Phe	Thr	Ala	Leu	Met	Ile	Thr	Val	Pro	Ile	Gly	Leu	Tyr	Phe	Thr	Thr
		35				40						45			
Lys	Ser	Tyr	Ile	Phe	Glu	Gly	Ala	Leu	Gly	Met	Ser	Asn	Arg	Asp	Ser
	50					55					60				
Tyr	Phe	Tyr	Ala	Ala	Ile	Val	Ala	Val	Val	Ala	Val	His	Val	Val	Leu
65					70					75					80
Ala	Leu	Phe	Val	Tyr	Val	Ala	Trp	Asn	Glu	Gly	Ser	Arg	Gln	Xaa	Arg
				85					90					95	
Glu	Gly	Lys	Gln	Asp											
			100												

<210> 462

<211> 93

<212> PRT

<213> Homo sapiens

<400> 462

Met	Asp	Ser	Leu	Arg	Lys	Met	Leu	Ile	Ser	Val	Ala	Met	Leu	Gly	Ala
1				5					10					15	
Gly	Ala	Gly	Val	Gly	Tyr	Ala	Leu	Leu	Val	Ile	Val	Thr	Pro	Gly	Glu

			20					25				30			
Arg	Arg	Lys	Gln	Glu	Met	Leu	Lys	Glu	Met	Pro	Leu	Gln	Asp	Pro	Arg
		35					40					45			
Ser	Arg	Glu	Glu	Ala	Ala	Arg	Thr	Gln	Gln	Leu	Leu	Leu	Ala	Thr	Leu
	50					55					60				
Gln	Glu	Ala	Ala	Thr	Thr	Gln	Glu	Asn	Val	Ala	Trp	Arg	Lys	Asn	Trp
65					70					75					80
Met	Val	Gly	Gly	Glu	Gly	Gly	Ala	Gly	Gly	Arg	Ser	Pro			
			85						90						

<210> 463
 <211> 133
 <212> PRT
 <213> Homo sapiens

Met	Gly	His	Gly	Asp	Glu	Ile	Val	Leu	Ala	Asp	Leu	Asn	Phe	Pro	Ala
1			5						10					15	
Ser	Ser	Ile	Cys	Gln	Cys	Gly	Pro	Met	Glu	Ile	Arg	Ala	Asp	Gly	Leu
		20					25					30			
Gly	Ile	Pro	Gln	Leu	Leu	Glu	Ala	Val	Leu	Lys	Leu	Leu	Pro	Leu	Asp
		35				40					45				
Thr	Tyr	Val	Glu	Ser	Pro	Ala	Ala	Val	Met	Glu	Leu	Val	Pro	Ser	Asp
	50					55					60				
Lys	Glu	Arg	Gly	Leu	Gln	Thr	Pro	Val	Trp	Thr	Glu	Tyr	Glu	Ser	Ile
65					70					75					80
Leu	Arg	Arg	Ala	Gly	Cys	Val	Arg	Ala	Leu	Ala	Lys	Ile	Glu	Arg	Phe
			85					90					95		
Glu	Phe	Tyr	Glu	Arg	Ala	Lys	Lys	Ala	Phe	Ala	Val	Val	Ala	Thr	Gly
		100					105					110			
Glu	Thr	Ala	Leu	Tyr	Gly	Asn	Leu	Ile	Leu	Arg	Lys	Gly	Val	Leu	Ala
		115				120						125			
Leu	Asn	Pro	Leu	Leu											
			130												

<210> 464
 <211> 95
 <212> PRT
 <213> Homo sapiens

Met	Gly	His	Gly	Asp	Glu	Ile	Val	Leu	Ala	Asp	Leu	Asn	Phe	Pro	Ala
1			5						10					15	
Ser	Ser	Ile	Cys	Gln	Cys	Gly	Pro	Met	Glu	Ile	Arg	Ala	Asp	Gly	Leu
		20					25					30			
Gly	Ile	Pro	Gln	Leu	Leu	Glu	Ala	Val	Leu	Ala	Ala	Ala	Pro	Gly	His
		35				40					45				
Leu	Cys	Gly	Glu	Ser	Gly	Cys	Ser	His	Gly	Ala	Gly	Ala	Gln	Arg	Gln
	50					55					60				
Gly	Glu	Gly	Pro	Ala	Asp	Pro	Ser	Val	Asp	Gly	Val	Arg	Val	His	Pro
65					70					75					80
Thr	Gln	Gly	Arg	Leu	Cys	Glu	Ser	Pro	Gly	Lys	Asp	Arg	Glu	Val	
			85						90					95	

<210> 465
 <211> 93
 <212> PRT
 <213> Homo sapiens

<400> 465

Met	Thr	Pro	Ile	Lys	Leu	Leu	Asn	Leu	Thr	Ser	Arg	Tyr	Asn	Phe	Arg
1				5					10					15	
Arg	Thr	Phe	Gly	Ile	Glu	Leu	Ser	Ser	Asn	Ser	Ser	Tyr	Cys	Lys	Arg
			20					25					30		
Gly	Asn	Gly	Tyr	Arg	Ser	Arg	Val	Pro	Lys	Glu	Cys	Glu	Cys	Asn	Trp
		35					40					45			
Leu	His	Leu	Glu	Ser	Asp	Thr	Leu	Lys	Lys	Leu	Pro	Ile	Ile	Ser	Pro
	50					55					60				
Ser	Trp	Thr	Cys	Arg	Ile	Ile	Leu	Phe	Leu	Tyr	Phe	Ser	Gly	Gln	Leu
65					70					75					80
Leu	Gln	Leu	Ser	Leu	Ser	Cys	Leu	Gln	Leu	Ile	Lys	Leu			
				85					90						

<210> 466

<211> 500

<212> PRT

<213> Homo sapiens

<400> 466

Met	Glu	Val	Ser	Thr	Asn	Pro	Ser	Ser	Asn	Ile	Asp	Pro	Gly	Asn	Tyr
1				5					10					15	
Val	Glu	Met	Asn	Asp	Ser	Ile	Thr	His	Leu	Pro	Ser	Lys	Val	Val	Ile
			20					25				30			
Gln	Asp	Ile	Thr	Met	Glu	Leu	His	Cys	Pro	Leu	Cys	Asn	Asp	Trp	Phe
		35					40					45			
Arg	Asp	Pro	Leu	Met	Leu	Ser	Cys	Gly	His	Asn	Phe	Cys	Glu	Ala	Cys
	50					55					60				
Ile	Gln	Asp	Phe	Trp	Arg	Leu	Gln	Ala	Lys	Glu	Thr	Phe	Cys	Pro	Glu
65					70					75					80
Cys	Lys	Met	Leu	Cys	Gln	Tyr	Asn	Asn	Cys	Thr	Phe	Asn	Pro	Val	Leu
			85						90					95	
Asp	Lys	Leu	Val	Glu	Lys	Ile	Lys	Lys	Leu	Pro	Leu	Leu	Lys	Gly	His
			100					105					110		
Pro	Gln	Cys	Pro	Glu	His	Gly	Glu	Asn	Leu	Lys	Leu	Phe	Ser	Lys	Pro
		115					120					125			
Asp	Gly	Lys	Leu	Ile	Cys	Phe	Gln	Cys	Lys	Asp	Ala	Arg	Leu	Ser	Val
	130					135					140				
Gly	Gln	Ser	Lys	Glu	Phe	Leu	Gln	Ile	Ser	Asp	Ala	Val	His	Phe	Phe
145					150					155					160
Met	Glu	Glu	Leu	Ala	Ile	Gln	Gln	Gly	Gln	Leu	Glu	Thr	Thr	Leu	Lys
			165						170					175	
Glu	Leu	Gln	Thr	Leu	Arg	Asn	Met	Gln	Lys	Glu	Ala	Ile	Ala	Ala	His
			180					185					190		
Lys	Glu	Asn	Lys	Leu	His	Leu	Gln	Gln	His	Val	Ser	Met	Glu	Phe	Leu
		195					200					205			
Lys	Leu	His	Gln	Phe	Leu	His	Ser	Lys	Glu	Lys	Asp	Ile	Leu	Thr	Glu
	210					215					220				
Leu	Arg	Glu	Glu	Gly	Lys	Ala	Leu	Asn	Glu	Glu	Met	Glu	Leu	Asn	Leu
225					230					235					240
Ser	Gln	Leu	Gln	Glu	Gln	Cys	Leu	Leu	Ala	Lys	Asp	Met	Leu	Val	Ser
				245					250					255	
Ile	Gln	Ala	Lys	Thr	Glu	Gln	Gln	Asn	Ser	Phe	Asp	Phe	Leu	Lys	Asp
		260						265					270		
Ile	Thr	Thr	Leu	Leu	His	Ser	Leu	Glu	Gln	Gly	Met	Lys	Val	Leu	Ala
	275						280					285			
Thr	Arg	Glu	Leu	Ile	Ser	Arg	Lys	Leu	Asn	Leu	Gly	Gln	Tyr	Lys	Gly

290	295	300
Pro Ile Gln Tyr Met Val Trp Arg Glu Met Gln Asp Thr Leu Cys Pro		
305	310	315
Gly Leu Ser Pro Leu Thr Leu Asp Pro Lys Thr Ala His Pro Asn Leu		320
	325	330
Val Leu Ser Lys Ser Gln Thr Ser Val Trp His Gly Asp Ile Lys Lys		335
	340	345
Ile Met Pro Asp Asp Pro Glu Arg Phe Asp Ser Ser Val Ala Val Leu		350
	355	360
Gly Ser Arg Gly Phe Thr Ser Gly Lys Trp Tyr Trp Glu Val Glu Val		365
	370	375
Ala Lys Lys Thr Lys Trp Thr Val Gly Val Val Arg Glu Ser Ile Ile		380
385	390	395
Arg Lys Gly Ser Cys Pro Leu Thr Pro Glu Gln Gly Phe Trp Leu Leu		400
	405	410
Arg Leu Arg Asn Gln Thr Asp Leu Lys Ala Leu Asp Leu Pro Ser Phe		415
	420	425
Ser Leu Thr Leu Thr Asn Asn Leu Asp Lys Val Gly Ile Tyr Leu Asp		430
	435	440
Tyr Glu Gly Gly Gln Leu Ser Phe Tyr Asn Ala Lys Thr Met Thr His		445
	450	455
Ile Tyr Thr Phe Ser Asn Thr Phe Met Glu Lys Leu Tyr Pro Tyr Phe		460
465	470	475
Cys Pro Cys Leu Asn Asp Gly Arg Glu Asn Lys Glu Pro Leu His Ile		480
	485	490
Leu His Pro Gln		495
500		

<210> 467

<211> 140

<212> PRT

<213> Homo sapiens

<400> 467

Met Val Leu Thr Lys Pro Leu Gln Arg Asn Gly Ser Met Met Ser Phe	
1	5
Glu Asn Val Lys Glu Lys Ser Arg Glu Gly Gly Pro His Ala His Thr	10
	20
Pro Glu Glu Glu Leu Cys Phe Val Val Thr His Tyr Pro Gln Val Gln	25
	30
Thr Thr Leu Asn Leu Phe Phe His Ile Phe Lys Val Leu Thr Gln Pro	35
	40
Leu Ser Leu Leu Trp Gly Cys Asp Gln Lys Pro Arg Thr Val Pro Thr	45
65	50
Leu Gly Asn Gly Ala Trp Asp Thr Cys Gln Gln His Ile Arg Thr Ser	55
	60
Ser Trp Thr Ala Asn Thr Leu Val Ile Gln Asn Gln His Ser Arg Glu	65
	70
Ser Thr Val Ser Val Cys Leu Phe Met Leu Ile Arg Met Gln His Ile	75
	80
Leu Lys Thr Asp Thr Leu Gln Phe Arg Ile Cys	85
	90
130	95
	100
	105
	110
	115
	120
	125
	130
	135
	140

<210> 468

<211> 100

<212> PRT

<213> Homo sapiens

<400> 468

Met Tyr Met Leu Leu Ser Pro His Arg Leu Arg Glu Gln Ala Gly Val
1 5 10 15
Arg Gly Ser Ile Arg Thr Ala Asn Arg Thr Glu Asp Gly Leu Lys Ile
20 25 30
Arg Glu Ala Glu Ser Leu Pro Gln Ser Asn Thr Ala Asp Phe Lys Cys
35 40 45
Leu His Ser Ala Ser Leu Gln Gln Ala Pro Gly Gly Ile Leu Met Gly
50 55 60
Pro Ala Ser Ser Pro Trp Thr Leu Ala Val Glu Gly Glu Lys Arg Thr
65 70 75 80
Ser Ala Pro Pro Leu Arg Glu Ser Leu Met Pro Thr Lys Gly Leu Gly
85 90 95
Trp Trp Thr Gln
100

<210> 469

<211> 119

<212> PRT

<213> Homo sapiens

<400> 469

Met Ala Ser Tyr Ser Gly Phe Ser Gly Leu Leu Glu Ile Arg Tyr Gly
1 5 10 15
Pro Gly His Arg Ser Cys Leu Pro Gln Phe Ala Phe Phe Pro Gln Pro
20 25 30
Pro Leu Pro Arg Pro Arg Ile Cys Met Trp Val Leu Ala Glu Leu Leu
35 40 45
Glu Leu Gly Cys Pro Glu Gln Ser Leu Arg Asp Ala Ile Thr Leu Asp
50 55 60
Leu Phe Cys His Ala Leu Ile Phe Cys Arg Gln Gln Gly Phe Ser Leu
65 70 75 80
Glu Gln Thr Ser Ala Ala Cys Ala Leu Leu Gln Asp Leu His Lys Ala
85 90 95
Cys Ile Gly Glu Arg Gly Gln Leu Pro Gly Leu Ser Pro Arg Glu Lys
100 105 110
Arg Asn Arg Ala Trp His Lys
115

<210> 470

<211> 140

<212> PRT

<213> Homo sapiens

<400> 470

Met Arg Ser Glu Cys Val Leu Gly Ala Ala Ser Asp Ser Gly Gln Glu
1 5 10 15
Ala Pro Arg Asp Thr Trp Phe Leu Gln Gly Trp Lys Ala Ser Arg Arg
20 25 30
Phe Leu Ile Lys Gly Ser Val Ala Gly Gly Ala Val Tyr Leu Val Tyr
35 40 45
Asp Gln Glu Leu Leu Gly Pro Ser Asp Lys Ser Gln Ala Ala Leu Gln
50 55 60
Lys Ala Gly Glu Val Val Pro Pro Ala Met Tyr Gln Phe Ser Gln Tyr
65 70 75 80
Val Cys Gln Gln Thr Gly Leu Gln Ile Pro Gln Leu Pro Ala Pro Pro
85 90 95
Lys Ile Tyr Phe Pro Ile Arg Asp Ser Trp Asn Ala Gly Ile Met Thr

			100					105					110			
Val	Met	Ser	Ala	Leu	Ser	Val	Ala	Pro	Ser	Lys	Ala	Arg	Glu	Tyr	Ser	
		115					120					125				
Lys	Glu	Gly	Trp	Glu	Tyr	Val	Lys	Ala	Arg	Thr	Lys					
	130					135					140					

<210> 471
 <211> 109
 <212> PRT
 <213> Homo sapiens

<400> 471

Met	Phe	His	Leu	Arg	Thr	Cys	Ala	Ala	Lys	Leu	Arg	Pro	Leu	Thr	Ala	
1			5						10					15		
Ser	Gln	Thr	Val	Lys	Thr	Phe	Ser	Gln	Asn	Arg	Pro	Ala	Ala	Ala	Arg	
			20					25					30			
Thr	Phe	Gln	Gln	Ile	Arg	Cys	Tyr	Ser	Ala	Pro	Val	Ala	Ala	Glu	Pro	
		35				40						45				
Phe	Leu	Ser	Gly	Thr	Ser	Ser	Asn	Tyr	Val	Glu	Glu	Met	Tyr	Cys	Ala	
	50				55					60						
Trp	Leu	Glu	Asn	Pro	Lys	Ser	Val	His	Lys	Thr	Gly	Ser	His	Cys	Cys	
65				70					75					80		
Pro	Gly	Trp	Ser	Ala	Val	Ala	Gly	Ser	Arg	Leu	Ala	Ala	Thr	Ser	Asp	
			85					90					95			
Ser	Trp	Val	Gln	Val	Ile	Leu	Met	Pro	Gln	Pro	Pro	Glu				
		100					105									

<210> 472
 <211> 100
 <212> PRT
 <213> Homo sapiens

<400> 472

Met	Phe	His	Leu	Arg	Thr	Cys	Ala	Ala	Lys	Leu	Arg	Pro	Leu	Thr	Ala	
1			5						10					15		
Ser	Gln	Thr	Val	Lys	Thr	Phe	Ser	Gln	Asn	Arg	Pro	Ala	Ala	Ala	Arg	
			20					25					30			
Thr	Phe	Gln	Gln	Ile	Arg	Ala	Ile	Leu	His	Leu	Leu	Leu	Leu	Ser	Pro	
		35				40						45				
Phe	Ser	Val	Gly	Leu	Val	Arg	Thr	Met	Trp	Arg	Arg	Cys	Thr	Val	Leu	
	50				55					60						
Gly	Trp	Lys	Thr	Pro	Lys	Val	Tyr	Ile	Arg	Gln	Gly	Pro	Thr	Val	Val	
65				70					75					80		
Gln	Ala	Gly	Val	Gln	Trp	Arg	Asp	Leu	Gly	Leu	Leu	Gln	Pro	Pro	Thr	
			85					90					95			
Pro	Gly	Phe	Lys													
		100														

<210> 473
 <211> 141
 <212> PRT
 <213> Homo sapiens

<400> 473

Met	Ala	Pro	Lys	Val	Phe	Arg	Gln	Tyr	Trp	Asp	Ile	Pro	Asp	Gly	Thr	
1			5						10					15		
Asp	Cys	His	Arg	Lys	Ala	Tyr	Ser	Thr	Ser	Ile	Ala	Ser	Val	Ala		
		20					25					30				

Gly Leu Thr Ala Ala Ala Tyr Arg Val Thr Leu Asn Pro Pro Gly Thr
 35 40 45
 Phe Leu Glu Gly Val Ala Lys Val Gly Gln Tyr Thr Phe Thr Ala Ala
 50 55 60
 Ala Val Gly Ala Val Phe Gly Leu Thr Thr Cys Ile Ser Ala His Val
 65 70 75 80
 Arg Glu Lys Pro Asp Asp Pro Leu Asn Tyr Phe Leu Gly Gly Cys Ala
 85 90 95
 Gly Gly Leu Thr Leu Gly Ala Arg Thr His Asn Tyr Gly Ile Gly Ala
 100 105 110
 Ala Ala Cys Val Tyr Phe Gly Ile Ala Ala Ser Leu Val Lys Met Gly
 115 120 125
 Arg Leu Glu Gly Trp Glu Val Phe Ala Lys Pro Lys Val
 130 135 140

<210> 474
 <211> 134
 <212> PRT
 <213> Homo sapiens

<400> 474
 Met Ala Thr His Pro Asp Gly Phe Arg Leu Glu Gly Pro Leu Ala Ala
 1 5 10 15
 Ala His Ser Pro Gly Pro Cys Thr Val Leu Tyr Glu Gly Pro Val Arg
 20 25 30
 Gly Leu Cys Pro Phe Ala Pro Arg Asn Ser Asn Thr Met Ala Ala Ala
 35 40 45
 Ala Leu Ala Ala Pro Ser Leu Gly Phe Asp Gly Val Ile Gly Val Leu
 50 55 60
 Val Ala Asp Thr Ser Leu Thr Asp Met His Val Val Asp Val Glu Leu
 65 70 75 80
 Ser Gly Pro Arg Gly Pro Thr Gly Arg Ser Phe Ala Val His Thr Arg
 85 90 95
 Arg Glu Asn Pro Ala Glu Pro Gly Ala Val Thr Gly Ser Ala Thr Val
 100 105 110
 Thr Ala Phe Trp Arg Ser Leu Leu Ala Cys Cys Gln Leu Pro Ser Arg
 115 120 125
 Pro Gly Ile His Leu Cys
 130

<210> 475
 <211> 134
 <212> PRT
 <213> Homo sapiens

<400> 475
 Met Ala Thr His Pro Asp Gly Phe Arg Leu Glu Gly Pro Leu Ala Ala
 1 5 10 15
 Ala His Ser Pro Gly Pro Cys Thr Val Leu Tyr Glu Gly Pro Val Arg
 20 25 30
 Gly Leu Cys Pro Phe Ala Pro Arg Asn Ser Asn Thr Met Ser Ala Ala
 35 40 45
 Ala Leu Ala Ala Pro Ser Leu Gly Phe Asp Gly Val Ile Gly Val Leu
 50 55 60
 Val Ala Asp Thr Ser Leu Thr Asp Met His Val Val Asp Val Glu Leu
 65 70 75 80
 Ser Gly Pro Arg Gly Pro Thr Cys Arg Ser Phe Ala Val His Thr Arg
 85 90 95

Arg Glu Asn Pro Ala Glu Pro Gly Ala Val Thr Gly Ser Ala Thr Val
 100 105 110
 Thr Ala Phe Trp Arg Ser Leu Leu Ala Cys Cys Gln Leu Pro Ser Arg
 115 120 125
 Pro Gly Ile His Leu Cys
 130

<210> 476
 <211> 85
 <212> PRT
 <213> Homo sapiens

<400> 476
 Met Leu Lys Val Glu Ala Thr Gly Ser Pro Glu Glu Gly Trp Ala Gly
 1 5 10 15
 Gly Glu Pro Arg Thr Gly Ala Pro Ala Asn Ser Pro Ser Cys Pro Gln
 20 25 30
 Glu Met Pro Leu Gln Asp Pro Arg Ser Arg Glu Glu Ala Ala Arg Thr
 35 40 45
 Gln Gln Leu Leu Leu Ala Thr Leu Gln Glu Ala Ala Thr Thr Gln Glu
 50 55 60
 Asn Val Ala Trp Arg Lys Asn Trp Met Val Gly Gly Glu Gly Gly Ala
 65 70 75 80
 Ser Gly Arg Ser Pro
 85

<210> 477
 <211> 116
 <212> PRT
 <213> Homo sapiens

<400> 477
 Met Gly Arg Pro Trp Met Val Met Ile Leu Glu Ser Lys Ser Glu Glu
 1 5 10 15
 Lys Met Trp Tyr Gly Val Phe Leu Trp Ala Leu Val Ser Ser Leu Phe
 20 25 30
 Phe His Val Pro Ala Gly Leu Leu Ala Leu Phe Thr Leu Arg His His
 35 40 45
 Lys Tyr Gly Arg Phe Met Ser Val Ser Ile Leu Leu Met Gly Ile Val
 50 55 60
 Gly Pro Ile Thr Ala Gly Ile Leu Thr Ser Ala Ala Ile Ala Gly Val
 65 70 75 80
 Tyr Arg Ala Ala Gly Lys Glu Met Ile Pro Phe Glu Ala Leu Thr Leu
 85 90 95
 Gly Thr Gly Gln Thr Phe Cys Val Leu Val Val Ser Phe Leu Arg Ile
 100 105 110
 Leu Ala Thr Leu
 115

<210> 478
 <211> 104
 <212> PRT
 <213> Homo sapiens

<400> 478
 Met Asn Arg Tyr Cys Gly Lys Ile Phe Val Ser Val Met Val Lys Leu
 1 5 10 15
 Gln Lys Asn Lys Leu Thr Ser Phe Pro Arg Gln Pro Leu Leu Thr Phe

20 25 30
 Phe Glu Tyr Leu Glu Lys Val Leu Cys Ser Gly Leu Phe Ser His Ser
 35 40 45
 Ala Lys Ser His His Asp Leu Thr Arg His Pro Tyr Glu Thr Ala
 50 55 60
 Ala Pro Leu Leu Ser Ser His Leu Ile Leu Thr Glu Ala Leu Arg Asn
 65 70 75 80
 Gly Leu Gly Lys Cys His Asp Pro His Phe Thr Gly Glu Glu Thr Glu
 85 90 95
 Ala Gln Arg Gly Lys Leu Thr Thr
 100

<210> 479
 <211> 439
 <212> PRT
 <213> Homo sapiens

<400> 479
 Leu Gly Asp His Gly Trp Glu Leu Ser Leu Glu Glu Asp Ala Gln Leu
 1 5 10 15
 Trp Gly Gly Val Val Lys Ser Cys Phe Glu Gly Lys Gly Pro Gln Arg
 20 25 30
 Glu Ala Gln Pro Ala Ser Pro Gln Ala Ala Pro Pro Gly Pro Thr Asn
 35 40 45
 Glu Ala Gln Met Ala Ala Ala Ala Leu Ala Arg Leu Glu Gln Lys
 50 55 60
 Gln Ser Arg Ala Trp Gly Pro Thr Ser Gln Asp Thr Ile Arg Asn Gln
 65 70 75 80
 Val Arg Lys Glu Leu Gln Ala Glu Ala Thr Val Ser Gly Ser Pro Glu
 85 90 95
 Ala Pro Gly Thr Asn Val Val Ser Glu Pro Arg Glu Glu Gly Ser Ala
 100 105 110
 His Leu Ala Val Pro Gly Val Tyr Phe Thr Cys Pro Leu Thr Gly Ala
 115 120 125
 Thr Leu Arg Lys Asp Gln Arg Asp Ala Cys Ile Lys Glu Ala Ile Leu
 130 135 140
 Leu His Phe Ser Thr Asp Pro Val Ala Ala Ser Ile Met Lys Ile Tyr
 145 150 155 160
 Thr Phe Asn Lys Asp Gln Asp Arg Val Lys Leu Gly Val Asp Thr Ile
 165 170 175
 Ala Lys Tyr Leu Asp Asn Ile His Leu His Pro Glu Glu Glu Lys Tyr
 180 185 190
 Arg Lys Ile Lys Leu Gln Asn Lys Val Phe Gln Glu Arg Ile Asn Cys
 195 200 205
 Leu Glu Gly Thr His Glu Phe Phe Glu Ala Ile Gly Phe Gln Lys Val
 210 215 220
 Leu Pro Ala Gln Asp Gln Glu Asp Pro Glu Glu Phe Tyr Val Leu
 225 230 235 240
 Ser Glu Thr ~ Leu Ala Gln Pro Gln Ser Leu Glu Arg His Lys Glu
 250 255
 Gln Leu Leu Ala Ala Pro Val Arg Ala Lys Leu Asp Arg Gln Arg
 260 265 270
 Arg Val Phe Gln Pro Ser ~ Ala Ser Gln Phe Glu Leu Pro Gly
 275 285
 Asp Phe Phe Asn Leu Thr Ala Glu Lys Arg Glu Gln Arg Leu
 290 295 300
 Arg Ser Glu Ala Val Glu Arg Leu Ser Val ~ Thr Lys Ala Met
 305 310 315 320

Figure 1. Schematic representation of the experimental design. The subjects were divided into two groups: a control group and an experimental group. The control group received a standard training program, while the experimental group received a modified training program. The results of the training program were compared between the two groups.

<211> 116

<213> Homo sapiens

[illegible]

<211> 171

<213> Homo sapiens

396

Gln Leu Leu Gln Gly Glu Arg Asn Pro Arg Leu Glu Asp Ala Ile Arg
 100 105 110
 Thr Asp Leu Asn Arg Thr Phe Pro Asp Asn Val Lys Phe Arg Lys Thr
 115 120 125
 Thr Asp Pro Cys Leu Gln Arg Thr Leu Tyr Asn Val Leu Leu Ala Tyr
 130 135 140
 Gly His His Asn Gln Gly Val Gly Tyr Cys Gln Gly Met Asn Phe Ile
 145 150 155 160
 Ala Gly Tyr Leu Ile Leu Ile Thr Asn Asn Glu
 165 170

<210> 482

<211> 177

<212> PRT

<213> Homo sapiens

<400> 482

Met Gln Pro Ala Glu Arg Ser Arg Val Pro Arg Ile Asp Pro Tyr Gly
 1 5 10 15
 Phe Glu Arg Pro Glu Asp Phe Asp Asp Ala Ala Tyr Glu Lys Phe Phe
 20 25 30
 Ser Ser Tyr Leu Val Thr Leu Thr Arg Arg Ala Ile Lys Trp Ser Arg
 35 40 45
 Leu Leu Gln Gly Gly Gly Val Pro Arg Ser Arg Thr Val Lys Arg Tyr
 50 55 60
 Val Arg Lys Gly Val Pro Leu Glu His Arg Ala Arg Val Trp Met Val
 65 70 75 80
 Leu Ser Gly Ala Gln Ala Gln Met Asp Gln Asn Pro Gly Tyr Tyr His
 85 90 95
 Gln Leu Leu Gln Gly Glu Arg Asn Pro Arg Leu Glu Asp Ala Ile Arg
 100 105 110
 Thr Asp Leu Asn Arg Thr Phe Pro Asp Asn Val Lys Phe Arg Lys Thr
 115 120 125
 Thr Asp Pro Cys Leu Gln Arg Thr Leu Tyr Asn Val Leu Leu Ala Tyr
 130 135 140
 Gly His His Asn Gln Gly Val Gly Tyr Cys Gln Gly Met Asn Phe Ile
 145 150 155 160
 Ala Gly Tyr Leu Ile Leu Ile Thr Asn Asn Asp Lys Asn Leu Phe Gly
 165 170 175

Cys